

Publication No. US20030049619A1
GENERAL INFORMATION:

APPLICANT: Delagrave, Simon
APPLICANT: Marrs, Barry
TITLE OF INVENTION: Methods For The Synthesis Of Polynucleotides And Combinatorial Libraries
FILE REFERENCE: HER0041
CURRENT APPLICATION NUMBER: US/09/813,408
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 85
SOFTWARE: PatentIn version 3.0
SEQ ID NO 27
LENGTH: 440
TYPE: PRT
ORGANISM: Aeropyrum pernix
US-09-813-408-27

Query Match 64.8%; Score 35; DB 9; Length 440;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EVVPGXGMDY 10
II:II:II:II

Db 120 EVLPWGVDY 128

RESULT 7

US-09-815-242-5111
Sequence 5111, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5111
LENGTH: 1062
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-815-242-5111

Query Match 63.0%; Score 34; DB 10; Length 1062;
Best Local Similarity 85.7%; Pred. No. 2,4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PXGMDYS 11
II:II:II:II

Db 321 PQGMDYS 327

RESULT 8

US-10-027-806-4
Sequence 4, Application US/10027806
Patent No. US20020160476A1
GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCRP.002A
CURRENT APPLICATION NUMBER: US/10/027,806
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 3472
TYPE: PRT
ORGANISM: Cenarchaeum symbiosum
US-10-027-806-4

Query Match 63.0%; Score 34; DB 9; Length 3472;
Best Local Similarity 45.5%; Pred. No. 9.1e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
I:II:II:II

Db 2294 EDVIPRGISFS 2304

RESULT 9

US-10-034-623-4
Sequence 4, Application US/10034623
Publication No. US20020198365A1
GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.
APPLICANT: Schleper, Christa
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
FILE REFERENCE: DCRP.002A
CURRENT APPLICATION NUMBER: US/10/034,623
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/408,020
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 60/102,294
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 4
LENGTH: 3472
TYPE: PRT
ORGANISM: Cenarchaeum symbiosum
US-10-034-623-4

Query Match 63.0%; Score 34; DB 9; Length 3472;
Best Local Similarity 45.5%; Pred. No. 9.1e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
I:II:II:II

Db 2294 EDVIPRGISFS 2304

RESULT 10

US-10-027-801-4
Sequence 4, Application US/10027801
Publication No. US20030054364A1
GENERAL INFORMATION:
APPLICANT: Swanson, Ronald V.
APPLICANT: Feldman, Robert A.

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; APPLICANT: Schleper, Christa
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCRP.002A
; CURRENT APPLICATION NUMBER: US/10/027,801
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3472
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-801-4

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Query Match      63.0%; Score 34; DB 9; Length 3472;
Best Local Similarity 45.5%; Pred. No. 9.1e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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QY 1 EEVVPXGMDYS 11
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Db 2294 EDVIPRGISF 2304

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RESULT 11
US-09-948-080-14
; Sequence 14, Application US/09948080
; Patent No. US20020102702A1
; GENERAL INFORMATION:
; APPLICANT: VAN DER OSTEN, CLAUS
; APPLICANT: HALKIER, TORDEN
; APPLICANT: ANDERSEN, CARSTEN
; APPLICANT: BAUDITZ, PETER
; APPLICANT: HANSEN, PETER KAMP
; TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
; FILE REFERENCE: 4946,200-US
; CURRENT APPLICATION NUMBER: US/09/948,080
; CURRENT FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: 2001-09-06
; PRIOR FILING DATE: 1997-11-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-948-080-14

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Query Match      61.1%; Score 33; DB 10; Length 59;
Best Local Similarity 45.5%; Pred. No. 15;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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QY 1 EEVVPXGMDYS 11
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Db 38 EXHIPGLEYS 48

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RESULT 12
US-09-738-626-4881
; Sequence 4881, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

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; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4881
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4881

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Query Match      61.1%; Score 33; DB 9; Length 283;
Best Local Similarity 75.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 4 VPXGMDYS 11
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Db 56 VPAGADYS 63

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RESULT 13
US-09-815-242-10697
; Sequence 10697, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10697
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10697

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Query Match      61.1%; Score 33; DB 10; Length 299;
Best Local Similarity 40.0%; Pred. No. 94;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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QY 1 EEVVPXGMDY 10
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Db 218 EQITPTGIEY 227

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RESULT 14

US-09-978-295A-526
 ; Sequence 526, Application US/09978295A
 ; Patent No. US20020156006A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David.
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Hurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C11
 ; CURRENT APPLICATION NUMBER: US/09/978,295A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/064249
 ; PRIOR FILING DATE: 1997-11-03
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
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 ; PRIOR APPLICATION NUMBER: 60/079294
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 ; PRIOR APPLICATION NUMBER: 60/083495

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; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-04-29
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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
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; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
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; PRIOR FILING DATE: 1998-05-13
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
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; PRIOR FILING DATE: 1998-05-15
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

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Query Match 61.1% Score 33; DB 9; Length 736;
 Best Local Similarity 70.0%; Pred. No. 2.6e+02;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 EEVVPXGMDY 10
Db 331 EPVVYVGYMDY 340

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RESULT 15

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; US-09-978-697-526
; Sequence 526, Application US/09978697
; Patent No. US2002016284A1
; GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630PIC27
; CURRENT APPLICATION NUMBER: US/09/978.697
; CURRENT FILING DATE: 2001-10-16
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
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us-09-909-164-13.rapb

;; PRIOR FILING DATE: 1998-03-27
;; PRIOR APPLICATION NUMBER: 60/079786
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;; PRIOR APPLICATION NUMBER: 60/081819
;; PRIOR FILING DATE: 1998-04-15
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;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 61.1%; Score 33; DB 9; Length 736;
Best Local Similarity 70.0%; Pred. NO. 2.6e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
DB 331 EPVVYVGYMDY 340

RESULT 16
US-09-978-192A-526
; Sequence 526, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PIC9
CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
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;; PRIOR FILING DATE: 1998-04-29
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;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 61.1%; Score 33; DB 9; Length 736;
Best Local Similarity 70.0%; Pred. NO. 2.6e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
Db 331 EPVVVYGM DY 340

RESULT 17
US-09-999-832A-526
; Sequence 526, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
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; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
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;; APPLICANT: Kljavin, Ivar J.
;; APPLICANT: Kuo, Sophia S.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James;
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Shelton, David L.
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2630PLC63
;; CURRENT FILING DATE: 2001-10-24
;; PRIOR APPLICATION NUMBER: 09/918585
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; PRIOR APPLICATION NUMBER: 60/085697

Query Match 61.1% Score 33; DB 9; Length 736;
Best Local Similarity 70.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
| | | | |
Db 331 EPVVVYGM DY 340

RESULT 18

US-09-978-189-526
; Sequence 526, Application US/09978189
; Publication No. US20030004102A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napler, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.

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APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT FILING DATE: 2001-10-15
CURRENT APPLICATION NUMBER: US/09/978,189
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/080194
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080327
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080328
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080333
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/080334
PRIOR FILING DATE: 1998-04-01
PRIOR APPLICATION NUMBER: 60/081070
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081049
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081071
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081195
PRIOR FILING DATE: 1998-04-08
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081817
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081819
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082569
PRIOR FILING DATE: 1998-04-21
PRIOR APPLICATION NUMBER: 60/082704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082700
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
PRIOR APPLICATION NUMBER: 60/083336
PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083496
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083499
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083554
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083558
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083559
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083500
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084640

;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084598
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084600
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084627
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/084643
;; PRIOR FILING DATE: 1998-05-07
;; PRIOR APPLICATION NUMBER: 60/085339
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085338
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085323
;; PRIOR FILING DATE: 1998-05-13
;; PRIOR APPLICATION NUMBER: 60/085582
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085700
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085689
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085579
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085580
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085573
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085704
;; PRIOR FILING DATE: 1998-05-15
;; PRIOR APPLICATION NUMBER: 60/085697

Query Match 61.1%; Score 33; DB 9; Length 736;
Best Local Similarity 70.0%; Pred. No. 2.6e+02;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
Db 331 EPVVYGYMDY 340

RESULT 19

US-10-174-590-420
; Sequence 420, Application US/10174590
; Publication No. US20030008352A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430R1C42

; CURRENT APPLICATION NUMBER: US/10/174,590

; PRIOR APPLICATION REMOVED - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 420

; LENGTH: 736

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-174-590-420

Query Match

Best Local Similarity 61.1%; Score 33; DB 9; Length 736;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
Db 331 EPVVYGYMDY 340

RESULT 20

US-10-176-758-420

; Sequence 420, Application US/10176758

; Publication No. US20030008353A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430R1C104

; CURRENT APPLICATION NUMBER: US/10/176,758

; PRIOR APPLICATION REMOVED - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 420

; LENGTH: 736

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-176-758-420

Query Match

Best Local Similarity 61.1%; Score 33; DB 9; Length 736;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
Db 331 EPVVYGYMDY 340

RESULT 21

US-10-175-737-420

; Sequence 420, Application US/10175737

; Publication No. US20030013153A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3430R1C50

; CURRENT APPLICATION NUMBER: US/10/175,737

; PRIOR APPLICATION REMOVED - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 420

; LENGTH: 736

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-175-737-420

Query Match

Best Local Similarity 61.1%; Score 33; DB 9; Length 736;

Best Local Similarity 70.0%; Pred. No. 2.6e+02; DB 9; Length 736;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGMDY 10
| | | | |
Db 331 EPVVYGM DY 340

RESULT 22
US-10-173-706-420
; Sequence 420, Application US/10173706
; Publication No. US2003002293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173,706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-706-420

Query Match 61.1%; Score 33; DB 9; Length 736;
Best Local Similarity 70.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGMDY 10
| | | | |
Db 331 EPVVYGM DY 340

RESULT 23
US-10-175-738-420
; Sequence 420, Application US/10175738
; Publication No. US2003002294A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C45
; CURRENT APPLICATION NUMBER: US/10/175,738
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo Sapien

US-10-175-738-420

Query Match 61.1%; Score 33; DB 9; Length 736;
Best Local Similarity 70.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGMDY 10
| | | | |
Db 331 EPVVYGM DY 340

RESULT 24
US-10-175-752-420
; Sequence 420, Application US/10175752
; Publication No. US2003002295A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C60
; CURRENT APPLICATION NUMBER: US/10/175,752
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-752-420

Query Match 61.1%; Score 33; DB 9; Length 736;
Best Local Similarity 70.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGMDY 10
| | | | |
Db 331 EPVVYGM DY 340

RESULT 25
US-10-176-482-420
; Sequence 420, Application US/10176482
; Publication No. US2003002296A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C70
; CURRENT APPLICATION NUMBER: US/10/176,482
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420

; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-482-420

Query Match 61.1%; Score 33; DB 9; Length 736;
Best Local Similarity 70.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
| | | | |
Db 331 EPVVVYGMDY 340

Search completed: June 10, 2003, 14:35:44
Job time : 16.0714 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:31:15 ; Search time 11.2143 Seconds
(without alignments)
94.297 Million cell updates/sec

Title: US-09-909-164-13
Perfect score: 54
Sequence: 1 EFWVPXGMDYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_73:*

1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	74.1	156	S54619	hypothetical prote
2	38	70.4	363	D69551	conserved hypothet
3	36	66.7	102	A42452	V1 protein - tobac
4	36	66.7	341	S72649	sucrose-phosphate
5	36	66.7	348	S72650	sucrose-phosphate
6	36	66.7	460	G96764	unknown protein F2
7	36	66.7	1049	J04783	sucrose-phosphate
8	36	66.7	1068	J01329	sucrose-phosphate
9	36	66.7	1081	T09837	sucrose-phosphate
10	36	66.7	1083	T04062	sucrose-phosphate
11	36	66.7	1084	T04103	sucrose-phosphate
12	35	64.8	425	T24111	hypothetical prote
13	35	64.8	433	H87660	peptidoglycan-bind
14	35	64.8	440	H2784	probable alkaline
15	35	64.8	1150	T20173	hypothetical prote
16	35	64.8	1474	F69009	probable membrane
17	35	64.8	2747	B49132	fat facets (faf) s
18	34	63.0	99	S00210	plastocyanin b - L
19	34	63.0	155	S38255	plastocyanin precu
20	34	63.0	168	S38208	plastocyanin b pre
21	34	63.0	290	D98182	O6-methylguanidine-D
22	34	63.0	290	AG3104	6-O-methylguanine-
23	34	63.0	296	F72745	hypothetical prote
24	34	63.0	357	G69290	probable hexosyltr
25	34	63.0	366	G69350	L-lactate dehydrog
26	34	63.0	565	E86665	ABC transporter AT
27	34	63.0	566	A70164	phenylalanine-trna
28	34	63.0	587	F81138	succinate dehydrog
29	34	63.0	906	T48898	disease resistance

30	34	63.0	908	2	T48899	disease resistance
31	34	63.0	1062	2	F83335	RND multidrug effl
32	34	63.0	1062	2	T30830	hypothetical prote
33	34	63.0	3472	2	T31308	hypothetical 367K
34	33	61.1	97	2	A99427	partial transposas
35	33	61.1	128	2	A90471	hypothetical prote
36	33	61.1	172	2	S27021	fibroblast growth
37	33	61.1	184	2	E90335	hypothetical prote
38	33	61.1	225	2	S57810	hypothetical prote
39	33	61.1	247	2	A96001	conserved hypothet
40	33	61.1	257	2	A95546	unknown protein [i
41	33	61.1	262	2	F90298	transposase ISC105
42	33	61.1	267	2	C90307	transposase ISC105
43	33	61.1	276	2	C64417	hypothetical prote
44	33	61.1	283	2	G83055	pantoate-beta-alan
45	33	61.1	299	2	E90487	transposase ISC105
46	33	61.1	299	2	H90352	transposase ISC105
47	33	61.1	307	2	F84330	hypothetical prote
48	33	61.1	394	2	F82491	ferrisiderophore r
49	33	61.1	421	1	DETCM	acyl-CoA dehydroge
50	33	61.1	670	2	S22293	zinc finger protei
51	33	61.1	797	2	S38579	fibroblast growth
52	33	61.1	800	1	TVH02F	fibroblast growth
53	33	61.1	801	2	I55363	heparin-binding gr
54	33	61.1	801	2	I55363	fibroblast growth
55	33	61.1	806	2	A35963	protein-tyrosine k
56	33	61.1	840	2	AG0526	penicillin-binding
57	33	61.1	840	2	T39116	probable sulfate p
58	33	61.1	846	2	S57580	penicillin-binding
59	33	61.1	877	2	T40413	sulfate permease -
60	33	61.1	982	1	VCLJLK	env polyprotein -
61	33	61.1	1064	2	F86182	hypothetical prote
62	33	61.1	1401	2	G82336	DNA-directed RNA p
63	33	61.1	2717	2	A34203	DNA-binding protei
64	33	61.1	2831	2	T31419	cyclic beta 1-2 gl
65	33	61.1	2867	2	AG3481	cellobiose-phospho
66	32.5	60.2	472	1	B53236	transcription fact
67	32	59.3	97	2	JW0011	plastocyanin - car
68	32	59.3	165	2	AG1272	thiol peroxidases
69	32	59.3	165	2	AH1635	thiol peroxidases
70	32	59.3	175	2	S36749	transcription fact
71	32	59.3	180	2	AG0504	fimbrial chain fim
72	32	59.3	231	1	I5ECB4	L-ribulose-phospha
73	32	59.3	231	1	A90637	L-ribulose-5-phosp
74	32	59.3	231	2	A85488	L-ribulose-5-phosp
75	32	59.3	231	2	AB0515	L-ribulose-5-phosp

ALIGNMENTS

RESULT 1

S54619
Hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein O2612; hypothetical protein YOL303.3
C;Species: Saccharomyces cerevisiae
C;Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C;Accession: S54619; S66879
R;de Haan, M.; Maarse, A.C.; Grivell, L.A.
submitted to the EMBL Data Library, May 1995
A;Reference number: S54617
A;Accession: S54619
A;Molecule type: DNA
A;Residues: 1-156 <DEH>
A;Cross-references: EMBL:X87331; NID:q1041652; PIDN:CAA60762.1; PID:q829123
R;de Haan, M.; Grivell, L.A.; Maarse, A.C.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66877
A;Accession: S66879
A;Molecule type: DNA
A;Residues: 1-156 <DEW>
A;Cross-references: EMBL:Z74920; NID:q1420109; PIDN:CAA99201.1; PID:q1420111; MIPS
A;Experimental source: strain S288C

C:Genetics:
A:Cross-references: SGD:S0005539
A:Map position: 15R
C:Superfamily: hypothetical protein YOR013w

Query Match 74.1%; Score 40; DB 2; Length 156;
Best Local Similarity 77.8%; Pred. No. 1;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EVVPXGMDY 10
||| ||||
DB 50 EVMPGLGMDY 58

RESULT 2

D69551
conserved hypothetical protein AF2411 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: D69551
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glocke, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Ventet, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: D69551
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-363 <KLE>
A:Cross-references: GB:AE001109; GB:AE000782; NID:g2689432; PIDN:AA891255.1; PID:g265068

Query Match 70.4%; Score 38; DB 2; Length 363;
Best Local Similarity 54.5%; Pred. No. 6.8;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
|:|:|:|:|:|
DB 120 ENIVPYGIDFS 130

RESULT 3

A42452
V1 protein - tobacco yellow dwarf virus (strain Australia)
C:Species: tobacco yellow dwarf virus
C>Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C:Accession: A42452
R:Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Virology 187, 633-642, 1992
A:Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yell
A:Reference number: A42452; MUID:92188538; PMID:1546458
A:Accession: A42452
A:Molecule type: DNA
A:Residues: 1-102 <MOR>
A:Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284

Query Match 66.7%; Score 36; DB 2; Length 102;
Best Local Similarity 60.0%; Pred. No. 4.2;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EVVPXGMDYS 11
||| |:
DB 7 QVVPISGINS 16

RESULT 4

S72649
sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Citrus unshiu (fragment)
C:Species: Citrus unshiu
C>Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C:Accession: S72649

R:Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
Mol. Gen. Genet. 252, 346-351, 1996
A:Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate
A:Reference number: S72648; MUID:96439842; PMID:8842155
A:Accession: S72649
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-341 <KOM>
A:Cross-references: EMBL:AB006319; NID:g2588891; PIDN:BAA23215.1; PID:g2588892
A:Experimental source: fruit, cv. Miyagawa-Wase
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1999
C:Genetics:
A:Gene: SPS2
C:Function:
A:Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fr
A:Pathway: sucrose biosynthesis
C:Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homo
C:Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F:1-341/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>

Query Match 66.7%; Score 36; DB 2; Length 341;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
|:|:|:|:|
DB 228 VIPPGMDFS 236

RESULT 5

S72650
sucrose-phosphate synthase (EC 2.4.1.14) isoform 3 - Citrus unshiu (fragment)
C:Species: Citrus unshiu
C>Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
C:Accession: S72650
R:Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
Mol. Gen. Genet. 252, 346-351, 1996
A:Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate
A:Reference number: S72648; MUID:96439842; PMID:8842155
A:Accession: S72650
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-348 <KOM>
A:Cross-references: EMBL:AB006660; NID:g2351059; PIDN:BAA22071.1; PID:g2351060
A:Experimental source: fruit, cv. Miyagawa-Wase
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
C:Genetics:
A:Gene: SPS3
C:Function:
A:Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fr
A:Pathway: sucrose biosynthesis
C:Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homo
C:Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F:1-348/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>

Query Match 66.7%; Score 36; DB 2; Length 348;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
|:|:|:|:|
DB 234 VIPPGMDFS 242

RESULT 6

G96764
unknown protein F25P22.17 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G96764
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Al
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar
ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: G96764
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-460 <STO>
A:Cross-references: GB:AE005173; NID:g6692750; PIDN:AAF24856.1; GSPDB:GN00141
C:Genetics:
A:Gene: F25P22.17
A:Map position: 1

Query Match 66.7%; Score 36; DB 2; Length 460;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 BEVVPXGMDY 10
DB 218 EEDVPSAMDY 227

RESULT 7
JC4783
sucrose-phosphate synthase (EC 2.4.1.14) - rice
C:Species: Oryza sativa (rice)
C:Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 18-Jun-1999
C:Accession: JC4783
R:Valdez-Alarcon, J.J.; Ferrando, M.; Salerno, G.; Jimenez-Morilla, B.; Herrera-Estrella
Gene 170, 217-222, 1996
A:Title: Characterization of a rice sucrose-phosphate synthase-encoding gene.
A:Reference number: JC4783; MUID:96235138; PMID:8666248
A:Accession: JC4783
A:Molecule type: mRNA
A:Residues: 1-1049 <VAL>
A:Cross-references: GB:U33175; NID:g1449931; PIDN:RAC49379.1; PID:g988270
A:Note: UDPglucose-fructose-phosphate glucosyltransferase; Sucrosephosphate-UDPglucosylt
C:Comment: This enzyme catalyzes the formation of sucrose-phosphate form UDP-glucose and
C:Genetics:
A:Gene: Sps1
A:Introns: 24/1; 103/3; 183/3; 205/3; 435/3; 475/3; 519/3; 578/3; 596/3; 617/3; 931/3; 9
C:Function:
A:Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc
A:Pathway: sucrose biosynthesis
A:Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C:Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F:180-663/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match 66.7%; Score 36; DB 2; Length 1049;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
DB 436 VIPPGMDFS 444

RESULT 8
JQ1329
sucrose-phosphate synthase (EC 2.4.1.14) - maize
C:Species: Zea mays (maize)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JQ1329; PQ0260
R:Worrell, A.C.; Bruneau, J.M.; Summerfelt, K.; Boersig, M.; Voelker, T.A.
Plant Cell 3, 1121-1130, 1991
A:Title: Expression of a maize sucrose phosphate synthase in tomato alters leaf carbohyd
A:Reference number: JQ1329; MUID:92338837; PMID:1840396
A:Accession: JQ1329
A:Molecule type: mRNA

A:Residues: 1-1068 <WOR>
A:Cross-references: GB:M97550; NID:g168625; PIDN:AAA33513.1; PID:g168626
A:Accession: PQ0260
A:Molecule type: protein
A:Residues: 71-74; 206-212; 471-481; 872-892 <WOR1>
C:Comment: This enzyme transfers the glucosyl group from UDPglucose to fructose-6-ph
C:Comment: This enzyme is involved in the regulation of carbon partitioning in the l
C:Function:
A:Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D
A:Pathway: sucrose biosynthesis
A:Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homol
C:Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F:178-666/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match 66.7%; Score 36; DB 1; Length 1068;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
DB 435 VIPPGMDFS 443

RESULT 9
T09837
sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Craterostigma plantagineum
C:Species: Craterostigma plantagineum
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T09837
R:Ingram, J.; Chandler, J.W.; Gallagher, L.; Salamini, F.; Bartels, D.
Plant Physiol. 115, 113-121, 1997
A:Title: Analysis of cDNA clones encoding sucrose-phosphate synthase in relation to
A:Reference number: T16874; MUID:97451773; PMID:9306694
A:Accession: T09837
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1081 <INC>
A:Cross-references: EMBL:Y11795; NID:g2190349; PIDN:CAA72491.1; PID:g2190350
A:Experimental source: EMBL:ABA-treated callus
C:Genetics:
A:Gene: sps2
C:Function:
A:Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and l
A:Pathway: sucrose biosynthesis
A:Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homol
C:Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F:176-674/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match 66.7%; Score 36; DB 2; Length 1081;
Best Local Similarity 66.7%; Pred. No. 60;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
DB 445 VIPPGMDFS 453

RESULT 10
T04062
sucrose-phosphate synthase homolog F28M11.40 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 16-Jul-1999
C:Accession: T04062
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer,
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z15184
A:Accession: T04062
A:Molecule type: DNA
A:Residues: 1-1083 <BEV>
A:Cross-references: EMBL:AL049487
A:Experimental source: cultivar Columbia; BAC clone F28M11
C:Genetics:
A:Map position: 4

A: Introns: 86/3; 116/3; 255/3; 322/2; 482/3; 526/3; 570/3; 629/3; 647/3; 668/3; 949/3; 9
A: Note: F28M11.40
C: Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
F: 230-714/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match
Best Local Similarity 66.7%; Score 36; DB 2; Length 1083;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
I: I I I I I

Db 483 VIPPGMDFS 491

RESULT 11
T04103
sucrose-phosphate synthase (EC 2.4.1.14) 1 - rice
C: Species: Oryza sativa (rice)
C: Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C: Accession: T04103
R: Sakamoto, M.; Satozawa, T.; Kishimoto, N.; Higo, K.; Shimada, H.; Fujimura, T.
Plant Sci. 112, 207-217, 1995
A: Title: Structure and RFLP mapping of a rice sucrose phosphate synthase (SPS) gene that
A: Reference number: Z15212
A: Accession: T04103
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-1084 <SAK>
A: Cross-references: EMBL:D45890; PIDN: BAA08304.1
A: Experimental source: subsp. Japonica
C: Genetics:
A: Gene: Sps1
A: Map position: 1
A: Introns: 120/3; 200/2; 221/3; 452/3; 492/3; 536/3; 595/3; 613/3; 634/3; 946/3; 989/2
C: Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C: Keywords: glycosyltransferase; hexosyltransferase
F: 196-680/Domain: sucrose/sucrose-phosphate synthase homology <SSPS>

Query Match
Best Local Similarity 66.7%; Score 36; DB 2; Length 1084;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
I: I I I I I

Db 453 VIPPGMDFS 461

RESULT 12
T24111
hypothetical protein R10D12.10 - Caenorhabditis elegans
C: Species: Caenorhabditis elegans
C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C: Accession: T24111
R: Percy, C.
submitted to the EMBL Data Library, October 1996
A: Reference number: Z19842
A: Accession: T24111
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-425 <WIL>
A: Cross-references: EMBL:Z81109; PIDN: CAB03241.1; GSPDB: GN00023; CESP: R10D12.10
A: Experimental source: clone R10D12
C: Genetics:
A: Gene: CESP:R10D12.10
A: Map position: 5
A: Introns: 23/3; 56/3; 113/3; 257/2

Query Match
Best Local Similarity 64.8%; Score 35; DB 2; Length 425;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
I: I I I I I

Db 335 EQIVPGLQY 344

RESULT 13

H87660

peptidoglycan-binding protein, probable [Imported] - Caulobacter crescentus
C: Species: Caulobacter crescentus
C: Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C: Accession: H87660

R: Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.;
O. J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Shapero, J.C.; Fraser,
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A: Title: Complete genome sequence of *Caulobacter crescentus*.

A: Reference number: A87249; MUID: 21173698; PMID: 11259647

A: Accession: H87660

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-433 <STO>

A: Cross-references: GB:AE005673; NID: gl3425020; PIDN: AAK25284.1; GSPDB: GN00148

C: Genetics:

A: Gene: CC3322

Query Match

Best Local Similarity 64.8%; Score 35; DB 2; Length 433;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11

I: I I I I I

Db 266 EVILPPGFDYS 276

RESULT 14

H72784

probable alkaline proteinase APE0263 - *Aeropyrum pernix* (strain K1)

C: Species: *Aeropyrum pernix*

C: Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C: Accession: H72784

R: Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.;
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.

DNA Res. 6, 83-101, 1999

A: Title: Complete genome sequence of an aerobic hyper-thermophilic *Crenarchaeon*, *Aer*

A: Reference number: A72450; MUID: 99310339; PMID: 10382966

A: Accession: H72784

A: Status: preliminary

A: Molecule type: DNA

A: Residues: 1-440 <KAW>

A: Cross-references: DDBJ: AP000058; NID: g5103388; PIDN: BAA79178.1; PID: g5103657

A: Experimental source: strain K1

C: Genetics:

A: Gene: APE0263

C: Superfamily: subtilisin; subtilisin homology

Query Match

Best Local Similarity 64.8%; Score 35; DB 2; Length 440;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EVVPXGMDY 10

I: I I I I I

Db 120 EVLPWGVY 128

RESULT 15

T20173

hypothetical protein C53A5.2 - *Caenorhabditis elegans*

C: Species: *Caenorhabditis elegans*

C: Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C: Accession: T20173; T23857

R: Mortimore, B.

submitted to the EMBL Data Library, November 1996

A: Reference number: Z19232

A: Accession: T20173

A: Status: preliminary; translated from GB/EMBL/DBJ

A;Cross-references: GB:I04959; NID:g157411; PIDN:AAF01345.1; PID:g6013474
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:127836, NCBIN:129008, NCBIP:129008)
A;Accession: A49132
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-2704, 'VR', 2707, 'ANNU', '<T>
A;Cross-references: GB:I04958; NID:g157410; PIDN:AAF01346.1; PID:g6013475
A;Note: sequence extracted from NCBI backbone (NCBIN:127936, NCBIN:129008, NCBIP:129008)
C;Keywords: alternative splicing

```

Query Match      64.8%; Score 35; DB 2; Length 2747;
Best Local Similarity 54.5%; Pred: No; 2.7e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 EEVVPXGMDYS ll
        | : | | | : |
Db      1394 EVIVPDGDQDFS 1404

```

RESULT 18

plastocyanin b - Lombardy poplar
C.Species: Populus nigra var. italica (Lombardy poplar)
C.Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 20-Apr-2000
C.Accession: S00210

FEBS Lett. 226, 17-22, 1987

A:Reference number: S00210
A:Accession: S00210
A:Molecule type: Protein
A:Residues: 1-99 <DM>
C:Superfamily: plastocyanin
C:Keywords: chloroplast; copper; electron transfer; metalloprotein
F:37,84,87,92/Binding site: copper (His, Cys, His, Met) (type 1) #status predicted

Query Match	63.0%	Score 34;	DB 2;	Length 99;
Best Local Similarity	54.5%	Pred. No. 11;		
		2. Matches	3. Indels	0: Gaps 0:

[illegible]

Db 43 EDVPSGYDVS 53

RESULT 19
S38255
electronic precursor - barlev

C:Species: Hordeum vulgare (barley)
C:Date: 13-Jan-1995 #sequence_revision
C:Accession: S38255; S00206

Eur. J. Biochem. 217, 97-104, 1993
A; Title: In vitro binding of nuclear proteins to the barley plastocyanin gene promoter
A; Reference number: S38255; MUID:94039081; PMID:8223592

A;Residues: 1-155 <NTEI>
A;Cross-references: EMBL:Z28347; NID:g431919; PIDN:CAA82201.1; PID:g431920
A;Experimental source: strain NK 1558
R;Nielsen, P.S.; Gausing, K.
FEBS Lett. 225, 159-162, 1987
A;Title: The precursor of barley plastocyanin: sequence of cDNA clones and gene expression
A;Reference number: S00206
A;Accession: S00206
A;Status: not compared with conceptual translation
A;Molecule type: mRNA

A:Residues: 1-119, 121-135 <NLE2>
A:Cross-references: EMBL:Y00704; NID:g22704
A:Note: not compared to nucleotide translation
C:Genetics:
A:Genome: nuclear

C;Function:
A;Description: mediates the transfer of electrons from cytochrome b6/f to photosystem I
C;Superfamily: plastocyanin
C;Keywords: chloroplast; copper; electron transfer; metalloprotein
F;1-58/Domain: transit peptide (chloroplast) #status predicted <TNP>
F;59-155/Product: plastocyanin #status predicted <MAT>
F;95,140,143,148/Binding site: copper (His, Cys, His, Met) (type 1) #status predicted

Query Match 63.0%; Score 34; DB 2; Length 155;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
: : : : :
Db 101 EDAPVSGVDVS 111

RESULT 20
S38208
plastocyanin b precursor - black poplar
C;Species: Populus nigra (black poplar)
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-May-2000
C;Accession: S58208
R;Reichert, J.; Jenzewski, V.; Haehnel, W.
submitted to the EMBL Data Library, July 1995
A;Description: Kinetic studies of recombinant poplar plastocyanins.
A;Reference number: S58208
A;Accession: S58208
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-168 <REI>
C;Cross-references: EMBL:Z50186; NID:g929814; PIDN:CAA90565.1; PID:g929815
C;Superfamily: plastocyanin
C;Keywords: copper; electron transfer; metalloprotein
F;106,153,156,161/Binding site: copper (His, Cys, His, Met) (type 1) #status predicted

Query Match 63.0%; Score 34; DB 2; Length 168;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
: : : : :
Db 112 EDAPVSGVDVS 122

RESULT 21
D98182
O6-methylguanine-DNA methyltransferase PA2118 [imported] - Agrobacterium tumefaciens (st
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C;Accession: D98182
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; PMID:11743194
A;Accession: D98182
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-290 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK88982.1; PID:gl5158766; GSPDB:GN00170
C;Genetics:
A;Gene: AGR_L_818
A;Map position: linear chromosome

Query Match 63.0%; Score 34; DB 2; Length 290;
Best Local Similarity 50.0%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
: : : : :
Db 9 EDITPIGSDY 18

RESULT 22

AG3104

6-O-methylguanine-DNA methyltransferase [imported] - Agrobacterium tumefaciens (str
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AG3104
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; W
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; M
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; PMID:11743193
A;Accession: AG3104
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-290 <KUR>
A;Cross-references: PIDN:AAI45253.1; PID:gl7742937; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: ada
A;Map position: linear chromosome

Query Match 63.0%; Score 34; DB 2; Length 290;

Best Local Similarity 50.0%; Pred. No. 35;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10

: : : : :

Db 9 EDITPIGSDY 18

RESULT 23

F72745

hypothetical protein APE0493 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000
C;Accession: F72745
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.;
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki,
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aer
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: F72745
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-296 <KAW>
A;Cross-references: DDBJ:AP0000059; NID:g5103911; PIDN:BAA79458.1; PID:dl043244; PID:
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0493
C;Superfamily: Aeropyrum pernix hypothetical protein APE0493

Query Match 63.0%; Score 34; DB 2; Length 296;

Best Local Similarity 50.0%; Pred. No. 36;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGMDYS 11

: : : : :

Db 3 EFLPGGLDYT 12

RESULT 24

G69290

probable hexosyltransferase (EC 2.4.1.-) AF0327 [similarity] - Archaeoglobus fulgidu
C;Species: Archaeoglobus fulgidus
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C;Accession: G69290
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Do
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness,
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Wed Jun 11 15:42:45 2003

us-09-909-164-13.rpr

Nature 390, 364-370, 1997
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
 A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: G69290

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-357 <KLE>

A:Cross-references: GB:AE001082; GB:AE000782; NID:g2689405; PIDN:AAB90909.1; PID:g265031

C:Superfamily: probable hexosyltransferase ytxN

C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 63.0%; Score 34; DB 1; Length 357;

Best Local Similarity 55.6%; Pred. No. 44;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EVVPXGMDY 10

DB 170 EVIPNGIDF 178

RESULT 25

G69350

L-lactate dehydrogenase, cytochrome-type (l1dd) homolog - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C>Date: 05-Dec-1997 #sequence-revision 05-Dec-1997 #text-change 17-Mar-2000

C:Accession: G69350

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: G69350

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-366 <KLE>

A:Cross-references: GB:AE001049; GB:AE000782; NID:g2689372; PIDN:AAB90435.1; PID:g264980

C:Superfamily: (S)-2-hydroxy-acid oxidase; (S)-2-hydroxy-acid oxidase homology

Query Match

Best Local Similarity 63.0%; Score 34; DB 2; Length 366;

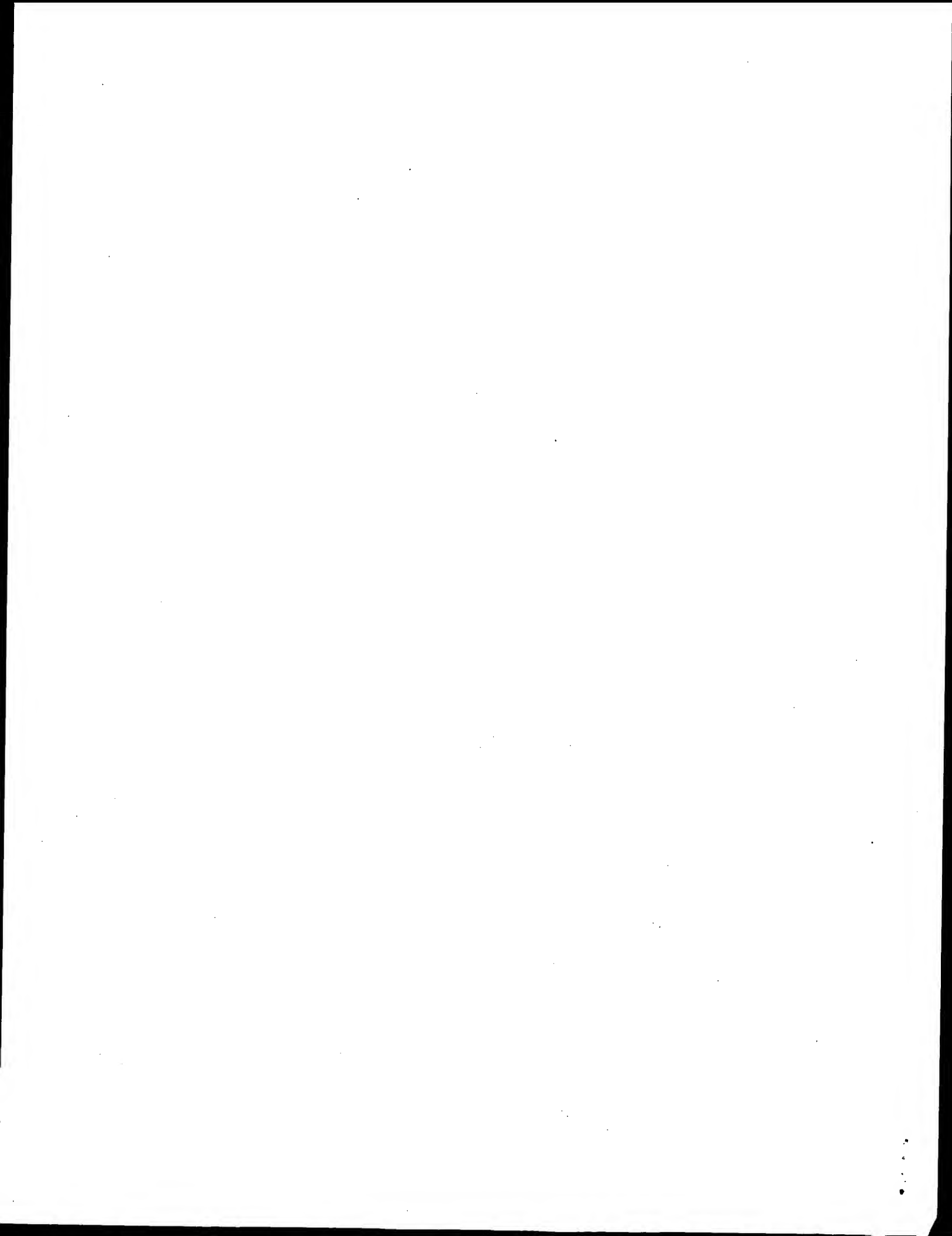
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGMD 9

DB 289 EKVPTGVD 297

Search completed: June 10, 2003, 13:49:15

Job time : 12.2143 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:25:04 ; Search time 4.5 Seconds
(without alignments)
101.387 Million cell updates/sec

Title: US-09-909-164-13
Perfect score: 54
Sequence: 1 EEWVFXGMDYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	38	70.4	1058	1 CARB_FUSNN	Q8rg86 fusbacteri
2	36	66.7	102	1 Y1LK_TYDVA	P31619 tobacco yel
3	36	66.7	1049	1 SPS_ORYSA	Q43802 oryza sativ
4	36	66.7	1068	1 SPS_MAIZE	P31927 zea mays (m
5	36	66.7	1081	1 SPS2_CRAPL	O04933 craterostig
6	35	64.8	2747	1 FAF_DROME	P55824 drosophila
7	34.5	63.9	748	1 KHL1_HUMAN	Q9nr64 homo sapien
8	34	63.0	154	1 PLAS_ORYSA	P20423 oryza sativ
9	34	63.0	155	1 PLAS_HORVU	P08248 hordeum vul
10	34	63.0	168	1 PLAT_POPNI	P11970 populus nig
11	34	63.0	566	1 SYFB_BORBU	P94283 borrelia bu
12	33	61.1	276	1 Y339_METJA	Q58349 methanococc
13	33	61.1	283	1 PANC_PSEAE	Q9nv69 pseudomonas
14	33	61.1	394	1 HMPA_VIBCH	Q9kmy3 vibrio chol
15	33	61.1	421	1 ACDM_RAT	P08503 rattus norv
16	33	61.1	421	1 ECB2_HALEL	O52250 halomonas e
17	33	61.1	423	1 ECB1_HALEL	Q9zeu7 halomonas e
18	33	61.1	787	1 ECB2_HUMAN	O60344 homo sapien
19	33	61.1	801	1 FGR3_MOUSE	Q61851 mus musculu
20	33	61.1	806	1 CRK2_CHICK	P18460 gallus gall
21	33	61.1	877	1 SULH_SCHPO	O74377 schizosacch
22	33	61.1	982	1 ENV_SFV3L	P27399 simian foam
23	33	61.1	1401	1 RPOC_VIBCH	Q9kv29 vibrio chol
24	33	61.1	2717	1 ZEP1_HUMAN	P15922 homo sapien
25	32.5	60.2	472	1 ET2A_XENLA	P20422 daucus caro
26	32	59.3	97	1 PLAS_DAUCA	Q04667 rattus norv
27	32	59.3	175	1 HES3_RAT	P08203 escherichia
28	32	59.3	231	1 ARAD_ECOLI	P06190 salmonella
29	32	59.3	231	1 ARAD_SALTY	Q9wrl1 thermotoga
30	32	59.3	233	1 H1S9_THEMA	Q04827 rattus norv
31	32	59.3	288	1 CGD2_RAT	P30279 homo sapien
32	32	59.3	289	1 CGD2_HUMAN	P30280 mus musculu
33	32	59.3	289	1 CGD2_MOUSE	

34	32	59.3	291	1 CGD1_BRARE	Q90459 brachydanio
35	32	59.3	291	1 CGD1_XENLA	P50755 xenopus lae
36	32	59.3	291	1 CGD2_CHICK	P49706 gallus gall
37	32	59.3	291	1 CGD2_XENLA	P53782 xenopus lae
38	32	59.3	292	1 CGD1_CHICK	P55169 gallus gall
39	32	59.3	292	1 CGD3_HUMAN	P30281 homo sapien
40	32	59.3	295	1 CGD1_HUMAN	P24385 homo sapien
41	32	59.3	295	1 CGD1_MOUSE	P25322 mus musculu
42	32	59.3	295	1 CGD1_RAT	P39948 rattus norv
43	32	59.3	338	1 MTBA_METBA	Q30640 methanosarc
44	32	59.3	372	1 ET2B_XENLA	Q91712 xenopus lae
45	32	59.3	561	1 HNPB_XENLA	Q91910 xenopus lae
46	32	59.3	759	1 SCTL_YEAST	P32784 saccharomyc
47	32	59.3	866	1 RECE_ECOLI	P00292 escherichia
48	32	59.3	995	1 HIP1_HUMAN	O00291 homo sapien
49	32	59.3	1176	1 NIR_NEUCR	P38681 neurospora
50	32	59.3	1258	1 ACN1_MOUSE	O61137 mus musculu
51	32	59.3	1394	1 LTBS_HUMAN	P22054 homo sapien
52	32	59.3	1498	1 Y1A9_CLOAB	Q04351 clostridium
53	32	59.3	1595	1 LTBL_HUMAN	Q14766 homo sapien
54	32	59.3	1712	1 LTBL_RAT	Q00918 rattus norv
55	32	59.3	3174	1 CHAC_HUMAN	Q96r17 homo sapien
56	31	57.4	98	1 PLAS_ENTPR	P07465 enteromorph
57	31	57.4	98	1 PLAS_ULVPE	P13133 ulva arasak
58	31	57.4	98	1 PLAS_TOMOB	P56274 ulva pertus
59	31	57.4	99	1 PLAS_TOBAC	P00298 rumex obtus
60	31	57.4	99	1 REV_SIVCZ	P35476 nicotiana t
61	31	57.4	124	1 HES3_MOUSE	P17280 chimpanzee
62	31	57.4	175	1 YC10_MOUSE	Q61657 mus musculu
63	31	57.4	258	1 YC10_METJA	O58607 methanococc
64	31	57.4	319	1 YHAI_CAPEL	P10941 cryptonectr
65	31	57.4	327	1 YK14_CAPEL	P34338 caenorhabdi
66	31	57.4	338	1 MTBA_METAC	P58869 methanosarc
67	31	57.4	346	1 HYPE_BRAJA	P31906 bradyrhizob
68	31	57.4	391	1 LE11_METTH	Q37667 methanobact
69	31	57.4	427	1 TOLE_HAEIN	P44677 haemophilus
70	31	57.4	469	1 LET1_KLOLA	P53998 kluyveromyc
71	31	57.4	529	1 ENP3_HUMAN	O53355 homo sapien
72	31	57.4	529	1 GUAA_MYCLE	P46810 mycobacteri
73	31	57.4	625	1 GIDA_STAM	Q99qt4 staphylococ
74	31	57.4	692	1 DNK1_SYNV3	Q55154 synechocyst
75	31	57.4	788	1 CY14_NEUCR	P23622 neurospora

ALIGNMENTS

RESULT 1
CARB_FUSNN STANDARD: PRT: 1058 AA.
ID CARB_FUSNN
AC Q8RG86;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
GN CARB OR FN0422.
OS Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterium.
NCBI_TaxID=76856;
[1]
SEQUENCE FROM N.A.
STRAIN=ATCC 25586;
MEDLINE=21886394; PubMed=11889109;
RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykdis A., Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fontaine M., Kyprides N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586."
J. Bacteriol. 184:2005-2018(2002).
CC -1- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +

CC phosphate + L-glutamate + carboxymethyl phosphate.
 CC -1- COFACTOR: Binds three manganese ions (By similarity).
 CC -1- PATHWAY: Arginine biosynthesis.
 CC -1- PATHWAY: Pyrimidine biosynthesis; first step.
 CC -1- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carboxymethyl phosphate. (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE CARB FAMILY.
 CC -----
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 CC -----
 CC EMBL; AE010554; AAL04625.1; ALT_INIT.
 CC InterPro; IPR005483; CPase_L.
 CC InterPro; IPR005479; CPase_L_D2.
 CC InterPro; IPR005480; CPase_L_D3.
 CC InterPro; IPR005481; CPase_L_N.
 CC InterPro; IPR004362; MGS-like.
 CC Pfam; PF00289; CPase_L_chain; 2.
 CC Pfam; PF02786; CPase_L_D2; 2.
 CC Pfam; PF02787; CPase_L_D3; 1.
 CC Pfam; PF02142; MGS; 1.
 CC PRINTS; PR00098; CPASE.
 CC PROSITE; PS00866; CPASE_1; 2.
 CC PROSITE; PS00867; CPASE_2; 2.
 CC Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
 CC ATP-binding; Manganese; Complete proteome.
 CC DOMAIN 1 401 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
 CC DOMAIN 402 546 OLIGOMERIZATION DOMAIN.
 CC DOMAIN 547 929 CARBOXYL PHOSPHATE SYNTHETIC DOMAIN.
 CC DOMAIN 930 1058 ALLOSTERIC DOMAIN.
 CC REPEAT 1 546
 CC REPEAT 547 1058
 CC NP_BIND 153 210
 CC NP_BIND 302 352
 CC METAL 284 284
 CC METAL 298 298
 CC METAL 300 300
 CC METAL 820 820
 CC METAL 832 832
 CC SEQUENCE 1058 AA; 117451 MW; ED/037AF77C1E39F CRC64;
 CC
 CC Query Match 70.4%; Score 38; DB 1; Length 1058;
 CC Best Local Similarity 60.0%; Pred. No. 7.8;
 CC Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC QY 2 EVVPXGMDYS 11
 CC Db 190 EIVPGLNYS 199
 CC
 CC RESULT 2
 CC Y1LK TYDVA
 CC ID Y1LK TYDVA STANDARD; PRT; 102 AA.
 CC AC P31619;
 CC DT 01-JUL-1993 (Rel. 26, Created)
 CC DT 01-JUL-1993 (Rel. 26, Last sequence update)
 CC DT 01-OCT-1993 (Rel. 27, Last annotation update)
 CC DE Hypothetical 11.2 kDa protein.
 CC GN V1.
 CC OS Tobacco yellow dwarf virus (strain Australia) (TYDV).
 CC OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
 CC OX NCBI_TaxID=31599;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=92188538; PubMed=1546458;
 CC RA Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;

RT "The nucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants.";
 RT Virology 187:633-642(1992).
 CC -----
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 CC -----
 CC EMBL; M81103; AAA47947.1; -
 CC PIR; A42452; A42452.
 CC InterPro; IPR002621; Gemini_mov.
 CC Pfam; PF01708; Gemini_mov; 1.
 CC KW Hypothetical protein.
 CC SQ SEQUENCE 102 AA; 11178 MW; A40ECF1E0AF5B67 CRC64;
 CC
 CC Query Match 66.7%; Score 36; DB 1; Length 102;
 CC Best Local Similarity 60.0%; Pred. No. 1.7;
 CC Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC QY 2 EVVPXGMDYS 11
 CC Db 7 QVVPGLNYS 16
 CC
 CC RESULT 3
 CC SPS_ORYSA
 CC ID SPS_ORYSA STANDARD; PRT; 1049 AA.
 CC AC Q43802;
 CC DT 15-DEC-1998 (Rel. 37, Created)
 CC DT 15-DEC-1998 (Rel. 37, Last sequence update)
 CC DT 15-DEC-1998 (Rel. 37, Last annotation update)
 CC DE Sucrose-phosphate synthase (EC 2.4.1.14)
 CC DE (UDP-glucose-fructose-phosphate glucosyltransferase).
 CC OS Oryza sativa (Rice).
 CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 CC OC Ehrhartoideae; Oryzaceae; Oryza.
 CC NCBI_TaxID=4530;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=cv. Indica-IR36; TISSUE=Leaf;
 CC RX MEDLINE=96235138; PubMed=8666248;
 CC RA Valdez-Alarcon J.J., Ferrando M., Jimenez-Moraila B.,
 CC RA Herrera-Estrella L.;
 CC RT "Characterization of a rice sucrose-phosphate synthase-encoding gene".
 CC RL Gene 170:217-222(1996).
 CC -1- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND THEREFORE PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF PHOTOASSIMILATES OUT OF THE LEAF.
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate -> UDP + sucrose 6-phosphate.
 CC -1- ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.
 CC -1- PATHWAY: Sucrose synthesis.
 CC -1- SUBUNIT: HOMODIMER OR HOMOTETRAMER (BY SIMILARITY).
 CC -1- PTM: PHOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR ENZYME FUNCTION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
 CC -----
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 CC -----

DR Pfam; PF00534; Glycos_transf_1; 1.
KW Transferase; Glycosyltransferase; Phosphorylation.
FT DOMAIN 25 31 POLY-GLY.

QY 3 VVPXGMDYS 11
|:| | | |:
Dh 445 VIPPGMDFS 453

Db 445 VIPPGMDES 453

KW	TTA
ET	DOM

QY 3 VVPXGMDYS 11
|:| | | |:
Dh 445 VIPPGMDFS 453

RESULT 6
FAF_DROME
ID FAF_DROME STANDARD; PRT; 2747 AA.
AC P55824;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable ubiquitin C-terminal hydrolase FAF (EC 3.1.2.15)
DE (Ubiquitin thiolesterase FAF) (Ubiquitin-specific protease
FAF) (Deubiquitinating enzyme FAF) (Fat facets protein).
GN FAF.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
ON NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93202020; PubMed=1295747;
RA Fischer-Vize J.A., Rubin G.M., Lehmann R.;
RT "The fat facets gene is required for Drosophila eye and embryo
development.";
RL Development 116:985-1000(1992).
CC -1- FUNCTION: REQUIRED FOR EYE AND EMBRYO DEVELOPMENT, AND PLAYS A
ROLE IN COMPOUND EYE ASSEMBLY AND OCOGENESIS RESPECTIVELY. IN THE
LARVAL EYE DISKS, CELLS OUTSIDE THE ASSEMBLING FACETS REQUIRE THIS
PROTEIN FOR SHORT-RANGE CELL INTERACTIONS THAT PREVENT THE MYSTERY
CELLS FROM BECOMING PHOTORECEPTORS. IT IS ALSO REQUIRED FOR
NUCLEAR MIGRATION AND CELLULARIZATION IN EARLY EMBRYOGENESIS AND
COULD PLAY A ROLE IN POLE CELL DETERMINATION, DEVELOPMENT OR
FUNCTION.
CC -1- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
ubiquitin + a thiol.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: EYE DISKS AND OVARIES.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C19.
CC
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or send an email to license@isb-sib.ch).
CC
CC EMBL; L04959; AAF01345.1; -;
CC EMBL; L04958; AAF01346.1; -;
CC MEROPS; C19.007; -;
CC FlyBase; FBgn0005632; faf.
CC InterPro; IPR001394; UCH-2.
CC Pfam; PF00442; UCH-1; 1.
CC Pfam; PF00443; UCH-2; 1.
CC PROSITE; PS00972; UCH_2_1; 1.
CC PROSITE; PS00973; UCH_2_2; 1.
CC PROSITE; PS50235; UCH_2_3; 1.
CC Ubl conjugation pathway; Hydrolase; Thiol protease;
KW Developmental protein; Vision; Alternative splicing.
FT ACT_SITE 1677 1677 BY SIMILARITY.
FT ACT_SITE 1978 1978 BY SIMILARITY.
FT ACT_SITE 1986 1986 BY SIMILARITY.
FT VARSPIC 2705 2747 KCRVLIKKLVSKDEEDATSAATTAATVTTSPATAS
FT VARIANT 2725 2725 S -> T.
FT ORQQL -> VTRANNV (IN SHORT ISOFORM).
SQ SEQUENCE 2747 AA; 307954 MW; 1D97659F7A7B2ADE CRC64;
Query Match 64.8%; Score 35; DB 1; Length 2747;
Best Local Similarity 54.5%; Pred. No. 91;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
OY 1 EEVVPXGMDYS 11

Db 1394 EVIYDQDQFS 1404
RESULT 7
KHL1_HUMAN
ID KHL1_HUMAN STANDARD; PRT; 748 AA.
AC Q9NR64; Q9NR65; Q9P238; Q9H4X4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kelch-like protein 1.
GN KHL1 OR KIAA1490.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20347694; PubMed=10888605;
RA Koob M.D., Nemes J.P., Benzow K.A.;
RT "The SCAR transcript is an antisense RNA to a brain-specific
transcript encoding a novel actin-binding protein (KHL1).";
RL Hum. Mol. Genet. 9:1543-1551(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20277482; PubMed=10819331;
RA Nagase T., Kikuno R., Ishikawa K.-I., Hirose M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVII.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
RL DNA Res. 7:143-150(2000).
RN [3]
RP SEQUENCE OF 179-409 FROM N.A.
RA Ray N.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MAY PLAY A ROLE IN ORGANIZING THE ACTIN CYTOSKELETON OF
THE BRAIN CELLS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
CC -1- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
CC -1- SIMILARITY: CONTAINS 6 KELCH REPEATS.
CC
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CC
CC EMBL; AF252283; AAF81719.1; -;
CC EMBL; AF252279; AAF81716.1; -;
CC EMBL; AB040923; BAA96014.1; ALT_INIT.
CC EMBL; AL353736; CAC16128.1; -;
CC Genew; HGNC:6352; KHL1.
CC MIM; 605332; -;
CC InterPro; IPR000210; BTB_POZ.
CC InterPro; IPR001798; Kelch.
CC Pfam; PF00651; BTB; 1.
CC Pfam; PF01344; Kelch; 6.
CC PRINTS; PR00501; KELCHREPEAT.
CC SMART; SM00225; BTB; 1.
CC PROSITE; PS50097; BTB; 1.
CC Cytoskeleton; Actin-binding; Repeat.
KW DOMAIN 43 88
FT DOMAIN 212 279 BTB.
FT REPEAT 460 506 KELCH 1.
FT REPEAT 507 553 KELCH 2.
FT REPEAT 555 600 KELCH 3.
FT REPEAT 601 647 KELCH 4.
FT REPEAT 649 700 KELCH 5.

```

FT REPEAT 701 747 KELCH 6.
SQ SEQUENCE 748 AA; 82680 MW; CILC43D8282F9FF9 CRC64;

Query Match 63.9%; Score 34.5; DB 1; Length 748;
Best Local Similarity 80.0%; Pred. No. 29;
Matches 8; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EVVVPXGMDY 10
DB 127 EVVVP-GMDF 135

RESULT 8
PLAS_ORYSA STANDARD; PRT: 154 AA.
ID PLAS_ORYSA
AC P20423; Q9SBB8;
DT 01-FEB-1991 (Rel. 17, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Plastocyanin, chloroplast precursor.
GN PETE.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OC NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Lipoom; TISSUE=Leaf;
RA Lee J.-S.;
RT "Molecular cloning and characterization of plastocyanin precursor in
RL rice."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 58-154.
RC STRAIN=cv. Japonica;
RX MEDLINE=89386623; PubMed=2780537;
RA Yano H., Kamo M., Tsugita A., Aso K., Nozu Y.;
RT "The amino acid sequence of plastocyanin from rice (Oryza sativa,
RT subspecies japonica)."
RL Protein Seq. Data Anal. 2:385-389(1989).
CC -!- FUNCTION: Participates in electron transfer between P700 and the
CC cytochrome b6-f complex in photosystem I.
CC -!- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID
CC MEMBRANE SURFACE IN CHLOROPLASTS.
CC -!- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
CC
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FT METAL 148 148 COPPER (BY SIMILARITY).
 FT VARIANT 120 120 T -> N (IN CV. NK 1558).
 SQ SEQUENCE 155 AA; 15709 MW; DAA7EABE3F6F4F91 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 155;
 Best Local Similarity 54.5%; Pred. No. 6.9;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 EEVVPXGMDYS 11
 I: | | | | |
 Db 101 EDAPVSGVDVS 111

RESULT 10
 PLAT_POPNI STANDARD; PRT; 168 AA.
 AC P11970;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Plastocyanin B, chloroplast precursor.
 GN PETE.
 OS Populus nigra (Lombardy poplar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Malpighiales; Salicaceae; Populus.
 OX NCBI_TaxID=3691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-cv. Italica; TISSUE=Leaf;
 RA Reichert J., Jenzelewski V., Haehnel W.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 70-168.
 RC STRAIN-cv. Italica;
 RA Dimitrov M.I., Egorov C.A., Donchev A.A., Atanasov B.P.;
 RT "Complete amino acid sequence of poplar plastocyanin B";
 RL FEBS Lett. 226:17-22(1987).
 CC -1- FUNCTION: Participates in electron transfer between P700 and the
 CC cytochrome b6-f complex in photosystem I.
 CC -1- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID
 CC MEMBRANE SURFACE IN CHLOROPLASTS.
 CC -1- SIMILARITY: THERE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF
 CC POPLAR PLASTOCYANINS A AND B.
 CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.

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EMBL; 250186; CAA90565.1; -
 PIR; S00210; S00210.
 DR HSP; P00299; IPII.
 DR InterPro; IPR000923; BlueCu.1.
 DR InterPro; IPR001235; Copper_blue.
 DR Pfam; PF00127; copper-bind; 1.
 DR PRINTS; PK00156; COPPERBLUE.
 DR ProDom; PK001235; Copper_blue; 1.
 DR PROSITE; PS00196; COPPER_BLUE; 1.
 DR Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
 TRANSIT peptide; Multigene family.
 FT TRANSIT 1 69
 FT CHAIN 70 168 CHLOROPLAST.
 FT DOMAIN 70 168 PLASTOCYANIN B.
 FT METAL 106 106 COPPER.
 FT METAL 153 153 COPPER.
 FT METAL 156 156 COPPER.
 FT METAL 161 161 COPPER.
 SQ SEQUENCE 168 AA; 16981 MW; F20DAGEA2038AEEA CRC64;

Query Match 63.0%; Score 34; DB 1; Length 168;
 Best Local Similarity 54.5%; Pred. No. 7.5;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 EEVVPXGMDYS 11
 I: | | | | |
 Db 112 EDAPVSGVDVS 122

RESULT 11
 SYFB_BORBU STANDARD; PRT; 566 AA.
 ID SYFB_BORBU
 AC P94283;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--
 DE tRNA ligase beta chain) (PHERS).
 GN PHER OR BB0514.
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 35210 / B31;
 RA Barbour A.G., Hinnebusch J.;
 RT "Phenylalanyl-tRNA synthetase genes (alpha and beta subunits) and
 RT thioredoxin reductase gene of Borrelia burgdorferi";
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 35210 / B31;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 RA Peterson J., Tomb J.F., Fleischmann R.D., Richardson D.,
 RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
 RA Utterback T., Wathey L., McDonald L., Artiach P., Bowman C.,
 RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
 RA Smith H.O., Venter J.C.;
 RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
 RT burgdorferi";
 RL Nature 390:580-586(1997).
 CC -1- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +
 CC diphosphate + L-phenylalanyl-tRNA(Phe).
 CC -1- SUBUNIT: Tetramer of two alpha and two beta chains (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE PHENYLALANYL-TRNA SYNTHETASE BETA
 CC CHAIN FAMILY. SUBFAMILY 2.

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EMBL; U82978; AAB41019.1; -
 DR EMBL; AE001153; AAC66870.1; -
 DR TIGR; BB0514; -
 DR InterPro; IPR005147; B5.
 DR InterPro; IPR004531; PheT_arch.
 DR Pfam; PF03484; B5; 1.
 DR TIGRFAMS; TIGR00471; pheT_arch; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 SQ SEQUENCE 566 AA; 65173 MW; 9D48CB5D6D3B74B CRC64;

Query Match 63.0%; Score 34; DB 1; Length 566;

Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VFXGMDY 10
DB 169 VFXGMDY 175

RESULT 12
Y939.METJA
ID Y939.METJA STANDARD; PRT; 276 AA.
AC Q58349;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0939.
GN MJ0939.

OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;

[1]
SEQUENCE FROM N.A.
RC STRAIN-TAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1038-1073(1996).

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EMBL: AF004886; AAG08116.1;
InterPro: IPR003721; Pantoate_ligase.
Pfam: PF02569; Pantoate_ligase; 1.
DR TIGR: TIGR000018; pncC; 1.
DR Pantothenate biosynthesis; Ligase; Complete proteome.
KW Pantothenate biosynthesis; Ligase; Complete proteome.
SQ SEQUENCE 283 AA; 30836 MW; C494949AB40E14E7 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 283;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMD 9
DB 96 EEMYPGMD 104

RESULT 14
HMPA_VIBCH STANDARD; PRT; 394 AA.
ID HMPA_VIBCH
AC Q9KMY3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Flavohemoprotein (Hemoglobin-like protein) (Flavohemoglobin).
GN HMP OR VCA0183.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;

[1]
SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA Ermolaeva M.D., Uterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).

-1- DOMAIN: CONSISTS OF TWO DISTINCT DOMAINS; ONE IS A HEME-CONTAINING
OXYGEN BINDING DOMAIN IN THE N-TERMINAL REGION AND THE OTHER IS AN
FAD-CONTAINING REDUCTASE DOMAIN FOUND IN THE C-TERMINAL REGION.
-1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY. TWO-DOMAIN
FLAVOHEMOPROTEINS SUBFAMILY.

Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VFXGMDY 10
DB 169 VFXGMDY 175

RESULT 13
PANC_PSEAE STANDARD; PRT; 283 AA.
ID PANC_PSEAE
AC Q9HV69;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pantoate-beta-alanine ligase (EC 6.3.2.1) (Pantothenate synthetase)
DE (Pantoate activating enzyme).
GN PANC OR PA4730.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;

[1]
SEQUENCE FROM N.A.
RC STRAIN-TAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kervatage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1038-1073(1996).

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EMBL: U67537; AAB98946.1;
TIGR: MJ0939;
Hypothetical protein; Complete proteome.
SQ SEQUENCE 276 AA; 33454 MW; 97BD69D392BC8FDF CRC64;

Query Match 61.1%; Score 33; DB 1; Length 276;
Best Local Similarity 45.5%; Pred. No. 21;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
DB 141 EEIENGHEHS 151

RESULT 13
PANC_PSEAE STANDARD; PRT; 283 AA.
ID PANC_PSEAE
AC Q9HV69;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pantoate-beta-alanine ligase (EC 6.3.2.1) (Pantothenate synthetase)
DE (Pantoate activating enzyme).
GN PANC OR PA4730.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;

```
CC -|- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
CC step.
CC
CC -|- SUBUNIT: HOMOTETRAMER.
CC
CC -|- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC
CC -|- MISCELLANEOUS: A NUMBER OF STRAIGHT-CHAIN ACYL-COA DEHYDROGENASES
CC OF DIFFERENT SUBSTRATE SPECIFICITIES ARE PRESENT IN MAMMALIAN
CC TISSUES
CC
CC -|- SIMILARITY: BELONGS TO THE ACYL-COA DEHYDROGENASE FAMILY.
CC -----
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CC -----
DR EMBL; J02791; AAA40670.1; -.
DR PIR; A28436; DERTCM.
DR HSP; P11310; LEGD.
DR InterPro; IPR001552; Acyl-CoA_dh.
DR Pfam; PF00441; Acyl-CoA_dh_1.
DR Pfam; PF02770; Acyl-CoA_dh_M; 1.
DR Pfam; PF02771; Acyl-CoA_dh_N; 1.
DR PROSITE; PS00072; ACYL_COA_DH_1; 1.
DR PROSITE; PS00073; ACYL_COA_DH_2; 1.
DR Oxidoreductase; Flavoprotein; FAD; Fatty acid metabolism;
KW Mitochondrion; Transit peptide.
FT TRANSIT 1 25 MITOCHONDRION.
FT CHAIN 26 421 ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN
FT FT SPECIFIC.
FT ACT_SITE 193 193 FORMS A HYDROGEN-BOND WITH THE FLAVIN
FT ACT_SITE 401 401 N(5) OF THE FAD COFACTOR (BY SIMILARITY).
FT SEQUENCE 421 AA; 46555 MW; 2CF076F8C919BDE8 CRC64;
SQ
Query Match 61.1%; Score 33; DB 1; Length 421;
Best Local Similarity 50.0%; Pred. No. 32;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 EEVVPXGMDY 10
Db |||::|||
58 EEIIPVAPDY 67
RESULT 16
ECB2_HALEL STANDARD; PRT; 421 AA.
AC O52250;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Diaminobutyrate--pyruvate aminotransferase (EC 2.6.1.46) (L-
DE diaminobutyric acid transaminase) (Diaminobutyrate transaminase).
GN ECB.
OS Halomonas elongata.
OC Bacteria; Proteobacteria; gamma subdivision; Halomonadaceae;
OC Halomonas.
OX NCBI_TaxID=2746;
[1]
SEQUENCE FROM N.A.
RC STRAIN=DSM 2581T;
RX MEDLINE=98231640; PubMed=9570121;
RA Goller K., Ofer A., Galinski E.A.;
RT "Construction and characterization of an NaCl-sensitive mutant of
RT Halomonas elongata impaired in ectoine biosynthesis.";
RL FEMS Microbiol. Lett. 161:293-300(1998)
CC -|- CATALYTIC ACTIVITY: L-2,4-diaminobutanoate + pyruvate = L-
CC aspartate 4-semialdehyde + L-alanine.
CC -|- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -|- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF ECTOINE (1,4,5,6-
CC TETRAHYDRO-2-METHYL-4-PYRIMIDINE CARBOXYLIC ACID).
CC -|- SUBUNIT: HOMOPOLYMER (BY SIMILARITY).
```

CC CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC CC AMINOTRANSFERASES.
CC CC
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CC CC or send an email to license@isb-sib.ch).
CC CC
CC CC EMBL; AF031489; AAC15882.1; -
CC CC HSPSP; P12995; 1QJ3
CC CC InterPro; IPR000954; AminoTran_3.
CC CC InterPro; IPR004637; Dat.
CC CC Pfam; PF00202; aminotran_3; 1.
CC CC TIGRFAMs; TIGR00709; dat; 1.
CC CC PROSITE; PS00600; AA_TRANSFER_CLASS_3; FALSE_NEG.
CC CC Transfrase; AminoTransferase; PYRIDOXAL PHOSPHATE (POTENTIAL).
CC CC BINDING 267 267
CC CC SEQUENCE 421 AA; 46166 MW; A4A2E21596E1E16C CRC64;
CC CC
CC CC Query Match 61.1%; Score 33; DB 1; Length 421;
CC CC Best Local Similarity 58.3%; Pred. No. 32;
CC CC Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
CC CC
CC CC QY 1 EVVV--PXGMDY 10
CC CC |||: | |:
CC CC 91 EEVILKPRGLDY 102
CC CC
CC CC RESULT 17
CC CC ECBI_HALEL STANDARD; PRT; 423 AA.
CC CC ID ECBI_HALEL
CC CC AC Q9ZEU7;
CC CC DT 30-MAY-2000 (Rel. 39, Created)
CC CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
CC CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC CC DE Diaminobutyrate-pyruvate aminotransferase (EC 2.6.1.46) (L-
CC CC diaminobutyrate acid transaminase) (diaminobutyrate transaminase).
CC CC GN ECTB.
CC CC OS Halomonas elongata.
CC CC OC Bacteria; Proteobacteria; gamma subdivision; Halomonadaceae;
CC CC OC Halomonas.
CC CC OX NCBI_TaxID=2746;
CC CC RN [1]
CC CC RP SEQUENCE FROM N.A.
CC CC RC STRAIN=DSM 3043;
CC CC RX MEDLINE=99123891; PubMed=9924816;
CC CC RA Canovas D., Vargas C., Calderon M.I., Ventosa A., Nieto J.J.;
CC CC RT "Characterization of the genes for the biosynthesis of the compatible
CC CC solute ectoine in the moderately halophilic bacterium Halomonas
CC CC elongata DSM 3043.";
CC CC RT Syst. Appl. Microbiol. 21:487-497(1998).
CC CC CC -1- CATALYTIC ACTIVITY: L-2,4-diaminobutanoate + pyruvate = L-
CC CC aspartate 4-semialdehyde + L-alanine.
CC CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC CC -1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF ECTOINE (1,4,5,6-
CC CC TETRAHYDRO-2-METHYL-4-PYRIMIDINE CARBOXYLIC ACID).
CC CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
CC CC AMINOTRANSFERASES.
CC CC
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CC CC or send an email to license@isb-sib.ch).
CC CC
CC CC EMBL; AJ011103; CAA09484.1; -
CC CC HSPSP; P12995; 1QJ3.
CC CC

DR InterPro; IPR000954; AminoTran_3.
DR InterPro; IPR004637; Dat.
DR Pfam; PF00202; aminotran_3; 1.
DR TIGRFAMs; TIGR00709; dat; 1.
DR PROSITE; PS00600; AA_TRANSFER_CLASS_3; FALSE_NEG.
DR Transfrase; AminoTransferase; PYRIDOXAL PHOSPHATE (POTENTIAL).
DR FT BINDING 267 267
DR SEQUENCE 423 AA; 46200 MW; 735C6BCF5A89288C CRC64;
DR
DR Query Match 61.1%; Score 33; DB 1; Length 423;
DR Best Local Similarity 58.3%; Pred. No. 32;
DR Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
DR
DR QY 1 EVVV--PXGMDY 10
DR |||: | |:
DR 91 EEVILKPRGLDY 102
DR
DR RESULT 18
DR EC22_HUMAN STANDARD; PRT; 787 AA.
DR ID EC22_HUMAN
DR AC O60344; O96NX4; O96NX3;
DR DT 30-MAY-2000 (Rel. 39, Created)
DR DT 15-JUN-2002 (Rel. 41, Last sequence update)
DR DT 15-JUN-2002 (Rel. 41, Last annotation update)
DR DE Endothelin-converting enzyme 2 (EC 3.4.24.71) (ECE-2).
DR GN ECE2 OR KIAA0604.
DR OS Homo sapiens (Human).
DR CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
DR CC Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.
DR OX NCBI_TaxID=9606;
DR RN [1]
DR RP SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
DR RA Lorenzo M.-N., Khan R.Y., Wang Y., Tai S.C., Chan G.C., Cheung A.H.,
DR Marsden P.A.;
DR RT "Human endothelin converting enzyme-2 (ECE2): characterization of mRNA
DR species and chromosomal localization.";
DR RL Biochim. Biophys. Acta 0:0-0(2002).
DR RN [2]
DR RP SEQUENCE FROM N.A. (ISOFORM B).
DR RC TISSUE=Brain;
DR RX MEDLINE=98290545; PubMed=9628581;
DR RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
DR Nomura N., Ohara O.;
DR RT "Prediction of the coding sequences of unidentified human genes. IX.
DR The complete sequences of 100 new cDNA clones from brain which can
DR code for large proteins in vitro.";
DR RL DNA Res. 5:31-39(1998).
DR CC -1- FUNCTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1 (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
CC Trp-1-Val-22 bond in the precursor.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- ALTERNATIVE PRODUCTS: 3 isoforms: ECE-2A (shown here), ECE-2B and
CC ECE-2C; are produced by alternative splicing.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
CC
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CC
CC EMBL; AF428263; AAL30386.1; -
CC EMBL; AF428264; AAL30387.1; -
CC EMBL; AF192531; AAG28399.1; -
CC EMBL; AB011176; BAA25530.1; -
CC HSPSP; P08473; 1DMT.
CC MEROPS; M13.003; -
CC InterPro; IPR000718; Peptidase_M13.
CC InterPro; IPR000130; Zn_Mtpeptdse.
CC

DR Pfam: PF01431; Peptidase_M13; 1.
 DR PRINTS; PRO0786; NEPRILYSIN.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;
 KW Signal-anchor; Alternative splicing.
 FT DOMAIN 1 82 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 83 103 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
 FT DOMAIN 104 787 EXTRACELLULAR (POTENTIAL).
 FT METAL 624 624 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 625 625 BY SIMILARITY.
 FT METAL 628 628 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 684 684 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 688 688 PROTON DONOR (BY SIMILARITY).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 187 187 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 228 228 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 288 288 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 400 400 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 556 556 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 649 649 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 657 657 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARSPLIC 1 63 MOARHVPOLRWETMDVRKLDFFSASDFVLEKGTLDALL
 AGERDPWTYSSEGVHTVDQLS -> MNVALQELGAGSNMV
 EYKRALRDEDAPEPPVGGASPDAM (IN ISOFORM ECE-2B).
 VARSPLIC 1 64 MOARHVPOLRWETMDVRKLDFFSASDFVLEKGTLDALL
 AGERDPWTYSSEGVHTVDQLSE -> MNVALQELGAGSN
 (IN ISOFORM ECE-2C).
 SQ SEQUENCE 787 AA; 89221 MW; CC2D2B0F0EB7239 CRC64;

Query Match 61.18; Score 33; DB 1; Length 787;
 Best Local Similarity 70.08; Pred. No. 63;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGMDY 10
 I I I I I I I I I I
 Db 382 EPVVVYGM DY 391

RESULT 19
 FGR3_MOUSE
 ID FGR3_MOUSE STANDARD; PRT; 801 AA.
 AC Q61851; Q63834; Q61564;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Fibroblast growth factor receptor 3 precursor (EC 2.7.1.112) (FGR-3)
 DE (heparin-binding growth factor receptor).
 GN FGR3 OR MFR3 OR SAM3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=92355591; PubMed=1379594;
 RA Ornitz D.M., Leder P.;
 RT "Ligand specificity and heparin dependence of fibroblast growth
 factor receptors 1 and 3.";
 RL J. Biol. Chem. 267:16305-16311(1992).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=93177694; PubMed=8382556;
 RA Katoh O., Hattori Y., Sasaki H., Sakamoto H., Fujimoto K.,
 RA Fujii T., Sugimura T., Terada M.;
 RT "Isolation of the complementary DNA encoding a mouse heparin-binding
 growth factor receptor with the use of a unique kinase insert
 sequence.";
 RL Cancer Res. 53:1136-1141(1993).
 RN [3]

RP SEQUENCE OF 242-364 FROM N.A. (ISOFORM 2).
 RX MEDLINE=94203351; PubMed=7512569;
 RA Chellalan A.T., McEwen D.G., Werner S., Xu J., Ornitz D.M.;
 RT "Fibroblast growth factor receptor (FGR) 3. Alternative splicing in
 immunoglobulin-like domain III creates a receptor highly specific for
 acidic FGF/FGF-1.";
 RL J. Biol. Chem. 269:11620-11627(1994).
 CC -1- FUNCTION: RECEPTOR FOR ACIDIC AND BASIC FIBROBLAST GROWTH
 FACTORS. PREFERENTIALLY BINDS FGF1.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1/IIc (shown here) and 2/IIb;
 are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: IN EMBRYO, EXPRESSED IN HEART, LUNG, KIDNEY,
 SKIN, HEAD AND LIVER BUT NOT IN MUSCLE. IN ADULT, HIGHEST LEVELS
 IN BRAIN. ALSO EXPRESSED IN LIVER, LUNG, KIDNEY, TESTIS, OVARY
 AND UTERUS. VERY LOW LEVELS IN HEART, THYMUS, SPLEEN AND MUSCLE.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN EMBRYO FROM MID-GESTATION AND
 IN ADULT.
 CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR
 FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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 CC -----
 CC EMBL: M81342; AAA39535.1; -
 DR EMBL: S56291; AAB25535.1; -
 DR EMBL: L26492; AAB21490.2; -
 DR HSSP: P11362; IFGK.
 DR MGD: MGI:95524; Fgfr3.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR003006; Iq_MHC.
 DR InterPro: IPR003598; Iq_c2.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00047; Iq; 4.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS; PRO0109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART; SM00408; IGC2; 3.
 DR SMART; SM00219; TyrKC; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 DR Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
 KW Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;
 KW Repeat; Signal; Alternative splicing.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 801 FIBROBLAST GROWTH FACTOR RECEPTOR 3.
 FT DOMAIN 21 369 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 370 390 POTENTIAL.
 FT DOMAIN 391 801 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 52 114 IG-LIKE C2-TYPE DOMAIN 1.
 FT DOMAIN 163 229 IG-LIKE C2-TYPE DOMAIN 2.
 FT DOMAIN 262 340 IG-LIKE C2-TYPE DOMAIN 3.
 FT DOMAIN 466 756 PROTEIN KINASE.
 FT NP_BIND 472 481 ATP (BY SIMILARITY).
 FT BINDING 502 502 ATP (BY SIMILARITY).
 FT ACT_SITE 611 611 BY SIMILARITY.
 FT MOD_RES 642 642 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT DISULFID 170 222 POTENTIAL.
 FT DISULFID 269 333 POTENTIAL.
 FT CARBOHYD 96 96 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 219 219 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 256 256 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 288 288 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 322 322 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 305 352 TAGANTTDKEVLSLHNVTFFDAGEYTCLAGNSIGFSHRS
FT AMLVLP -> SWISENVEADARLRLANVSERDGGVLCRA
FT TNGVAKAFWLRVHGPOA (IN ISOFORM 2).
FT P -> L (IN REF. 2).
FT MISSING (IN REF. 2).
FT SEQUENCE 801 AA; 87758 MW; 68BC110212691705 CRC64;
Query Match 61.1%; Score 33; DB 1; Length 801;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 PXGMDYS 11
DB 566 PPGMDYS 572
RESULT 20
CEK2_CHICK STANDARD; PRT; 806 AA.
AC P18460;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine kinase receptor CEK2 precursor (EC 2.7.1.112).
GN Gallus (Chicken).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90332672; PubMed=2165604;
RA Pasquale E.B.;
RT "A distinctive family of embryonic protein-tyrosine kinase
receptors";
RL Proc. Natl. Acad. Sci. U.S.A. 87:5812-5816(1990).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR
FAMILY.
CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
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DR EMBL: M35195; AAA48664.1; -;
DR HSP: A35963; A35963.
DR HGSP: P11362; IFGK.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003598; Ig_C2.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00047; Ig_3.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00408; IGG2; 3.
DR SMART: SM00219; TyrcK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
KW Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;
KW Repeat; Signal.

FT SIGNAL 1 19
FT CHAIN 20 806
FT DOMAIN 20 806
FT TRANSMEM 365 389
FT DOMAIN 390 806
FT DOMAIN 54 114
FT DOMAIN 163 229
FT DOMAIN 262 340
FT DOMAIN 131 141
FT DOMAIN 466 755
FT NP_BIND 472 480
FT BINDING 502 502
FT ACT_SITE 611 611
FT MOD_RES 642 642
FT DISULFID 61 107
FT DISULFID 170 222
FT DISULFID 269 333
FT CARBOHYD 83 83
FT CARBOHYD 96 96
FT CARBOHYD 118 118
FT CARBOHYD 219 219
FT CARBOHYD 256 256
FT CARBOHYD 288 288
FT CARBOHYD 309 309
FT CARBOHYD 322 322
SQ SEQUENCE 806 AA; 89730 MW; B38B3C6D5F2314B6 CRC64;
Query Match 61.1%; Score 33; DB 1; Length 806;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 5 PXGMDYS 11
DB 566 PPGMDYS 572
RESULT 21
SULH_SCHPO STANDARD; PRT; 877 AA.
AC 074377;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable sulfate permease C3H7.02.
GN SPBC3H7.02.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gholroyd S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Stevens K.,
RA Skelton J., Simmonds M., Squares R., Walsh S.V., Warren T., Whitehead S.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Schaefer M., Mueller-Auer S.,
RA Welljens I., Vanstreels E., Rieger M., Schaefer M., Hilbert H.,
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Leinach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler R., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT "The genome sequence of Schizosaccharomyces pombe";
RL Nature 415:871-880(2002).
CC -!- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -!- SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS.
CC -!- SIMILARITY: CONTAINS 1 STAS DOMAIN.
CC
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CC
CC EMBL; AL031261; CAA20298.1; -
CC InterPro; IPR002645; STAS.
CC Pfam; PF001902; Sulfate_transp.
CC Pfam; PF00916; Sulfate_transp; 1.
CC Pfam; PF01740; STAS; 1.
CC TIGRFAMs; TIGR00815; sulp; 1.
CC PROSITE; PS01130; SLC26A; 1.
CC PROSITE; PS0801; STAS; 1.
CC Transmembrane.
CC Transmembrane.
CC TRANSMEM 133 153 POTENTIAL.
CC TRANSMEM 161 181 POTENTIAL.
CC TRANSMEM 186 206 POTENTIAL.
CC TRANSMEM 221 241 POTENTIAL.
CC TRANSMEM 243 263 POTENTIAL.
CC TRANSMEM 292 312 POTENTIAL.
CC TRANSMEM 329 349 POTENTIAL.
CC TRANSMEM 384 404 POTENTIAL.
CC TRANSMEM 424 444 POTENTIAL.
CC TRANSMEM 461 481 POTENTIAL.
CC TRANSMEM 484 504 POTENTIAL.
CC TRANSMEM 518 538 POTENTIAL.
CC TRANSMEM 543 563 POTENTIAL.
CC DOMAIN 594 747 STAS.
CC SEQUENCE 877 AA; 96373 MW; 56995A8493371E43 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 877;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
||| |||
Db 148 VVPQMSYA 156

RESULT 22
ENV_SFV3L
ID ENV_SFV3L STANDARD; PRT; 982 AA.
AC P27399;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE DNA-directed RNA polymerase (coat polyprotein).
DE ENV.
GN ENV.
OS Simian foamy virus (type 3 / strain LK3) (SFV-3).
OC Viruses: Retroviridae; Retroviridae; Spumavirus.
OX NCBI_TaxID=11644;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=92124734; PubMed=1310187;
RA Renne R., Friedl E., Schweizer M., Fleps U., Turek R.,
RA Neumann-Haefelin D.;
RT "Genomic organization and expression of simian foamy virus type 3

(SFV-3).";
Virology 186:597-608(1992).

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CC
CC EMBL; M74895; AAA47798.1; ALT_INIT.
CC PIR; C40820; VCLJLK.
CC InterPro; IPR005070; Foamy_env.
CC Pfam; PF03408; Foamy_virus_ENV; 1.
CC Coat protein; Transmembrane; Polyprotein; Glycoprotein.
CC TRANSMEM 68 88 I (POTENTIAL).
CC TRANSMEM 955 975 II (POTENTIAL).
CC CARBOHYD 17 17 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 25 25 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 109 109 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 346 346 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 404 404 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 412 412 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 484 484 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 522 522 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 551 551 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 776 776 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 802 802 N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 827 827 N-LINKED (GLCNAC. .) (POTENTIAL).
CC SEQUENCE 982 AA; 113313 MW; 721F2F8929D604FF CRC64;

Query Match 61.1%; Score 33; DB 1; Length 982;
Best Local Similarity 66.7%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVXPXGMD 9
||| |||
Db 44 EEVPIPRMD 52

RESULT 23
RPOC_VIBCH
ID RPOC_VIBCH STANDARD; PRT; 1401 AA.
AC Q9KV29;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
DE beta' chain) (RNA polymerase beta' subunit).
DE RPOC OR VC0329.
GN Vibrio cholerae.
OS Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Emolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae";
RL Nature 406:477-483(2000).
CC -!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION

CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA](N).
CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AE004121; AAF93502.1; -
CC HSP; Q9K06; 1HQ.
CC TIGR: VC0329; -
CC InterPro: IPR000722; RNA_pol_A.
CC InterPro: IPR002879; RNA_pol_A2.
CC Pfam: PF00623; RNA_pol_A; 1.
CC Pfam: PF01854; RNA_pol_A2; 2.
CC Transferase; DNA-directed RNA polymerase; Transcription;
CC Complete proteome.
CC KW
CC SEQUENCE 1401 AA; 155021 MW; DFD80F2B514504F CRC64;
CC -----
CC Query Match 61.1%; Score 33; DB 1; Length 1401;
CC Best Local Similarity 50.0%; Pred. No. 1.2e+02;
CC Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
CC -----
CC QY 2 EVVPXGMDYS 11
CC :|||: ||
CC 581 QIVPKGLPYS 590
CC -----
CC RESULT 24
CC ID ZEP1_HUMAN STANDARD; PRT; 2717 AA.
CC AC P15822;
CC DT 01-APR-1990 (Rel. 14, Created)
CC DT 01-APR-1990 (Rel. 14, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Zinc finger protein 40 (Human immunodeficiency virus type I enhancer-
CC binding protein 1) (HIV-Ep1) (Major histocompatibility complex binding
CC protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
CC (PRDII-BF1).
CC DE HIVEP1 OR ZNF40.
CC GN Homo sapiens (Human).
CC OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC [1]
CC SEQUENCE FROM N.A.
CC MEDLINE=90169514; PubMed=2106471;
CC Fan C.M., Maniatis T.;
CC RA "A DNA-binding protein containing two widely separated zinc finger
CC motifs that recognize the same DNA sequence.";
CC Genes Dev. 4:29-42(1990).
CC [2]
CC STRUCTURE BY NMR OF 2113-2142.
CC MEDLINE=91064333; PubMed=2248949;
CC Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
CC Gronenborn A.M.;
CC RA "High-resolution three-dimensional structure of a single zinc finger
CC from a human enhancer binding protein in solution.";
CC RL Biochemistry 29:9324-9334(1990).
CC [3]
CC STRUCTURE BY NMR OF 2087-2142.
CC RP MEDLINE=92232684; PubMed=1567844;
CC RA Omichinski J.G., Clore G.M., Roblen M., Sakaguchi K., Appella E.,
CC Gronenborn A.M.;

RT "High-resolution solution structure of the double Cys2His2 zinc
RT finger from the human enhancer binding protein MBP-1.";
RL Biochemistry 31:3907-3917(1992).
CC -1- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE
CC 5'-GGGACTTCC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF
CC NUMEROUS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CMV, OR HIV1.
CC IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS
CC OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I
CC MHC, INTERLEUKIN-2 RECEPTOR, AND INTERFERON-BETA GENES. IT MAY ACT
CC IN T-CELL ACTIVATION.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- INDUCTION: BY MITOGEN AND PHORBOL ESTER.
CC -1- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY
CC SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
CC ZINC-FINGER IN-BETWEEN.
CC -1- SIMILARITY: STRONG, TO HIVEP2.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X51435; CAA35798.1; -
CC PIR: A34203; A34203.
CC PDB: 3ZNF; 15-JAN-92.
CC PDB: 4ZNF; 15-JAN-92.
CC PDB: 1BBO; 31-OCT-93.
CC TRANSFAC: T00497; -
CC Genew; HGNC:4920; HIVEP1.
CC MIM: 194540; -
CC InterPro: IPR000822; Znf_C2H2.
CC Pfam: PF00096; Zf_C2H2; 5.
CC PRINTS: PR00048; ZINCFINGER.
CC SMART; SM00355; Znf_C2H2; 4.
CC PROSITE; PS00028; ZINC_FINGER_C2H2_1; 4.
CC PROSITE; PS0157; ZINC_FINGER_C2H2_2; 4.
CC Transcription regulation; zinc-finger; Metal-binding; DNA-binding;
CC KW Nuclear protein; Repeat; 3D-structure.
CC DOMAIN 406 456 ZINC FINGERS.
CC ZN_FING 406 428 C2H2-TYPE.
CC ZN_FING 434 456 C2H2-TYPE.
CC ZN_FING 434 456 POLY-SER.
CC ZN_FING 958 981 C2HC-TYPE (POTENTIAL).
CC ZN_FING 2087 2139 ZINC FINGERS.
CC ZN_FING 2087 2109 C2H2-TYPE.
CC ZN_FING 2115 2139 C2H2-TYPE.
CC STRAND 2088 2088
CC TURN 2090 2092
CC STRAND 2095 2095
CC HELIX 2099 2108
CC TURN 2109 2109
CC STRAND 2115 2116
CC STRAND 2123 2124
CC HELIX 2127 2135
CC SEQUENCE 2717 AA; 297217 MW; D45D3CA951FEA561 CRC64;
CC -----
CC Query Match 61.1%; Score 33; DB 1; Length 2717;
CC Best Local Similarity 66.7%; Pred. No. 2.3e+02;
CC Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
CC -----
CC QY 3 VVPXGMDYS 11
CC |||: ||
CC 2405 VVPAGLYYS 2413
CC -----
CC RESULT 25
CC ET2A_XENLA STANDARD; PRT; 472 AA.
CC ID ET2A_XENLA
CC AC P19102;
CC DT 01-NOV-1990 (Rel. 16, Created)

01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-ETS-2A protein.
ETS2A OR ETS-2A.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
[1]
SEQUENCE FROM N.A.
MEDLINE=92158632; PubMed=1741266;
Burdett L.A., Qi S.M., Chen Z.Q., Lautenberger J.A., Papas T.S.;
"Characterization of the cDNA sequences of two Xenopus ets-2 proto-
oncogenes.";
Nucleic Acids Res. 20:371-371(1992).
[2]
SEQUENCE OF 121-472 FROM N.A.
TISSUE=Oocyte;
MEDLINE=90356411; PubMed=2201951;
Wolff C.M., Stiegler P., Baltzinger M., Meyer D., Ghysdael J.,
Stehelin D., Befort N., Remy P.;
"Isolation of two different c-ets-2 proto-oncogenes in Xenopus
laevis.";
Nucleic Acids Res. 18:4603-4604(1990).
[3]
SEQUENCE OF 121-472 FROM N.A.
MEDLINE=92088972; PubMed=1751411;
Wolff C.M., Stiegler P., Baltzinger M., Meyer D., Ghysdael J.,
Stehelin D., Befort N., Remy P.;
"Cloning, sequencing, and expression of two Xenopus laevis c-ets-2
protooncogenes";
Cell Growth Differ. 2:447-456(1991).
-!- SUBCELLULAR LOCATION: Nuclear.
-!- SIMILARITY: BELONGS TO THE ETS FAMILY.
-!- SIMILARITY: CONTAINS 1 POINTED (PNT) DOMAIN.

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EMBL; M81583; AAA49705.1; -;
EMBL; X51826; CA36124.1; -;
PIR; S10994; S10994.
PIR; S28824; S28824.
HSP; P14921; 2STT.
TRANSFAC; T02041; -;
InterPro; IPR000418; Ets.
InterPro; IPR002341; HSF_ETs.
InterPro; IPR003118; SAM_PNT.
Pfam; PF00178; Ets; 1.
Pfam; PF02198; SAM_PNT; 1.
PRINTS; PR00454; ETSDOMAIN.
SMART; SM00413; ETS; 1.
SMART; SM00251; SAM_PNT; 1.
PROSITE; PS00345; ETS_DOMAIN_1; 1.
PROSITE; PS00346; ETS_DOMAIN_2; 1.
PROSITE; PS50061; ETS_DOMAIN_3; 1.
KW. DNA-binding; Nuclear protein.
FT DOMAIN 87 170 POINTED.
FT DNA_BIND 366 446 ETS-DOMAIN.
SQ SEQUENCE 472 AA; 53894 MW; E080808B5E6BF111 CRC64;

Query Match 60.2%; Score 32.5; DB 1; Length 472;
Best Local Similarity 58.3%; Pred. No. 46;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 EEVYPXGMD-YS 11
|:|:|:|:|

Db 49 EQAVPTGLDSYS 60

Search completed: June 10, 2003, 13:40:21
Job time : 4.5 secs

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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:30:25 ; Search time 25.7857 Seconds
(without alignments)
87.898 Million cell updates/sec

Title: US-09-909-164-13
Perfect score: 54
Sequence: 1 EEEVXPXGMDYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : SPTREMBL.21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mmc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriaph.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	74.1	156	3 Q12479	Q12479 saccharomyc
2	38	70.4	363	17 Q30260	Q30260 archaeoglob
3	38	70.4	1063	16 Q8RG86	Q8RG86 fusobacteri
4	36	66.7	341	10 Q22081	Q22081 citrus unsh
5	36	66.7	348	10 Q22096	Q22096 citrus unsh
6	36	66.7	452	10 Q8W568	Q8W568 arabidopsis
7	36	66.7	1047	10 Q9C9T7	Q9C9T7 arabidopsis
8	36	66.7	1047	10 P93782	P93782 saccharum o
9	36	66.7	1083	10 Q9SN30	Q9SN30 arabidopsis
10	36	66.7	1084	10 Q43010	Q43010 oryza sativ
11	36	66.7	1100	10 Q8S064	Q8S064 oryza sativ
12	35	64.8	219	5 Q8GQ04	Q8GQ04 eriocheir s
13	35	64.8	253	16 Q8XPA8	Q8XPA8 clostidium
14	35	64.8	298	2 Q52367	Q52367 rhizobium t
15	35	64.8	425	5 Q9XVK4	Q9XVK4 caenorhabdi
16	35	64.8	433	16 Q9A382	Q9A382 caulobacter

ALIGNMENTS

RESULT 1
Q12479 PRELIMINARY; PRT; 156 AA.
ID Q12479
AC Q12479
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Q9XVK4 caenorhabdi
GN YOR013W.

17	35	64.8	440	17	Q9YFI3	Q9YFI3 aeropyrum p
18	35	64.8	511	2	O52680	O52680 escherichia
19	35	64.8	517	16	Q8XZL5	Q8XZL5 ralstonia s
20	35	64.8	745	5	Q95PA6	Q95PA6 carinus ma
21	35	64.8	1031	5	Q9U6A3	Q9U6A3 callinectes
22	35	64.8	1150	5	O17704	O17704 caenorhabdi
23	35	64.8	1410	2	O52673	O52673 escherichia
24	35	64.8	1420	2	O52666	O52666 escherichia
25	35	64.8	1474	17	O27146	O27146 methanobact
26	35	64.8	1828	16	Q98K29	Q98K29 rhizobium l
27	35	64.8	2778	5	Q9V9I6	Q9V9I6 drosophila
28	34.5	63.9	748	4	Q8TBJ7	Q8TBJ7 homo sapien
29	34	63.0	143	5	Q9VSX8	Q9VSX8 drosophila
30	34	63.0	154	10	Q9SBB8	Q9SBB8 oryza sativ
31	34	63.0	215	16	Q8R9L5	Q8R9L5 thermoanaer
32	34	63.0	290	16	Q8U7J0	Q8U7J0 agrobacteri
33	34	63.0	296	17	Q9YEN8	Q9YEN8 aeropyrum p
34	34	63.0	357	17	O29920	O29920 archaeoglob
35	34	63.0	366	17	O29451	O29451 archaeoglob
36	34	63.0	387	16	Q98FX1	Q98FX1 rhizobium l
37	34	63.0	543	3	Q8TFF4	Q8TFF4 trichoderma
38	34	63.0	558	16	Q8R8Z2	Q8R8Z2 thermoanaer
39	34	63.0	565	16	Q9CINI	Q9CINI lactococcus
40	34	63.0	587	16	Q9JZF8	Q9JZF8 neisseria m
41	34	63.0	906	10	Q9ZSY4	Q9ZSY4 arabidopsis
42	34	63.0	908	10	Q9FJK8	Q9FJK8 arabidopsis
43	34	63.0	908	10	Q8W4J9	Q8W4J9 arabidopsis
44	34	63.0	908	10	Q9ZSV3	Q9ZSV3 arabidopsis
45	34	63.0	909	10	Q9M5A1	Q9M5A1 arabidopsis
46	34	63.0	1062	2	P95422	P95422 pseudomonas
47	34	63.0	1062	16	Q910X8	Q910X8 pseudomonas
48	34	63.0	3472	1	O74056	O74056 cenarchaeum
49	33	61.1	78	6	Q9XST4	Q9XST4 canis famil
50	33	61.1	97	17	Q97VR9	Q97VR9 sulfolobus
51	33	61.1	128	17	Q97US8	Q97US8 sulfolobus
52	33	61.1	172	13	Q92528	Q92528 oryzias lat
53	33	61.1	175	10	Q8VY88	Q8VY88 arabidopsis
54	33	61.1	183	2	Q9S1I0	Q9S1I0 sweet potat
55	33	61.1	184	17	Q97XJ2	Q97XJ2 sulfolobus
56	33	61.1	193	5	Q8SWL4	Q8SWL4 encephalito
57	33	61.1	209	13	Q9DEL6	Q9DEL6 brachydanio
58	33	61.1	210	10	O65890	O65890 cyclotella
59	33	61.1	217	4	O00404	O00404 homo sapien
60	33	61.1	225	10	Q40129	Q40129 lycopersico
61	33	61.1	230	17	Q9P9L6	Q9P9L6 pyrobaculum
62	33	61.1	247	16	Q92U66	Q92U66 rhizobium m
63	33	61.1	257	10	Q9C6J0	Q9C6J0 arabidopsis
64	33	61.1	262	17	Q97YB8	Q97YB8 sulfolobus
65	33	61.1	267	17	Q97Y57	Q97Y57 sulfolobus
66	33	61.1	299	4	Q90EE9	Q90EE9 homo sapien
67	33	61.1	299	17	Q97TV4	Q97TV4 sulfolobus
68	33	61.1	299	17	Q9UWN4	Q9UWN4 sulfolobus
69	33	61.1	307	17	Q9HP60	Q9HP60 halobacteri
70	33	61.1	396	17	Q8TIT9	Q8TIT9 methanosarc
71	33	61.1	441	17	Q9HIW6	Q9HIW6 thermoplasm
72	33	61.1	556	4	O43733	O43733 homo sapien
73	33	61.1	577	15	Q9QBR8	Q9QBR8 simian foam
74	33	61.1	577	15	Q9QBR7	Q9QBR7 simian foam
75	33	61.1	577	15	Q9QBR6	Q9QBR6 simian foam

OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RA De haan M., Grivell L.A., Maarse A.C.;
 RP Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RA De haan M., Grivell L.A., Maarse A.C.;
 RP Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RA MIPS;
 RP Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RA De haan M., Maarse A.C., Grivell L.A.;
 RP Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RA Sherman F.;
 RP "CYC2 encodes a factor involved in mitochondrial import of yeast
 cytochrome c.";
 RL Mol. Cell. Biol. 13:6442-6451(1993).
 RN [6]
 RA STRAIN=FY1679;
 RP STRAIN=FY1679;
 RN [7]
 RA MEDLINE=94019318; PubMed=8413243;
 RP Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlenny G.,
 Sherman F.;
 RT "CYC2 encodes a factor involved in mitochondrial import of yeast
 cytochrome c.";
 RL Mol. Cell. Biol. 13:6442-6451(1993).
 RN [8]
 RA STRAIN=FY1679;
 RP STRAIN=FY1679;
 RN [9]
 RA MEDLINE=94169519; PubMed=7764548;
 RP Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
 RT "Molecular cloning of a gene, DHS1, which complements a drug-
 hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
 RL Biosci. Biotechnol. Biochem. 58:391-395(1994).
 DR EMBL; Z74920; CAA99201.1;
 DR EMBL; X87331; CAA60762.1;
 DR SGD; S0005539; YOR013W.
 SQ SEQUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;
 Query Match 74.1%; Score 40; DB 3; Length 156;
 Best Local Similarity 77.8%; Pred. No. 1.7;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 EYVPXGMDY 10
 DB 50 EYVPLGMDY 58
 RESULT 2
 ID O30260 PRELIMINARY; PRT; 363 AA.
 AC O30260;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein AF2411.
 GN AF2411.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RA STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RP STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RN [2]
 RA MEDLINE=98049343; PubMed=9389475;
 RP Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
 Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 Peterson S., Reich C.I., McNeil L.K., Badger J.H., Zhou L.,
 Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 Cotton M.D., Spriggs T., Artach P., Kane B.P., Sykes S.M.,

RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 DR EMBL; AE001109; AAB91255.1;
 DR TIGR; AF2411;
 DR InterPro; IPR002103; Bac_luciferase.
 DR Pfam; PF00296; bac_luciferase; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 363 AA; 41736 MW; 0E976EAE788F4803 CRC64;
 Query Match 70.4%; Score 38; DB 17; Length 363;
 Best Local Similarity 54.5%; Pred. No. 12;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGMDYS 11
 DB 120 ENIVPGIDFS 130
 RESULT 3
 ID Q8RG86 PRELIMINARY; PRT; 1063 AA.
 AC Q8RG86;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Carbamoyl-phosphate synthase large chain (EC 6.3.5.5).
 GN FN0422.
 OS Fusobacterium nucleatum (subsp. nucleatum).
 OC Bacteria; Fusobacteria; Fusobacterium.
 OX NCBI_TaxID=76856;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 25586;
 RX MEDLINE=21886394; PubMed=11889109;
 RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
 RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
 RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
 RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
 RA Fongstein M., Kyrpides N., Overbeek R.;
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium
 nucleatum strain ATCC 25586.";
 RL J. Bacteriol. 184:2005-2018(2002).
 DR EMBL; AE010554; AAL94625.1;
 KW Ligase; Complete proteome.
 SQ SEQUENCE 1063 AA; 118008 MW; 39700E10B7CCE411 CRC64;
 Query Match 70.4%; Score 38; DB 16; Length 1063;
 Best Local Similarity 60.0%; Pred. No. 39;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 EYVPXGMDYS 11
 DB 195 EIVPGLNYS 204
 RESULT 4
 ID O22081 PRELIMINARY; PRT; 341 AA.
 AC O22081;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Sucrose-phosphate synthase (Fragment).
 GN CITSPS2.
 OS Citrus unshiu (Satsuma orange).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosids II; Sapindales; Rutaceae; Citrus.
 OX NCBI_TaxID=55188;

RP SEQUENCE FROM N.A.
RC STRAIN=CV. MIYAGAWA-WASE; TISSUE=JUICE SACS AND SEGMENT EPIDERMIS;
RX MEDLINE=96439842; PubMed=8842155;
RA Komatsu A., Takanokura Y., Omura M., Akihama T.;
RT "Cloning and molecular analysis of cDNA encoding three sucrose
phosphate synthase isoforms from a citrus fruit (Citrus unshiu
Marc.).";
RL Mol. Gen. Genet. 252:346-351(1996).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. MIYAGAWA-WASE; TISSUE=JUICE SACS AND SEGMENT EPIDERMIS;
RA Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;
RT "Differential expression of three sucrose-phosphate synthase isoforms
during sucrose accumulation in citrus fruits (Citrus unshiu Marc.).";
RL Plant Sci. 140:169-178(1999).
DR EMBL; AB006319; BAA23215.1; -.
FT NON_TER 1 341
FT SEQUENCE 341 AA; 38136 MW; 61417A59C4560777 CRC64;
SQ
Query Match 66.7%; Score 36; DB 10; Length 341;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 VVPXGMDYS 11
DB 228 VPPGMDFS 236
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. MIYAGAWA-WASE; TISSUE=JUICE SACS AND SEGMENT EPIDERMIS;
RX MEDLINE=96439842; PubMed=8842155;
RA Komatsu A., Takanokura Y., Omura M., Akihama T.;
RT "Cloning and molecular analysis of cDNA encoding three sucrose
phosphate synthase isoforms from a citrus fruit (Citrus unshiu
Marc.).";
RL Mol. Gen. Genet. 252:346-351(1996).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. MIYAGAWA-WASE; TISSUE=JUICE SACS AND SEGMENT EPIDERMIS;
RA Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;
RT "Differential expression of three sucrose-phosphate synthase isoforms
during sucrose accumulation in citrus fruits (Citrus unshiu Marc.).";
RL Plant Sci. 140:169-178(1999).
DR EMBL; AB006660; BAA22071.1; -.
FT NON_TER 1 348
FT SEQUENCE 348 AA; 38556 MW; EEIC21EBA6FF5C5E CRC64;
SQ
Query Match 66.7%; Score 36; DB 10; Length 348;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 VVPXGMDYS 11
DB 234 VPPGMDFS 242

RESULT 6
Q8W568 PRELIMINARY; PRT; 452 AA.
ID Q8W568;
AC Q8W568;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Atlg73750/F25P22.17
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RA "Arabidopsis cDNA clones.";
RT Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF419606; AAL31938.1; -.
DR InterPro; IPR002471; Prol_endopep_ser.
DR InterPro; IPR000379; Ser_estrs_site.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; UNKNOWN_1.
SQ SEQUENCE 452 AA; 49682 MW; A159955B21742C4A CRC64;
Query Match 66.7%; Score 36; DB 10; Length 452;
Best Local Similarity 70.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 EEVVPXGMDY 10
DB 210 EEDVPSAMDY 219
[1]
RESULT 7
Q9C9T7 PRELIMINARY; PRT; 460 AA.
ID Q9C9T7;
AC Q9C9T7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical 50.6 kDa protein.
GN F25P22.17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maiti R., Marziani A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney D., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

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RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
DR EMBL; AC012679; AAG52073.1; -.
DR InterPro; IPR002471; Prol_endopep_ser.
DR InterPro; IPR000379; Ser_estrs_site.
DR PROSITE; PS00708; PRO-ENDOPEP_SER; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 460 AA; 50564 MW; E94B27B5C4B249EC CRC64;

Query Match 66.7%; Score 36; DB 10; Length 460;
Best Local Similarity 70.0%; Pred. No. 41;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGMDY 10
Db 218 EEDVPSANDY 227
||| ||| |||

RESULT 8
P93782 PRELIMINARY; PRT; 1047 AA.
AC P93782;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Sucrose-phosphate synthase (EC 2.4.1.14) (Fragment).
GN SOSPS1.
OS Saccharum officinarum (Sugarcane).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoideae; Andropogoneae; Saccharum.
OX NCBI_TaxID=4547;
RN [1]
RP TISSUE=LEAF;
RC Sugiharto B., Sakakibara H., Sugiyama T.;
RT "Differential Expression of Two Genes for Sucrose-Phosphate Synthase
RT in Sugarcane: Molecular Cloning of the cDNAs and Comparative Analysis
RT of Gene Expression.";
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB001337; BAA19241.1; -.
DR InterPro; IPR001296; Glycos_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
KW Glycosyltransferase; Transferase.
FT NON_TER 1
SQ SEQUENCE 1047 AA; 116379 MW; D0EDB34961E1D83D CRC64;

Query Match 66.7%; Score 36; DB 10; Length 1047;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VVPXGMDYS 11
Db 414 VIPPGMDFS 422
||| ||| |||

RESULT 9
Q9SN30 PRELIMINARY; PRT; 1083 AA.
AC Q9SN30;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Sucrose-phosphate synthase-like protein (EC 2.4.1.14).
GN F28M11.40 OR At4G10120.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;

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[1]
RN SEQUENCE FROM N.A.
RP Bevan M., Murphy G., Ridley P., Hudson S., Bancroft I., Mewes H.W.,
RA Mayer K.F.X., Lemcke K., Schueller C.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE FROM N.A.
RP EU Arabidopsis sequencing project;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
[3]
RN SEQUENCE FROM N.A.
RP EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL049487; CAB39764.1; -.
DR EMBL; AL161516; CAB78135.1; -.
DR InterPro; IPR001296; Glycos_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
KW Glycosyltransferase; Transferase.
SQ SEQUENCE 1083 AA; 122688 MW; EFC126FCA2137BB1 CRC64;

Query Match 66.7%; Score 36; DB 10; Length 1083;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VVPXGMDYS 11
Db 483 VIPPGMDFS 491
||| ||| |||

RESULT 10
Q43010 PRELIMINARY; PRT; 1084 AA.
AC Q43010;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE L-lactate dehydrogenase (EC 1.1.1.27) (LDH).
GN SP51.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzoae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. JAPONICA;
RA Sakamoto M., Satozawa T., Kishimoto N., Higo K., Shimada H.,
RA Fujimura T.;
RT "Structure and RFLP mapping of a rice sucrose phosphate synthase (SPS)
RT gene that is specifically expressed in the source organ.";
RL Plant Sci. 112:207-217(1995).
CC -|- CATALYTIC ACTIVITY: (S)-LACTATE + NAD(+) -> PYRUVATE + NADH.
CC -|- PATHWAY: ANAEROBIC GLYCOLYSIS; FINAL STEP.
CC -|- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
DR EMBL; D45890; BAA08304.1; -.
DR InterPro; IPR001296; Glycos_transf_1.
DR Pfam; PF00534; Glycos_transf_1; 1.
DR PROSITE; PS00064; L_LDH; 1.
KW Glycolysis; NAD: Oxidoreductase.
SQ SEQUENCE 1084 AA; 119417 MW; 4D0D79AFEDD2F92B CRC64;

Query Match 66.7%; Score 36; DB 10; Length 1084;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VVPXGMDYS 11
Db 453 VIPPGMDFS 461
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RESULT 11
Q8S064

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us-09-909-164-13.rspt

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ID Q8S064 PRELIMINARY; PRT; 1100 AA.
AC Q8S064;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative sucrose-phosphate synthase.
GN P0678F11.14.
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. NIPPONBARE;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
clone:P0678F11." to the EMBL/GenBank/DBJ databases.
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP003437; BAB86107.1; -
SQ SEQUENCE 1100 AA; 121170 MW; 084F4604BA389CAD CRC64;

Query Match 66.7%; Score 36; DB 10; Length 1100;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
Db 469 VIPPGMDES 477

RESULT 12
Q9GQ04 PRELIMINARY; PRT; 219 AA.
AC Q9GQ04;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE Na+/K+/2Cl-cotransporter (Fragment).
OS Eriocheir sinensis (Chinese mitten crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Grapsoidae; Varunidae; Eriocheir.
OX NCBI_TaxID=95602;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GILL;
RA Wehrhau D., Towle D.W.;
RT "Na+/H+-exchanger and Na+/K+/2Cl- cotransporter are expressed in
gills of the euryhaline Chinese crab Eriocheir sinensis.";
RL Comp. Biochem. Physiol. 126:SI58-SI58(2000).
DR EMBL; AF301160; AAG39938.1; -
FT NON_TER 1
FT NON_TER 219
SQ SEQUENCE 219 AA; 24159 MW; 599442DA26F0D3F1 CRC64;

Query Match 64.8%; Score 35; DB 5; Length 219;
Best Local Similarity 75.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPXGMDYS 11
Db 107 VPQGLDYS 114

RESULT 13
Q8XPA8 PRELIMINARY; PRT; 253 AA.
AC Q8XPA8;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical protein CPE0057.

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GN CPE0057.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / TYPE A;
RX PubMed=11792842;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
RT "Complete genome sequence of Clostridium perfringens, an anaerobic
flesh-eater.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
DR EMBL; AP003185; BAB79763.1; -
DR InterPro; IPR000205; NAD_binding.
DR InterPro; IPR000594; THF_domain.
DR Pfam; PF00899; THF; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 253 AA; 27714 MW; 814DF79D3E0D7486 CRC64;

Query Match 64.8%; Score 35; DB 16; Length 253;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
Db 108 EEIIPDDVDY 117

RESULT 14
Q52367 PRELIMINARY; PRT; 298 AA.
AC Q52367;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Aryl-alcohol dehydrogenase homolog (Fragment).
GN XYL81.
OS Rhizobium tropici.
OG Plasmid pRCFN299a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=398;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CFN299;
RA Rosenblueth M., Hynes M.F., Martinez-Romero E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- COFACTOR: ZINC (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
FAMILY.
DR EMBL; AF036920; AAC04779.1; -
DR HSSP; P07846; ISDG.
DR InterPro; IPR002328; ADH_zinc.
DR InterPro; IPR002085; Adh_zn_family.
DR InterPro; IPR000205; NAD_binding.
DR Pfam; PF00107; adh_zinc; 1.
DR PROSITE; PS00059; ADH_ZINC; 1.
KW Oxidoreductase; Plasmid; Zinc.
FT NON_TER 298
FT NON_TER 298
SQ SEQUENCE 298 AA; 31092 MW; 49B2F8117C33AE87 CRC64;

Query Match 64.8%; Score 35; DB 2; Length 298;
Best Local Similarity 50.0%; Pred. No. 41;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGMDYS 11
Db 250 EEIIPGADFS 259

RESULT 15

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RT "Sequence and expression analysis of the Na+/K+/2Cl- cotransporter in
RT the euryhaline crabs Callinectes sapidus and Carcinus maenas."
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF044506; AAC622388.1; -
FT NON_TER 511 511
SQ SEQUENCE 511 AA; 55877 MW; C85402569450DBFF CRC64;

Query Match 64.8%; Score 35; DB 2; Length 511;
Best Local Similarity 60.0%; Pred. No. 75;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVVVPXGMDY 10
Db 381 EQVNPGLDY 390

RESULT 19
Q8XZL5 PRELIMINARY; PRT; 517 AA.
AC Q8XZL5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Probable SUBSTATE-binding periplasmic (PBP) ABC transporter
DE protein. OR RS04663.
GN RSC1380
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC Ralstonia.
OC NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21681879; PubMed-11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Cholsne N., Claudel-Renard C., Cunhac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
RL Nature 415:497-502(2002).
DR EMBL: AL646064; CAD15082.1; -
DR InterPro: IPR000914; SBP_bac_5.
DR Pfam: PF00496; SBP_bac_5; 1.
KW Complete proteome.
SQ SEQUENCE 517 AA; 57349 MW; 861EE836F645F2DA CRC64;

Query Match 64.8%; Score 35; DB 16; Length 517;
Best Local Similarity 66.7%; Pred. No. 76;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
Db 316 VVPQGVDA 324

RESULT 20
Q9SP46 PRELIMINARY; PRT; 745 AA.
AC Q9SP46;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Na+/K+/2Cl-cotransporter (Fragment).
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OC NCBI_TaxID=6759;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GILL;
RA Wehrauch D., Towle D.W.;

RT "Sequence and expression analysis of the Na+/K+/2Cl- cotransporter in
RT the euryhaline crabs Callinectes sapidus and Carcinus maenas."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY035548; AAK62044.1; -
DR InterPro: IPR002293; AA/rel_primeasel.
DR InterPro: IPR004841; Permease.
DR Pfam: PF00324; aa_permeases; 1.
FT NON_TER 745 745
FT NON_TER 1 1
SQ SEQUENCE 745 AA; 81249 MW; 08AE2D3E1F70C7BE CRC64;

Query Match 64.8%; Score 35; DB 5; Length 745;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPXGMDYS 11
Db 625 VPQGLDYS 632

RESULT 21
Q9U6A3 PRELIMINARY; PRT; 1031 AA.
AC Q9U6A3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Na+/K+/2Cl-cotransporter.
DE NCBI_TaxID=6763;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=GILL;
RA Towle D.W.;
RT "Cloning and sequencing a Na+/K+/2Cl- cotransporter from gills of the
RT euryhaline blue crab Callinectes sapidus."
RL Am. Zoologist 38:114A-114A(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=GILL;
RA Towle D.W., Wehrauch D.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF190129; AAF05702.1; -
DR InterPro: IPR002293; AA/rel_primeasel.
DR InterPro: IPR004842; KCl_cotransport.
DR InterPro: IPR002443; NaKCl_transporter.
DR PRINTS: PR01207; NAKCLTRNSPRT.
DR TIGRFAMs: TIGR00930; 2a30; 1.
SQ SEQUENCE 1031 AA; 113699 MW; F67773021AB05D71 CRC64;

Query Match 64.8%; Score 35; DB 5; Length 1031;
Best Local Similarity 75.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPXGMDYS 11
Db 737 VPQGLDYS 744

RESULT 22
O17704 PRELIMINARY; PRT; 1150 AA.
AC O17704; O17976;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE C53A5.2 protein.
GN C53A5.2.
OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peleoderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RL Mortimore B.;
 RA Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister N., Letellier P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.,
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans".
 RL Nature 368:32-38(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Matthews L.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; 281486; CAB03994.1; -;
 DR EMBL; 278015; CAB03994.1; JOINED.
 DR EMBL; 278015; CAB01437.1; -;
 DR EMBL; 281486; CAB01437.1; JOINED.
 DR InterPro; IPR001201; PAP_25A.Core.
 DR InterPro; IPR000051; SAM_Bind.
 DR InterPro; IPR003402; Unk_Met10.
 DR Pfam; PF02475; Met_10; I.
 SQ SEQUENCE 1150 AA; 133001 MW; BA130A251C1A12F8 CRC64;

Query Match 64.8%; Score 35; DB 5; Length 1150;
 Best Local Similarity 66.7%; Pred. No. 1.9e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 VVPXGMDYS 11
 DB 562 VLPVGDYS 570

RESULT 23

ID O52673 PRELIMINARY; PRT; 1410 AA.
 AC O52673;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Core protein.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EC11;
 RX MEDLINE=98361897; PubMed=9696756;
 RA Wang Y.D., Zhao S., Hill C.W.;
 RT "Rhs elements comprise three subfamilies which diverged prior to
 RT acquisition by Escherichia coli."
 RL J. Bacteriol. 180:4102-4110(1998).
 DR EMBL; AF044503; AAC32478.1; -;
 DR InterPro; IPR001826; RHS.
 DR Pfam; PF03527; RHS; 1.
 DR PRINTS; PR00394; RHPROTEIN.
 SO SEQUENCE 1410 AA; 158739 MW; 39ECB9F8C97FCB15 CRC64;

Query Match 64.8%; Score 35; DB 2; Length 1410;

Best Local Similarity 60.0%; Pred. No. 2.4e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 EEVVPXGMDY 10
 DB 382 EQVNPEGIDY 391

RESULT 24

ID O52666 PRELIMINARY; PRT; 1420 AA.
 AC O52666;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Core protein.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EC45;
 RX MEDLINE=98361897; PubMed=9696756;
 RA Wang Y.D., Zhao S., Hill C.W.;
 RT "Rhs elements comprise three subfamilies which diverged prior to
 RT acquisition by Escherichia coli."
 RL J. Bacteriol. 180:4102-4110(1998).
 DR EMBL; AF044501; AAC32471.1; -;
 DR InterPro; IPR001826; RHS.
 DR Pfam; PF03527; RHS; 1.
 DR PRINTS; PR00394; RHPROTEIN.
 DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
 SQ SEQUENCE 1420 AA; 159215 MW; E7851E4D48740621 CRC64;

Query Match 64.8%; Score 35; DB 2; Length 1420;
 Best Local Similarity 60.0%; Pred. No. 2.4e+02;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 EEVVPXGMDY 10
 DB 381 EQVNPEGIDY 390

RESULT 25

ID O27146 PRELIMINARY; PRT; 1474 AA.
 AC O27146;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Putative membrane protein.
 GN MTH1074.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DELTA H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT deltaH: functional analysis and comparative genomics."
 RL J. Bacteriol. 179:7135-7155(1997).
 DR EMBL; AE000878; AAB85563.1; -;

DR InterPro; IPR001434; DUF11.
DR Pfam; PF01345; DUF11; 9.
KW Complete proteome.
SQ SEQUENCE 1474 AA; 153713 MW; 11D4D27BD86255F0 CRC64;
Query Match 64.8%; Score 35; DB 17; Length 1474;
Best Local Similarity 55.6%; Pred. No. 2.5e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 2 EVVPXGMDY 10
Db 1238 DVLPAGLDY 1246
Search completed: June 10, 2003, 13:46:34
Job time : 26.7857 secs

Best Local Similarity 70.0%; Pred. No. 2.6e+02; DB 9; Length 736;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
| | | | |
Db 331 EPVVYGM DY 340

RESULT 22

US-10-173-706-420
; Sequence 420, Application US/10173706
; Publication No. US20030022293A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C7
; CURRENT APPLICATION NUMBER: US/10/173,706
; CURRENT FILING DATE: 2002-06-17
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-706-420

Query Match 61.1%; Score 33; DB 9; Length 736;
Best Local Similarity 70.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
| | | | |
Db 331 EPVVYGM DY 340

RESULT 23

US-10-175-738-420
; Sequence 420, Application US/10175738
; Publication No. US20030022294A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C45
; CURRENT APPLICATION NUMBER: US/10/175,738
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo Sapien

US-10-175-738-420

Query Match 61.1%; Score 33; DB 9; Length 736;
Best Local Similarity 70.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
| | | | |
Db 331 EPVVYGM DY 340

RESULT 24

US-10-175-752-420
; Sequence 420, Application US/10175752
; Publication No. US20030022295A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C60
; CURRENT APPLICATION NUMBER: US/10/175,752
; CURRENT FILING DATE: 2002-06-19
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420
; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-752-420

Query Match 61.1%; Score 33; DB 9; Length 736;
Best Local Similarity 70.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
| | | | |
Db 331 EPVVYGM DY 340

RESULT 25

US-10-176-482-420
; Sequence 420, Application US/10176482
; Publication No. US20030022296A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C70
; CURRENT APPLICATION NUMBER: US/10/176,482
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 420

; LENGTH: 736
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-482-420

Query Match 61.1%; Score 33; DB 9; Length 736;
Best Local Similarity 70.0%; Pred. No. 2.6e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
| | | | |
Db 331 EPVVVYGM DY 340

Search completed: June 10, 2003, 14:35:43
Job time : 15.0714 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:31:15 ; Search time 11.2143 Seconds
(without alignments)
94.297 Million cell updates/sec

Title: US-09-909-164-12
Perfect score: 54
Sequence: 1 EEVVPXGMDYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query %	Match	Length	ID	Description
1	40	74.1	156	2	S54619	hypothetical prote
2	38	70.4	363	2	D69551	conserved hypothet
3	36	66.7	102	2	A42452	VI protein - tobac
4	36	66.7	341	2	S72649	sucrose-phosphate
5	36	66.7	348	2	S72650	sucrose-phosphate
6	36	66.7	460	2	G96764	unknown protein F2
7	36	66.7	1049	2	JC4783	sucrose-phosphate
8	36	66.7	1068	1	JQ1329	sucrose-phosphate
9	36	66.7	1081	2	T09837	sucrose-phosphate
10	36	66.7	1083	2	T04062	sucrose-phosphate
11	36	66.7	1084	2	T04103	sucrose-phosphate
12	35	64.8	425	2	T24111	hypothetical prote
13	35	64.8	433	2	H87660	peptidoglycan-bind
14	35	64.8	440	2	H72784	probable alkaline
15	35	64.8	1150	2	T20173	hypothetical prote
16	35	64.8	1474	2	F69009	probable membrane
17	35	64.8	2747	2	B49132	fat facets (faf) s
18	34	63.0	99	2	S00210	plastoquinone b - L
19	34	63.0	155	2	S38255	plastoquinone b pre
20	34	63.0	168	2	S58208	plastoquinone b
21	34	63.0	290	2	D98182	6-O-methylguanine-D
22	34	63.0	290	2	AG3104	6-O-methylguanine-
23	34	63.0	296	2	F72745	hypothetical prote
24	34	63.0	357	1	G69290	probable hexosyltr
25	34	63.0	366	2	G69350	L-lactate dehydrog
26	34	63.0	565	2	E86665	ABC transporter AT
27	34	63.0	566	2	A70164	phenylalanine-tRNA
28	34	63.0	587	2	F81138	succinate dehydrog
29	34	63.0	906	2	T48898	disease resistance

ALIGNMENTS

RESULT 1

S54619
hypothetical protein YOR013w - yeast (Saccharomycetes cerevisiae)
N:Alternate names: hypothetical protein O2612; hypothetical protein YOL303.3
C:Species: Saccharomycetes cerevisiae
C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
C:Accession: S54619; S66879
R:de Haan, M.; Maarse, A.C.; Grivell, L.A.
A:Reference number: S54617
A:Accession: S54619
A:Molecule type: DNA
A:Residues: 1-156 <DEH>
A:Cross-references: EMBL:X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123
R:de Haan, M.; Grivell, L.A.; Maarse, A.C.
A:Reference number: S66877
A:Accession: S66879
A:Molecule type: DNA
A:Residues: 1-156 <DEH>
A:Cross-references: EMBL:Z74920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:
A:Experimental source: strain S288C

30	34	63.0	908	2	T48899	disease resistance
31	34	63.0	1062	2	F83335	RND multidrug effl
32	34	63.0	1062	2	T30830	hypothetical prote
33	34	63.0	3472	2	T31308	hypothetical 367K
34	33	61.1	97	2	A94427	partial transposas
35	33	61.1	128	2	A90471	hypothetical prote
36	33	61.1	172	2	S27021	fibroblast growth
37	33	61.1	184	2	E90335	hypothetical prote
38	33	61.1	225	2	S57810	hypothetical prote
39	33	61.1	247	2	A66001	conserved hypothet
40	33	61.1	257	2	A96546	unknown protein [1
41	33	61.1	262	2	F90298	transposase ISC105
42	33	61.1	267	2	C90307	transposase ISC105
43	33	61.1	276	2	C64417	hypothetical prote
44	33	61.1	283	2	G83055	pantoate-beta-alan
45	33	61.1	299	2	E90487	transposase ISC105
46	33	61.1	299	2	H90352	transposase ISC105
47	33	61.1	307	2	F84330	hypothetical prote
48	33	61.1	394	2	F82491	hypothetical prote
49	33	61.1	421	1	DETCM	acyl-CoA dehydrog
50	33	61.1	670	2	S22293	zinc finger protei
51	33	61.1	797	2	S38579	fibroblast growth
52	33	61.1	800	1	TVH02F	fibroblast growth
53	33	61.1	800	2	A48991	heparin-binding gr
54	33	61.1	801	2	I53363	fibroblast growth
55	33	61.1	806	2	A35963	protein-tyrosine k
56	33	61.1	840	2	AG0526	penicillin-binding
57	33	61.1	840	2	T39116	probable sulfate p
58	33	61.1	846	2	S57580	penicillin-binding
59	33	61.1	877	2	T40413	sulfate permease -
60	33	61.1	982	1	VCLJLK	hypothetical prote
61	33	61.1	1064	2	F86182	env polyprotein -
62	33	61.1	1401	2	G82336	DNA-directed RNA p
63	33	61.1	2717	2	A34203	DNA-binding protei
64	33	61.1	2831	2	T31419	cyclic beta 1-2 gl
65	33	61.1	2867	2	AG3481	cellobiose-phospho
66	33	61.1	472	1	B53236	transcription fact
67	32	59.3	97	2	JW0011	thiol peroxidases
68	32	59.3	165	2	AG1272	thiol peroxidases
69	32	59.3	165	2	AH1635	transcription fact
70	32	59.3	175	2	S36749	transcription fact
71	32	59.3	180	2	AG0504	transcription fact
72	32	59.3	231	1	I5ECP4	L-ribulose-phosph
73	32	59.3	231	2	A90637	L-ribulose-5-phosp
74	32	59.3	231	2	A85488	L-ribulose-5-phosp
75	32	59.3	231	2	AB0515	L-ribulose-5-phosp

C:Genetics:
 A:Cross-references: SGD:S0005539
 A:Map position: 15R
 C:Superfamily: hypothetical protein YOR013W

Query Match 74.1%; Score 40; DB 2; Length 156;
 Best Local Similarity 77.8%; Pred. No. 1;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EVVPXGMDY 10
 ||:| ||||
 Db 50 EVMPGLGMDY 58

RESULT 2

D69551
 conserved hypothetical protein AF2411 - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C:Accession: D69551
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
 A:Reference number: A69250; MUID:98049343; PMID:9389475
 A:Accession: D69551
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-363 <KLE>
 A:Cross-references: GB:AE001109; GB:AE000782; NID:g2689432; PIDN:AAB91255.1; PID:g265068

Query Match 70.4%; Score 38; DB 2; Length 363;
 Best Local Similarity 54.5%; Pred. No. 6.8;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
 | : || | : | : |
 Db 120 ENIVPXGIDFS 130

RESULT 3

A42452
 V1 protein - tobacco yellow dwarf virus (strain Australia)
 C:Species: tobacco yellow dwarf virus
 C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
 C:Accession: A42452
 R:Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
 Virology 187, 633-642, 1992
 A:Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yell
 A:Reference number: A42452; MUID:92188538; PMID:1546458
 A:Accession: A42452
 A:Molecule type: DNA
 A:Residues: 1-102 <MOR>
 A:Cross-references: GB:M81103; NID:g335283; PIDN:AAA7947.1; PID:g335284

Query Match 66.7%; Score 36; DB 2; Length 102;
 Best Local Similarity 60.0%; Pred. No. 4.2;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EVVPXGMDYS 11
 : ||| | : ||
 Db 7 QVVPGGINIS 16

RESULT 4

S72649
 sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Citrus unshiu (fragment)
 C:Species: Citrus unshiu
 C:Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
 C:Accession: S72649

R:Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
 Mol. Gen. Genet. 252, 346-351, 1996
 A:Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate sy
 A:Reference number: S72648; MUID:96439842; PMID:8842155
 A:Accession: S72649
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-341 <KOM>
 A:Cross-references: EMBL:AB006319; NID:g2588891; PIDN:BAA23215.1; PID:g2588892
 A:Experimental source: fruit, cv. Miyagawa-Wase
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
 C:Genetics:
 A:Gene: SPS2
 C:Function:

A:Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fruc
 A:Pathway: sucrose biosynthesis
 C:Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homolo
 C:Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
 F:1-341/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>

Query Match 66.7%; Score 36; DB 2; Length 341;
 Best Local Similarity 66.7%; Pred. No. 16;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
 | : | | | : |
 Db 228 VIPPGMDFS 236

RESULT 5

S72650
 sucrose-phosphate synthase (EC 2.4.1.14) isoform 3 - Citrus unshiu (fragment)
 C:Species: Citrus unshiu
 C:Date: 24-Oct-1998 #sequence_revision 24-Oct-1998 #text_change 21-Jul-2000
 C:Accession: S72650
 R:Komatsu, A.; Takanokura, Y.; Omura, M.; Akihama, T.
 Mol. Gen. Genet. 252, 346-351, 1996
 A:Title: Cloning and molecular analysis of cDNAs encoding three sucrose phosphate sy
 A:Reference number: S72648; MUID:96439842; PMID:8842155
 A:Accession: S72650
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-348 <KOM>
 A:Cross-references: EMBL:AB006660; NID:g2351059; PIDN:BAA22071.1; PID:g2351060
 A:Experimental source: fruit, cv. Miyagawa-Wase
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1997
 C:Genetics:
 A:Gene: SPS3
 C:Function:

A:Description: catalyzes formation of sucrose-6-phosphate from UDPglucose and D-fruc
 A:Pathway: sucrose biosynthesis
 C:Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homolo
 C:Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
 F:1-348/Domain: sucrose/sucrose-phosphate synthase homology (fragment) <SSPS>

Query Match 66.7%; Score 36; DB 2; Length 348;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
 | : | | | : |
 Db 234 VIPPGMDFS 242

RESULT 6

G96764
 unknown protein F25P22.17 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: G96764
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 ansen, N.F.; Hughes, B.; Huizlar, L.

Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khavkin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: G96764
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-460 <STO>
A:Cross-references: GB:AE0051173; NID:g6692750; PIDN:AAF24856.1; GSPDB:GN00141
C:Genetics:
A:Gene: F25P22.17
A:Map position: 1

Query Match 66.7%; Score 36; DB 2; Length 460;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
|| || |||
Db 218 EEDVPSAMDY 227

RESULT 7
JC4783
sucrose-phosphate synthase (EC 2.4.1.14) - rice
C:Species: Oryza sativa (rice)
C:Date: 10-May-1996 #sequence_revision 16-Aug-1996 #text_change 18-Jun-1999
C:Accession: JC4783
R:Valdez-Alarcon, J.J.; Ferrando, M.; Salerno, G.; Jimenez-Moralla, B.; Herrera-Estrella
Gene 170, 217-222, 1996
A:Title: Characterization of a rice sucrose-phosphate synthase-encoding gene.
A:Reference number: JC4783; MUID:96235138; PMID:8666248
A:Accession: JC4783
A:Molecule type: mRNA
A:Residues: 1-1049 <VAL>
A:Cross-references: GB:U33175; NID:g1449931; PIDN:AAC49379.1; PID:g988270
A:Note: UDPglucose-fructose-phosphate glucosyltransferase; Sucrosephosphate-UDPglucosyl
C:Comment: This enzyme catalyzes the formation of sucrose-phosphate form UDP-glucose and
C:Genetics:
A:Gene: Sps1
A:Introns: 24/1; 103/3; 183/3; 205/3; 435/3; 475/3; 519/3; 578/3; 596/3; 617/3; 931/3; 9
A:Function:
A:Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D-fruc
C:Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homology
C:Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F:180-663/Domain: sucrose/sucrose-phosphate synthase homology <SSFS>

Query Match 66.7%; Score 36; DB 2; Length 1049;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
|| || |||
Db 436 VIPPGMDFS 444

RESULT 8
JQ1329
sucrose-phosphate synthase (EC 2.4.1.14) - maize
C:Species: Zea mays (maize)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JQ1329; PQ0260
R:Worrell, A.C.; Bruneau, J.M.; Summerfelt, K.; Boersig, M.; Voelker, T.A.
Plant Cell 3, 1121-1130, 1991
A:Title: Expression of a maize sucrose phosphate synthase in tomato alters leaf carbohyd
A:Reference number: JQ1329; MUID:92338837; PMID:1840396
A:Accession: JQ1329
A:Molecule type: mRNA

A:Residues: 1-1068 <WOR>
A:Cross-references: GB:M97550; NID:g168625; PIDN:AAA33513.1; PID:g168626
A:Accession: PQ0260
A:Molecule type: protein
A:Residues: 71-74; 206-212; 471-481; 872-892 <WOR1>
C:Comment: This enzyme transfers the glucosyl group from UDPglucose to fructose-6-p
C:Function:
A:Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D
A:Pathway: sucrose biosynthesis
C:Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homol
C:Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F:178-666/Domain: sucrose/sucrose-phosphate synthase homology <SSFS>

Query Match 66.7%; Score 36; DB 1; Length 1068;
Best Local Similarity 66.7%; Pred. No. 59;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
|| || |||
Db 435 VIPPGMDFS 443

RESULT 9
T09837
sucrose-phosphate synthase (EC 2.4.1.14) isoform 2 - Craterostigma plantagineum
C:Species: Craterostigma plantagineum
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T09837
R:Ingram, J.; Chandler, J.W.; Gallagher, L.; Salamini, F.; Bartels, D.
Plant Physiol. 115, 113-121, 1997
A:Title: Analysis of cDNA clones encoding sucrose-phosphate synthase in relation to
A:Reference number: Z18874; MUID:97451773; PMID:9306694
A:Accession: T09837
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1081 <ING>
A:Cross-references: EMBL:Y11795; NID:g2190349; PIDN:CAA72491.1; PID:g2190350
A:Experimental source: ABA-treated callus
C:Genetics:
A:Gene: sps2
C:Function:
A:Description: catalyzes the formation of sucrose-6-phosphate from UDPglucose and D
C:Superfamily: sucrose-phosphate synthase; sucrose/sucrose-phosphate synthase homol
C:Keywords: glycosyltransferase; hexosyltransferase; sucrose biosynthesis
F:176-674/Domain: sucrose/sucrose-phosphate synthase homology <SSFS>

Query Match 66.7%; Score 36; DB 2; Length 1081;
Best Local Similarity 66.7%; Pred. No. 60;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
|| || |||
Db 445 VIPPGMDFS 453

RESULT 10
T04062
sucrose-phosphate synthase homolog F28M11.40 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 16-Jul-1999
C:Accession: T04062
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer
submitted to the Protein Sequence Database, March 1999
A:Reference number: Z15184
A:Accession: T04062
A:Molecule type: DNA
A:Residues: 1-1083 <BEV>
A:Cross-references: EMBL:AL049487
A:Experimental source: cultivar Columbia; BAC clone F28M11
C:Genetics:
A:Map position: 4

100

A:Molecule type: DNA
 A:Residues: 1-1150 <WIL>
 A:Cross-references: EMBL:281486; PIDN:CAB03994.1; GSPDB:GN00023; CESP:C53A5.2
 A:Experimental source: clone C53A5
 R:Matthews, L.
 submitted to the EMBL Data Library, August 1996
 A:Reference number: Z19808
 A:Accession: T23857
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1150 <WIL>
 A:Cross-references: EMBL:278015; PIDN:CAB01437.1; GSPDB:GN00023; CESP:C53A5.2
 A:Experimental source: clone R02D5
 C:Genetics:
 A:Gene: CESP:C53A5.2
 A:Map position: 5
 A:Introns: 33/3; 63/3; 132/3; 169/3; 221/3; 299/3; 379/2; 423/2; 438/2; 471/1; 513/2; 65

Query Match 64.8%; Score 35; DB 2; Length 1150;
 Best Local Similarity 66.7%; Pred. No. 1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
 I: I: I: I: I:
 Db 562 VLPVGIDYS 570

RESULT 16
 F69009
 probable membrane protein MTH1074 - Methanobacterium thermoautotrophicum (strain Delta H
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C:Accession: F69009
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
 ; Glu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiawani, N.
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
 A:Reference number: A69000; MUID:98037514; PMID:9371463
 A:Accession: F69009
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1474 <MTH>
 A:Cross-references: GB:AE000878; GB:AF000666; NID:32622171; PIDN:AAB85563.1; PID:3262217
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH1074
 C:Keywords: duplication

Query Match 64.8%; Score 35; DB 2; Length 1474;
 Best Local Similarity 55.6%; Pred. No. 1.4e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EVVPXGMDY 10
 I: I: I: I: I:
 Db 1238 DVLPAGLDY 1246

RESULT 17
 B49132
 fat facets (faf) splice form 1 - fruit fly (Drosophila melanogaster)
 C:Species: Drosophila melanogaster
 C:Date: 19-Dec-1993 #sequence_revision 25-Apr-1997 #text_change 01-Dec-2000
 C:Accession: B49132; A49132
 R:Fischer-Vize, J.A.; Rubin, G.M.; Lehmann, R.
 Development 116, 985-1000, 1992
 A:Title: The fat facets gene is required for Drosophila eye and embryo development.
 A:Reference number: A49132; MUID:93202020; PMID:1295747
 A:Contents: isogenic st
 A:Accession: B49132
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-2747 <FIS>

A:Cross-references: GB:L04959; NID:gl57411; PIDN:AAF01345.1; PID:g6013474
 A:Note: sequence inconsistent with the nucleotide translation
 A:Note: sequence extracted from NCBI backbone (NCBIN:127836, NCBIN:129008, NCBIP:12
 A:Accession: A49132
 A>Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-2704, 'VT', '2707', 'ANNV' <FI2>
 A:Cross-references: GB:L04958; NID:gl57410; PIDN:AAF01346.1; PID:g6013475
 A:Note: sequence extracted from NCBI backbone (NCBIN:127836, NCBIN:129008, NCBIP:12
 C:Keywords: alternative splicing

Query Match 64.8%; Score 35; DB 2; Length 2747;
 Best Local Similarity 54.5%; Pred. No. 2.7e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
 I: I: I: I: I:
 Db 1394 EVIVPDGODFS 1404

RESULT 18
 S00210
 plastocyanin b - Lombardy poplar
 C:Species: Populus nigra var. italica (Lombardy poplar)
 C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 20-Apr-2000
 C:Accession: S00210
 R:Dimitrov, M.I.; Egorov, C.A.; Donchev, A.A.; Atanasov, B.P.
 FEBS Lett. 226, 17-22, 1987
 A:Title: Complete amino acid sequence of poplar plastocyanin b.
 A:Reference number: S00210
 A:Accession: S00210
 A:Molecule type: protein
 A:Residues: 1-99 <DIM>
 C:Superfamily: plastocyanin
 C:Keywords: chloroplast; copper; electron transfer; metalloprotein
 F:37.84,87,92/Binding site: copper (His, Cys, His, Met) (type 1) #status predicted

Query Match 63.0%; Score 34; DB 2; Length 99;
 Best Local Similarity 54.5%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
 I: I: I: I: I:
 Db 43 EDAPVSGVDYS 53

RESULT 19
 S38255
 plastocyanin precursor - barley
 C:Species: Hordeum vulgare (barley)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jun-1999
 C:Accession: S38255; S00206
 R:Nielsen, P.S.; Gausing, K.
 Eur. J. Biochem. 217, 97-104, 1993
 A:Title: In vitro binding of nuclear proteins to the barley plastocyanin gene prom
 A:Reference number: S38255; MUID:94039081; PMID:8223592
 A:Accession: S38255
 A:Molecule type: DNA
 A:Residues: 1-155 <NIE1>
 A:Cross-references: EMBL:228347; NID:g431919; PIDN:CAA82201.1; PID:g431920
 A:Experimental source: strain NK 1558
 R:Nielsen, P.S.; Gausing, K.
 FEBS Lett. 225, 159-162, 1987
 A:Title: The precursor of barley plastocyanin: sequence of cDNA clones and gene exp

Query Match 63.0%; Score 34; DB 2; Length 99;
 Best Local Similarity 54.5%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
 I: I: I: I: I:
 Db 43 EDAPVSGVDYS 53

RESULT 19
 S38255
 plastocyanin precursor - barley
 C:Species: Hordeum vulgare (barley)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 11-Jun-1999
 C:Accession: S38255; S00206
 R:Nielsen, P.S.; Gausing, K.
 Eur. J. Biochem. 217, 97-104, 1993
 A:Title: In vitro binding of nuclear proteins to the barley plastocyanin gene prom
 A:Reference number: S38255; MUID:94039081; PMID:8223592
 A:Accession: S38255
 A:Molecule type: DNA
 A:Residues: 1-155 <NIE1>
 A:Cross-references: EMBL:228347; NID:g431919; PIDN:CAA82201.1; PID:g431920
 A:Experimental source: strain NK 1558
 R:Nielsen, P.S.; Gausing, K.
 FEBS Lett. 225, 159-162, 1987
 A:Title: The precursor of barley plastocyanin: sequence of cDNA clones and gene exp
 A:Reference number: S00206
 A:Accession: S00206
 A:Molecule type: mRNA
 A:Residues: 1-119, 'T', 121-155 <NIE2>
 A:Cross-references: EMBL:Y00704; NID:g22704
 A:Note: not compared to nucleotide translation
 C:Genetics:
 A:Genome: nuclear

C;Function: mediates the transfer of electrons from cytochrome b6/f to photosystem I
C;Superfamily: plastocyanin
C;Keywords: chloroplast; copper; electron transfer; metalloprotein
F;1-58/Domain: transit peptide (chloroplast) #status predicted <NP>
F;59-155/Product: plastocyanin #status predicted <MAR>
F;95,140,143,148/Binding site: copper (His, Cys, His, Met) (type 1) #status predicted

Query Match 63.0%; Score 34; DB 2; Length 155;
Best Local Similarity 54.5%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
| : | | | | |
Db 101 EDAVPSGVDYS 111

RESULT 20
S58208
Plastocyanin b precursor - black poplar
C;Species: Populus nigra (black poplar)
C;Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 05-May-2000
C;Accession: S58208
R;Reichert, J.; Jenzelewski, V.; Haehnel, W.
submitted to the EMBL Data Library, July 1995

A;Description: Kinetic studies of recombinant poplar plastocyanins.
A;Reference number: S58208
A;Accession: S58208
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-168 <PEL>
A;Cross-references: EMBL:Z50186; NID:929814; PIDN:CAA90565.1; PID:929815
C;Superfamily: plastocyanin
C;Keywords: copper; electron transfer; metalloprotein
F;106,153,156,161/Binding site: copper (His, Cys, His, Met) (type 1) #status predicted

Query Match 63.0%; Score 34; DB 2; Length 168;
Best Local Similarity 54.5%; Pred. No. 19;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
| : | | | | |
Db 112 EDAVPSGVDYS 122

RESULT 21
D98182
O6-methylguanine-DNA methyltransferase PA2118 [imported] - Agrobacterium tumefaciens (st
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C;Accession: D98182
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; PMID:11743194
A;Accession: D98182
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-290 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK88982.1; PID:915158766; GSPDB:GN00170
C;Genetics:
A;Gene: AGR_L_818
A;Map position: linear chromosome

Query Match 63.0%; Score 34; DB 2; Length 290;
Best Local Similarity 50.0%; Pred. No. 35;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
| : | | | | |
Db 9 EDITPTGSDY 18

RESULT 22

AG3104

6-O-methylguanine-DNA methyltransferase [imported] - Agrobacterium tumefaciens (str
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AG3104
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; W
; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; Mc
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Ka
ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58
A;Reference number: AB2577; PMID:11743193

A;Accession: AG3104

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-290 <KUR>

A;Cross-references: GB:AE008689; PIDN:AAL45253.1; PID:917742937; GSPDB:GN00187

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: ada

A;Map position: linear chromosome

Query Match 63.0%; Score 34; DB 2; Length 290;

Best Local Similarity 50.0%; Pred. No. 35;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10

| : | | | | |

Db 9 EDITPTGSDY 18

RESULT 23

F72745

hypothetical protein APE0493 - Aeropyrum pernix (strain K1)

C;Species: Aeropyrum pernix

C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jun-2000

C;Accession: F72745

R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; T
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.
DNA Res. 6, 83-101, 1999

A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aer
A;Reference number: A72450; MUID:99310339; PMID:10382966

A;Accession: F72745

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-296 <KAW>

A;Cross-references: DDBJ:AP000059; NID:95103911; PIDN:BAA79458.1; PID:91043244; PID:
A;Experimental source: strain K1

C;Genetics:

A;Gene: APE0493

C;Superfamily: Aeropyrum pernix hypothetical protein APE0493

Query Match 63.0%; Score 34; DB 2; Length 296;

Best Local Similarity 50.0%; Pred. No. 36;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVVPXGMDYS 11

| : | | | | |

Db 3 ETLPGGLDYT 12

RESULT 24

G69290

probable hexosyltransferase (EC 2.4.1.-) AF0327 [similarity] - Archaeoglobus fulgidu
C;Species: Archaeoglobus fulgidus

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000

C;Accession: G69290

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; DO
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness,
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997
 A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: G69290

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-357 <KLE>

A;Cross-references: GB:AE001082; GB:AE000782; NID:g2689405; PIDN:AAB90909.1; PID:g265031

C;Superfamily: probable hexosyltransferase ycxN

C;Keywords: glycosyltransferase; hexosyltransferase

Query Match 63.0%; Score 34; DB 1; Length 357;

Best Local Similarity 55.6%; Pred. No. 44;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EVVPXGMDY 10

Db 170 EVIPNGIDF 178

RESULT 25

G69350

L-lactate dehydrogenase, cytochrome-type (lldD) homolog - Archaeoglobus fulgidus

C;Species: Archaeoglobus fulgidus

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 17-Mar-2000

C;Accession: G69350

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: G69350

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-366 <KLE>

A;Cross-references: GB:AE001049; GB:AE000782; NID:g2689372; PIDN:AAB90435.1; PID:g264980

C;Superfamily: (S)-2-hydroxy-acid oxidase; (S)-2-hydroxy-acid oxidase homology

Query Match 63.0%; Score 34; DB 2; Length 366;

Best Local Similarity 66.7%; Pred. No. 46;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGMD 9

Db 289 EKVVTGVD 297

Search completed: June 10, 2003, 13:49:14

Job time : 11.2143 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2003, 13:25:04 ; Search time 4.5 Seconds
(without alignments)
101.387 Million cell updates/sec

Title: US-09-909-164-12
Perfect score: 54
Sequence: 1 BEVVPXGMDYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	70.4	1058	1 CARB_FUSNN	Q8rg86 fusobacteri
2	36	66.7	102	1 Y1LK_TVDVA	P31619 tobacco yel
3	36	66.7	1049	1 SPS_ORYSA	Q43802 oryza sativ
4	36	66.7	1068	1 SPS_MAIZE	P31927 zea mays (m
5	36	66.7	1081	1 SPS2_CRAPL	Q04933 craterostig
6	35	64.8	2747	1 FAF_DROME	P55824 drosophila
7	34.5	63.9	748	1 KHLI_HUMAN	Q9nr64 homo sapien
8	34	63.0	154	1 PLAS_ORYSA	P20423 oryza sativ
9	34	63.0	155	1 PLAS_HORVU	P08248 hordeum vul
10	34	63.0	168	1 PLAT_POPNI	P11970 populus nig
11	34	63.0	566	1 SYEB_BORBU	P94283 borrelia bu
12	33	61.1	276	1 Y939_METJA	Q58349 methanococc
13	33	61.1	283	1 PANC_PSAE	Q9hv69 pseudomonas
14	33	61.1	394	1 HMPA_VIBCH	P08503 vibrio chol
15	33	61.1	421	1 ECDM_RAT	P08503 rattus norv
16	33	61.1	421	1 ECDM_RAT	Q52250 halomonas e
17	33	61.1	423	1 ECDM_RAT	Q52250 halomonas e
18	33	61.1	787	1 ECE2_HUMAN	O60344 homo sapien
19	33	61.1	801	1 FGR3_MOUSE	Q61851 mus musculu
20	33	61.1	806	1 CEK2_CHICK	P18460 gallus gall
21	33	61.1	877	1 SULH_SCHPO	O74377 schizosacch
22	33	61.1	982	1 ENV_SFV3L	P27399 simian foam
23	33	61.1	1401	1 RPOC_VIBCH	Q9kv29 vibrio chol
24	33	61.1	2717	1 ZEPI_HUMAN	P15822 homo sapien
25	32.5	60.2	472	1 ET2A_XENLA	P19102 xenopus lae
26	32	59.3	97	1 PLAS_DAUCA	P20422 daucus caro
27	32	59.3	175	1 HES3_RAT	Q04667 rattus norv
28	32	59.3	231	1 ARAD_ECOLI	P08203 escherichia
29	32	59.3	231	1 ARAD_SALTY	P06190 salmonella
30	32	59.3	233	1 HIS9_THEMA	Q9wzrl thermotoga
31	32	59.3	288	1 CGD2_RAT	Q04627 rattus norv
32	32	59.3	289	1 CGD2_HUMAN	P30279 homo sapien
33	32	59.3	289	1 CGD2_MOUSE	P30280 mus musculu

34	32	59.3	291	1 CGD1_BRARE	Q90459 brachydanio
35	32	59.3	291	1 CGD1_XENLA	P50755 xenopus lae
36	32	59.3	291	1 CGD2_CHICK	P49706 gallus gall
37	32	59.3	291	1 CGD2_XENLA	P53782 xenopus lae
38	32	59.3	292	1 CGD1_CHICK	P55169 gallus gall
39	32	59.3	292	1 CGD3_HUMAN	P30281 homo sapien
40	32	59.3	295	1 CGD1_HUMAN	P24385 homo sapien
41	32	59.3	295	1 CGD1_MOUSE	P25322 mus musculu
42	32	59.3	295	1 CGD1_RAT	P39948 rattus norv
43	32	59.3	338	1 MTBA_METBA	O30640 methanosarc
44	32	59.3	472	1 ET2B_XENLA	Q91712 xenopus lae
45	32	59.3	561	1 HNFB_XENLA	Q91910 xenopus lae
46	32	59.3	759	1 SCTL_YEAST	P32784 saccharomyc
47	32	59.3	866	1 RECE_ECOLI	P15032 escherichia
48	32	59.3	995	1 HPI1_HUMAN	O00291 homo sapien
49	32	59.3	1176	1 NIR_NEUCR	P38661 neurospora
50	32	59.3	1258	1 ACNI_MOUSE	Q61137 mus musculu
51	32	59.3	1394	1 LTBS_HUMAN	P22084 homo sapien
52	32	59.3	1498	1 Y1A9_CLOAB	Q04351 clostridium
53	32	59.3	1595	1 Y1BL_HUMAN	Q14766 homo sapien
54	32	59.3	1712	1 LTBL_RAT	Q00918 rattus norv
55	32	59.3	3174	1 CHAC_HUMAN	Q96r17 homo sapien
56	31	57.4	98	1 PLAS_ENTPR	P07485 enteromorph
57	31	57.4	98	1 PLAS_ULVPE	P13133 ulva arasak
58	31	57.4	99	1 PLAS_TOBAC	P56274 ulva pertus
59	31	57.4	99	1 PLAS_TOBAC	P00298 rumex obtus
60	31	57.4	99	1 PLAS_TOBAC	P23476 nicotiana t
61	31	57.4	124	1 REV_SIVCZ	P17280 chimpanzee
62	31	57.4	175	1 HES3_MOUSE	Q61657 mus musculu
63	31	57.4	258	1 YC10_METJA	Q58607 methanococc
64	31	57.4	319	1 YHAI_CRYPA	P10941 cryphonectr
65	31	57.4	327	1 YK14_CAEEL	P34338 caenorhabdi
66	31	57.4	338	1 MTBA_METAC	P58869 methanosarc
67	31	57.4	346	1 HYPE_BRAJA	P31906 bradyrhizob
68	31	57.4	391	1 LEII_METTH	O27667 methanobact
69	31	57.4	427	1 TOLB_HAEIN	P44677 haemophilus
70	31	57.4	469	1 LET1_KLULA	P53998 kluyveromyc
71	31	57.4	529	1 ENP3_HUMAN	O75355 homo sapien
72	31	57.4	529	1 GUAA_MYLE	P46810 mycobacteri
73	31	57.4	625	1 GIDA_STAMM	Q99qt4 staphylococ
74	31	57.4	692	1 DNK1_SYNY3	Q55154 synechocyst
75	31	57.4	788	1 CY14_NEUCR	P32622 neurospora

ALIGNMENTS

RESULT 1

CARB_FUSNN	STANDARD;	PRT;	1058 AA.
AC	Q8RG86:		
DT	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).		
GN	CARB OR FN0422.		
OS	Fusobacterium nucleatum (subsp. nucleatum).		
OC	Bacteria; Fusobacteria; Fusobacterium.		
OX	NCBI_TaxID=76856;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-ATCC 25586;		
RX	MEDLINE-21986394; PubMed-11889109;		
RA	Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasileva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.;		
RT	Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586.;		
RL	J. Bacteriol. 184:2005-2018(2002).		
CC	- - CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +		

phosphate + L-glutamate + carbamoyl phosphate.
 -1- COFACTOR: Binds three manganese ions (By similarity).
 -1- PATHWAY: Arginine biosynthesis.
 -1- SUBUNIT: Pyrimidine biosynthesis; first step.
 -1- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).
 -1- SIMILARITY: BELONGS TO THE CARB FAMILY.

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EMBL: AE010554; AAL94625.1; ALT_INIT.
 InterPro: IPR005483; CPase_L.
 InterPro: IPR005479; CPase_L_D2.
 InterPro: IPR005480; CPase_L_D3.
 InterPro: IPR005481; CPase_L_N.
 InterPro: IPR004362; MGS_Like.
 Pfam: PF00289; CPase_L_chain; 2.
 Pfam: PF02786; CPase_L_D2; 2.
 Pfam: PF02787; CPase_L_D3; 1.
 Pfam: PF02142; MGS; 1.
 PRINTS: PR00098; CPASE.
 PROSITE: PS00866; CPASE_1; 2.
 PROSITE: PS00867; CPASE_2; 2.
 Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
 ATP-binding; Manganese; Complete proteome.
 FT DOMAIN 1 401
 FT DOMAIN 402 546
 FT DOMAIN 547 929
 FT DOMAIN 930 1058
 FT REPEAT 1 546
 FT REPEAT 547 1058
 FT NP_BIND 153 210
 FT NP_BIND 302 352
 FT METAL 284 284
 FT METAL 298 298
 FT METAL 300 300
 FT METAL 820 820
 FT METAL 832 832
 SEQUENCE 1058 AA; 117451 MW; ED7037AF77C1E39F CRC64;

Query Match 70.4%; Score 38; DB 1; Length 1058;
 Best Local Similarity 60.0%; Pred. No. 7.8;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EVVFXGMDYS 11
 :||| :|||
 Db 190 EIVPGLNYS 199

RESULT 2
 Y1LK_TYDVA STANDARD; PRT; 102 AA.
 AC P31619;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE Hypothetical 11.2 kDa protein.
 GN V1.
 OS Tobacco yellow dwarf virus (strain Australia) (TYDV).
 OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
 OX NCBI_TaxID=31599;
 [1]
 RN
 RP
 RX MEDLINE=92188538; PubMed=1546458;
 RA Morris B.A.M., Richardson K.A., Hailey A., Zhan X., Thomas J.E.;

 The nucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants.";
 Virology 187:633-642(1992).

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EMBL: M811103; AAA47947.1; -.
 PIR: A42452; A42452.
 InterPro: IPR002621; Gemini_mov.
 Pfam: PF01708; Gemini_mov; 1.
 Hypothetical protein.
 KW
 SQ SEQUENCE 102 AA; 11178 MW; A40ECF1E0AF5B67 CRC64;

Query Match 66.7%; Score 36; DB 1; Length 102;
 Best Local Similarity 60.0%; Pred. No. 1.7;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EVVFXGMDYS 11
 :||| :|||
 Db 7 QVPSGINYS 16

RESULT 3
 SPS_ORYSA STANDARD; PRT; 1049 AA.
 AC Q43802;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Sucrose-phosphate synthase (EC 2.4.1.14)
 DE (UDP-glucose-fructose-phosphate glucosyltransferase).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 [1]
 RN
 RP
 RX STRAIN=cv. Indica-IR36; TISSUE=Leaf;
 MEDLINE=96235138; PubMed=8666248;
 RA Valdez-Alarcon J.J., Ferrando M., Jimenez-Moralla B.,
 Herrera-Estrella L.;
 RT "Characterization of a rice sucrose-phosphate synthase-encoding gene.";
 RL Gene 170:217-222(1996).
 CC -1- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND THEREFORE PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF PHOTOASSIMILATES OUT OF THE LEAF.
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate -> UDP + sucrose 6-phosphate.
 CC -1- ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.
 CC -1- PATHWAY: Sucrose synthesis.
 CC -1- SUBUNIT: HOMODIMER OR HOMOTETRAMER (BY SIMILARITY).
 CC -1- PFM: PHOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR ENZYME FUNCTION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.

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CC -----
DR EMBL: U33175; AAC49379.1;
DR InterPro: IPR001296; Glycos_transf_1.
DR Pfam: PF00534; Glycosyltransferase; Phosphorylation.
KW Transferase; Glycosyltransferase; POLY-GLY.
FT DOMAIN 22 29 POLY-GLY.
FT DOMAIN 695 698 POLY-GLU.
FT DOMAIN 775 779 POLY-ARG.
SQ SEQUENCE 1049 AA; 116455 MW; ED862E2819AA4B04 CRC64;

Query Match 66.7%; Score 36; DB 1; Length 1049;
Best Local Similarity 66.7%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
Db 436 VIPPGMDFS 444
|:|:|:|:|

RESULT 4
SPS_MAIZE STANDARD; PRT; 1068 AA.
ID SPS_MAIZE STANDARD; PRT; 1068 AA.
AC F31927;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Sucrose-phosphate synthase (EC 2.4.1.14) (UDP-glucose-fructose-
phosphate glucosyltransferase).
GN SPS.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 71-74; 206-212; 471-481 AND
RP 872-892.
RX STRAIN=CV, PIONEER 3184; TISSUE=Leaf;
RX MEDLINE=92338837; PubMed=1840396;
RA Worrell A.C., Bruneau J.-M., Summerfelt K., Boersig M., Voelker T.A.;
RT "Expression of a maize sucrose phosphate synthase in tomato alters
leaf carbohydrate partitioning."
RL Plant Cell 3:1121-1130(1991).
CC -!- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN
THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND
THEREFORE PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF
PHOTOASSIMILATES OUT OF THE LEAF.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
sucrose 6-phosphate.
CC -!- ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND
MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.
CC -!- PATHWAY: Sucrose synthesis.
CC -!- SUBUNIT: HOMODIMER OR HOMOTETRAMER.
CC -!- DEVELOPMENTAL STAGE: GERMINATING SEEDS OR MATURE LEAVES.
CC -!- PTM: PHOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR
ENZYME FUNCTION.
CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
CC -----
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CC -----
DR EMBL: M97550; AAA33513.1;
DR DR PIR: JQ1329; JQ1329.
DR MaizeDB: 25294;
DR InterPro: IPR001296; Glycos_transf_1.
DR Pfam: PF00534; Glycosyltransferase; Phosphorylation.
KW Transferase; Glycosyltransferase; POLY-GLY.
FT DOMAIN 25 31 POLY-GLY.
SQ SEQUENCE 25 AA; 116455 MW; ED862E2819AA4B04 CRC64;

Query Match 66.7%; Score 36; DB 1; Length 1081;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
Db 445 VIPPGMDFS 453
|:|:|:|:|

RESULT 5
SPS2_CRAPL STANDARD; PRT; 1081 AA.
ID SPS2_CRAPL STANDARD; PRT; 1081 AA.
AC O04933;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Sucrose-phosphate synthase 2 (EC 2.4.1.14) (UDP-glucose-fructose-
phosphate glucosyltransferase 2).
GN SPS2.
OS Craterostigma plantagineum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Lamiales; Lamiales incertae sedis; Torenieae;
OC Craterostigma.
OX NCBI_TaxID=4153;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97451773; PubMed=9306694;
RA Ingram J., Chandler J.W., Gallagher L., Salamini F., Bartels D.;
RT "Analysis of cDNA clones encoding sucrose-phosphate synthase in
relation to sugar interconversions associated with dehydration in the
resurrection plant Craterostigma plantagineum Hochst."
RL Plant Physiol. 115:113-121(1997).
CC -!- FUNCTION: INVOLVED IN THE REGULATION OF CARBON PARTITIONING IN
THE LEAVES OF PLANTS. MAY REGULATE THE SYNTHESIS OF SUCROSE AND
THEREFORE PLAY A MAJOR ROLE AS A LIMITING FACTOR IN THE EXPORT OF
PHOTOASSIMILATES OUT OF THE LEAF.
CC -!- CATALYTIC ACTIVITY: UDP-glucose + D-fructose 6-phosphate = UDP +
sucrose 6-phosphate.
CC -!- ENZYME REGULATION: ACTIVITY REGULATED BY PHOSPHORYLATION AND
MODERATED BY CONCENTRATION OF METABOLITES AND LIGHT.
CC -!- PATHWAY: Sucrose synthesis.
CC -!- SUBUNIT: HOMODIMER OR HOMOTETRAMER (BY SIMILARITY).
CC -!- PTM: PHOSPHORYLATED. HOWEVER, PHOSPHORYLATION IS NOT ESSENTIAL FOR
ENZYME FUNCTION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 1.
CC -----
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RESULT 6
FAF_DROME STANDARD; PRT; 2747 AA.
AC P55824;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable ubiquitin carboxyl-terminal hydrolase FAF (EC 3.1.2.15)
DE (Ubiquitin thiolesterase FAF) (Ubiquitin-specific processing protease FAF) (Deubiquitinating enzyme FAF) (Fat facets protein).
GN FAF.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93202020; PubMed=1295747;
RA Fischer-Vize J.A., Rubin G.M., Lehmann R.;
RT "The fat facets gene is required for Drosophila eye and embryo development."
RL Development 116:985-1000(1992).
CC -!- FUNCTION: REQUIRED FOR EYE AND EMBRYO DEVELOPMENT, AND PLAYS A ROLE IN COMPOUND EYE ASSEMBLY AND OOGENESIS RESPECTIVELY. IN THE LARVAL EYE DISKS, CELLS OUTSIDE THE ASSEMBLING FACETS REQUIRE THIS PROTEIN FOR SHORT-RANGE CELL INTERACTIONS THAT PREVENT THE MYSTERY CELLS FROM BECOMING PHOTORECEPTORS. IT IS ALSO REQUIRED FOR NUCLEAR MIGRATION AND CELLULARIZATION IN EARLY EMBRYOGENESIS AND COULD PLAY A ROLE IN POLE CELL DETERMINATION, DEVELOPMENT OR FUNCTION.
CC -!- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O = ubiquitin + a thiol.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- TISSUE SPECIFICITY: EYE DISKS AND OVARIES.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C19.
CC
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CC
CC EMBL; L04959; AAF01345.1;
CC EMBL; L04958; AAF01346.1;
CC MEROPS; C19.007;
CC Flybase; FBgn0005632; faf.
CC InterPro; IPR001394; UCH-2.
CC Pfam; PF00442; UCH-1; 1.
CC Pfam; PF00443; UCH-2; 1.
CC PROSITE; PS00972; UCH_2.1; 1.
CC PROSITE; PS00973; UCH_2.2; 1.
CC PROSITE; PS00973; UCH_2.3; 1.
CC PROSITE; PS00973; UCH_2.3; 1.
KW Ubl conjugation pathway; Hydrolase; Thiol protease;
KW Developmental protein; Vision; Alternative splicing.
FT ACT_SITE 1677 1677 BY SIMILARITY.
FT ACT_SITE 1978 1978 BY SIMILARITY.
FT ACT_SITE 1986 1986 BY SIMILARITY.
FT VARSPPLIC 2705 2747 KCRVILKKLVESKDEEDATSAVTAATTEVTTSPATAS
FT VARIANT 2725 2725 S -> T.
FT ORQQL -> VTRANNV (IN SHORT ISOFORM).
SQ SEQUENCE 2747 AA; 307954 MW; 1D97659F7A7B2ADE CRC64;
Query Match 64.8%; Score 35; DB 1; Length 2747;
Best Local Similarity 54.5%; Pred. No. 91;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 ERWPKGMDYS 11

Db 1394 EVIVPDGQDFS 1404
RESULT 7
KHL1_HUMAN STANDARD; PRT; 748 AA.
ID KHL1_HUMAN
AC Q9NR64; Q9NR65; Q9P238; Q9H4X4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kelch-like protein 1.
DE Kelch-like protein 1.
GN KHL1 OR KIAA1490.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20347694; PubMed=10888605;
RA Koob M.D., Nemes J.P., Benzow K.A.;
RT "The SCA8 transcript is an antisense RNA to a brain-specific transcript encoding a novel actin-binding protein (KHL1).";
RL Hum. Mol. Genet. 9:1543-1551(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=20377482; PubMed=10819331;
RA Nagase T., Kikuno R., Ishikawa K.-I., Hirotsawa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."
RL DNA Res. 7:143-150(2000).
RN [3]
RP SEQUENCE OF 179-409 FROM N.A.
RA Kay M.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY PLAY A ROLE IN ORGANIZING THE ACTIN CYTOSKELETON OF THE BRAIN CELLS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
CC -!- SIMILARITY: CONTAINS 1 BTB/POZ DOMAIN.
CC -!- SIMILARITY: CONTAINS 6 KELCH REPEATS.
CC
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CC
CC EMBL; AF252283; AAF81719.1;
CC EMBL; AF252279; AAF81716.1;
CC EMBL; AB040923; BAA96014.1; AUT_INIT.
CC EMBL; AL353738; CAC16128.1;
CC Genew; HGNC:6352; KHL1.
CC MIM; 605332;
CC InterPro; IPR000210; BTB_POZ.
CC InterPro; IPR001798; Kelch.
CC Pfam; PF00651; BTB; 1.
CC Pfam; PF01344; Kelch; 6.
CC PRINTS; PR00501; KELCHREPEAT.
CC SMART; SM00225; BTB; 1.
CC PROSITE; PS50097; BTB; 1.
KW Cytoskeleton; Actin-binding; Repeat.
FT DOMAIN 43 88 SER-RICH.
FT DOMAIN 212 279 BTB.
FT REPEAT 460 506 KELCH 1.
FT REPEAT 507 553 KELCH 2.
FT REPEAT 555 600 KELCH 3.
FT REPEAT 601 647 KELCH 4.
FT REPEAT 649 700 KELCH 5.

FT REPEAT 701 747 KELCH 6.
SQ SEQUENCE 748 AA; 83680 MW; C11C43D8282F9FF9 CRC64;

Query Match 63.9%; Score 34.5; DB 1; Length 748;
Best Local Similarity 80.0%; Pred. No. 29;
Matches 8; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 EEVVPXGMDY 10
Db 127 EEVVP-GMDF 135

RESULT 8

PLAS_ORYSA
ID PLAS_ORYSA STANDARD; PRT; 154 AA.
AC P20423; Q9SBB8;
DT 01-FEB-1991 (Rel. 17, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Plastocyanin, chloroplast precursor.
GN PETE.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Ilpoom; TISSUE=Leaf;
RA Lee J.-S.;
RT "Molecular cloning and characterization of plastocyanin precursor in rice."
RL Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE OF 58-154.
RC STRAIN=cv. Japonica;
RX MEDLINE=89386623; PubMed=2780537;
RA Yano H., Kamo M., Tsugita A., Aso K., Nozu Y.;
RT "The amino acid sequence of plastocyanin from rice (Oryza sativa, subspecies japonica)."
RL Protein Seq. Data Anal. 2:385-389(1989).
CC -1- FUNCTION: Participates in electron transfer between P700 and the cytochrome b6-f complex in photosystem I.
CC -1- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID MEMBRANE SURFACE IN CHLOROPLASTS.
CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
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CC EMBL: AF093636; AAC78108.1; -;
DR PIR: S06105; S06105.
DR PIR: J03552; J03552.
DR HSSP: P00289; 2PCF.
DR InterPro: IPR000923; BlueCu_1.
DR Pfam: PF00127; copper_bind; 1.
DR PRINTS: PR00156; COPPERBLUE.
DR PRODOM: PD001235; Copper_blue; 1.
DR PROSITE: PS00196; COPPER_BLUE; 1.
KW Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
KW Transit peptide.
FT CHAIN 1 57 CHLOROPLAST.
FT CHAIN 58 154 PLASTOCYANIN.
FT DOMAIN 58 154 PLASTOCYANIN-LIKE.
FT METAL 94 154 COPPER (BY SIMILARITY).
FT METAL 139 139 COPPER (BY SIMILARITY).
FT METAL 142 142 COPPER (BY SIMILARITY).

FT METAL 147 147 COPPER (BY SIMILARITY).
SQ SEQUENCE 154 AA; 15577 MW; E45725D25B5F400D CRC64;

Query Match 63.0%; Score 34; DB 1; Length 154;
Best Local Similarity 54.5%; Pred. No. 6.8;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
Db 100 EDVPSGVDVS 110

RESULT 9

PLAS_HORVU
ID PLAS_HORVU STANDARD; PRT; 155 AA.
AC P08248;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Plastocyanin, chloroplast precursor.
GN PETE.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Bomli;
RA Nielsen O.S., Gausing K.;
RT "The precursor of barley plastocyanin: sequence of cDNA clones and gene expression in different tissues."
RL FEBS Lett. 225:159-162(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. NK 1558;
RX MEDLINE=94039081; PubMed=8223592;
RA Nielsen P., Gausing K.;
RT "In vitro binding of nuclear proteins to the barley plastocyanin gene promoter region."
RL Eur. J. Biochem. 217:97-104(1993).
CC -1- FUNCTION: Participates in electron transfer between P700 and the cytochrome b6-f complex in photosystem I.
CC -1- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID MEMBRANE SURFACE IN CHLOROPLASTS.
CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
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CC EMBL: Y00704; CAA8696.1; -;
DR EMBL: Z28347; CAA82201.1; -;
DR PIR: S00206; S00206.
DR HSSP: P00289; 2PCF.
DR InterPro: IPR000923; BlueCu_1.
DR Pfam: PF00127; copper_bind; 1.
DR PRINTS: PR00156; COPPERBLUE.
DR PRODOM: PD001235; Copper_blue; 1.
DR PROSITE: PS00196; COPPER_BLUE; 1.
KW Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
KW Transit peptide.
FT CHAIN 1 58 CHLOROPLAST.
FT CHAIN 59 155 PLASTOCYANIN.
FT DOMAIN 59 155 PLASTOCYANIN-LIKE.
FT METAL 95 95 COPPER (BY SIMILARITY).
FT METAL 140 140 COPPER (BY SIMILARITY).
FT METAL 143 143 COPPER (BY SIMILARITY).

FT METAL 148 148 COPPER (BY SIMILARITY).
 FT VARIANT 120 120 T -> N (IN CV. NK 1558).
 SQ SEQUENCE 155 AA; 15709 MW; DAA7EAB3F6F4F91 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 155;
 Best Local Similarity 54.5%; Pred. No. 6.9;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
 I: |||:
 Db 101 EDAPVSGVDVS 111

RESULT 10

PLAT_POPNI
 ID PLAT_POPNI STANDARD; PRT; 168 AA.
 AC P11970;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Plastocyanin B, chloroplast precursor.
 GN PETE.
 OS Populus nigra (lombardy poplar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Malpighiales; Salicaceae; Populus.
 OX NCBI_TaxID=3691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Italica; TISSUE=Leaf;
 RA Reichert J., Jenzelewski V., Haehnel W.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 70-168.
 RC STRAIN=cv. Italica;
 RA Dmitrov M.I., Egorov C.A., Donchev A.A., Atanasov B.P.;
 RT "Complete amino acid sequence of poplar plastocyanin b.";
 RL FEBS Lett. 226:17-22(1987).
 CC -I- FUNCTION: Participates in electron transfer between P700 and the
 CC cytochrome b6-f complex in photosystem I.
 CC -I- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID
 CC MEMBRANE SURFACE IN CHLOROPLASTS.
 CC -I- SIMILARITY: THERE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF
 CC POPLAR PLASTOCYANINS A AND B.
 CC -I- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.

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 EMBL; Z50186; CAA90565.1;
 FIR; S00210; S00210.
 HSP; P00299; IPIIC.
 InterPro; IPR000923; BlueCu1.
 InterPro; IPR001235; Copper_Blue.
 Pfam; PF00127; copper_bind; 1.
 PRINTS; PR00156; COPPERBLUE.
 ProDom; PD001235; Copper_blue; 1.
 PROSITE; PS00196; COPPER_BLUE; 1.
 Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
 Transit peptide; Multigene family.
 TRANSIT 1 69 CHLOROPLAST.
 FT CHAIN 70 168 PLASTOCYANIN B.
 FT DOMAIN 70 168 PLASTOCYANIN-LIKE.
 FT METAL 106 106 COPPER.
 FT METAL 153 153 COPPER.
 FT METAL 156 156 COPPER.
 FT METAL 161 161 COPPER.
 SQ SEQUENCE 168 AA; 16981 MW; F20DA6EA2038AEEA CRC64;

Query Match 63.0%; Score 34; DB 1; Length 168;
 Best Local Similarity 54.5%; Pred. No. 7.5;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
 I: |||:
 Db 112 EDAPVSGVDVS 122

RESULT 11

SYFB_BORBU
 ID SYFB_BORBU STANDARD; PRT; 566 AA.
 AC P94283;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20) (Phenylalanine--
 DE tRNA ligase beta chain) (PHERS).
 GN PHET OR B0514.
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35210 / B31;
 RA Barbour A.G., Hinnebusch J.;
 RT "Phenylalanyl-tRNA synthetase genes (alpha and beta subunits) and
 RT thiorodoxin reductase gene of Borrelia burgdorferi".
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35210 / B31;
 RX MEDLINE=98065943; PubMed=9403685;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
 RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
 RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
 RA Uitterback T., Wathey L., McDonald L., Artiach P., Bowman C.,
 RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
 RA Smith H.O., Venter J.C.;
 RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
 RT burgdorferi".
 RL Nature 390:580-586(1997).
 CC -I- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +
 CC diphosphate + L-phenylalanyl-tRNA(Phe).
 CC -I- SUBUNIT: Tetramer of two alpha and two beta chains (BY
 CC SIMILARITY).
 CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -I- SIMILARITY: BELONGS TO THE PHENYLALANYL-TRNA SYNTHETASE BETA
 CC CHAIN FAMILY, SUBFAMILY 2.

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 EMBL; U82978; AAB41019.1;
 DR EMBL; AE001153; AAC66870.1;
 DR TIGR; B0514;
 DR InterPro; IPR005147; B5.
 DR InterPro; IPR004531; PheT_arch.
 DR Pfam; PF03484; B5; 1.
 DR TIGRFAMS; TIGR00471; pheT_arch; 1.
 KW Aminoacyl-tRNA synthetase; protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 SQ SEQUENCE 566 AA; 65173 MW; 9D48C8B5D6D3B74B CRC64;

Query Match 63.0%; Score 34; DB 1; Length 566;

Best Local Similarity 85.7%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VPXGMDY 10
DB 169 VPFGMDY 175

RESULT 12
Y939_METJA STANDARD; PRT; 276 AA.
AC Q58349;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein M70939.
GN M70939.

OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID:2190;
RN
RP SEQUENCE FROM N.A.
RC STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RT
RL
SC Science 273:1058-1073(1996).

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EMBL: U67537; AAB98946.1; -
DR TIGR; M70939; -
DR
SQ SEQUENCE 276 AA; 33454 MW; 97BD69D32BC8FDF CRC64;

Query Match 61.1%; Score 33; DB 1; Length 276;
Best Local Similarity 45.5%; Pred. No. 21;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
DB 141 EEIENGMEHS 151

RESULT 13
PANC_PSEAE STANDARD; PRT; 283 AA.
AC Q9HV69;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pantoate-beta-alanine ligase (EC 6.3.2.1) (Pantothenate synthetase)
DE (Pantoate activating enzyme).
GN PANC OR PA4730.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;

[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warriner P.,
RA Hickey M.J., Brinkman F.S.L., Huinagie W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -1- CATALYTIC ACTIVITY: ATP + (R)-pantoate + beta-alanine = AMP +
CC diphosphate + (R)-pantothenate.
CC -1- PATHWAY: Pantothenate biosynthesis; last step.
CC -1- SIMILARITY: BELONGS TO THE PANTOTHENATE SYNTHETASE FAMILY.

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EMBL: AE004886; AAG08116.1; -
DR InterPro; IPR003721; Pantoate_ligase.
DR Pfam; PF02569; Pantoate_ligase; 1.
DR TIGR; TIGR000018; pncC; 1.
KW Pantothenate biosynthesis; Ligase; Complete proteome.
SQ SEQUENCE 283 AA; 30836 MW; C494949AB40E14E7 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 283;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMD 9
DB 96 EENYPDGMD 104

RESULT 14
HMPA_VIBCH STANDARD; PRT; 394 AA.
AC Q9KMX3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Flavohemoprotein (Hemoglobin-like protein) (Flavohemoglobin).
GN HMP OR VCA0183.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;

[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Unayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
CC -1- DOMAIN: CONSISTS OF TWO DISTINCT DOMAINS; ONE IS A HEME-CONTAINING
CC OXYGEN BINDING DOMAIN IN THE N-TERMINAL REGION AND THE OTHER IS AN
CC FAD-CONTAINING REDUCTASE DOMAIN FOUND IN THE C-TERMINAL REGION.
CC -1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY. TWO-DOMAIN
CC FLAVOHEMOPROTEINS SUBFAMILY.

CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.
 CC -----
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 CC -----
 CC EMBL: AF031489; AAC15882.1; -
 CC HSSP: P12995; 1QJ3.
 CC InterPro: IPR000954; Aminotran_3.
 CC Pfam: PF00202; aminotran_3; 1.
 CC PROSITE: PS00600; AA_TRANSFER_CLASS_3; FALSE_NEG.
 CC TRANSFERASE; Aminotransferase; Pyridoxal phosphate.
 CC BINDING 267 267 PYRIDOXAL PHOSPHATE (POTENTIAL).
 CC SEQUENCE 421 AA; 46166 MW; 44A2E21596E1E16C CRC64;
 CC -----
 CC Query Match 61.1%; Score 33; DB 1; Length 421;
 CC Best Local Similarity 58.3%; Pred. No. 32;
 CC Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
 CC
 CC QY 1 EEVW--PXGMDY 10
 CC |||: | | | |
 CC DB 91 EEVILKPRGLDY 102
 CC -----
 CC RESULT 17
 CC ECBI_HALEL STANDARD; PRT; 423 AA.
 CC ID ECBI_HALEL
 CC AC Q9ZEU7;
 CC DT 30-MAY-2000 (Rel. 39, Created)
 CC DT 30-MAY-2000 (Rel. 39, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Diaminobutyrate-pyruvate aminotransferase (EC 2.6.1.46) (L-
 CC diaminobutyric acid transaminase) (Diaminobutyrate transaminase).
 CC GN ECTB.
 CC OS Halomonas elongata.
 CC Bacteria; Proteobacteria; gamma subdivision; Halomonadaceae;
 CC Halomonas.
 CC NCBI_TaxID=2746;
 CC [1]
 CC SEQUENCE FROM N.A.
 CC STRAIN=DSM 3043;
 CC MEDLINE=99123891; PubMed=9924816;
 CC Canovas D., Vargas C., Calderon M.I., Ventosa A., Nieto J.J.;
 CC "Characterization of the genes for the biosynthesis of the compatible
 CC solute ectoine in the moderately halophilic bacterium Halomonas
 CC elongata DSM 3043.";
 CC Syst. Appl. Microbiol. 21:487-497(1998).
 CC -1- CATALYTIC ACTIVITY: L-2,4-diaminobutanate + pyruvate = L-
 CC aspartate 4-senialdehyde + L-alanine.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
 CC -1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF ECTOINE (1,4,5,6-
 CC TETRAHYDRO-2-METHYL-4-PYRIMIDINE CARBOXYLIC ACID).
 CC -1- SUBUNIT: HOMOHETEROMER (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 CC AMINOTRANSFERASES.
 CC -----
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 CC -----
 CC EMBL: AJ011103; CAA09484.1; -
 CC HSSP: P12995; 1QJ3.
 CC InterPro: IPR000130; Zn_MTpeptdse.

DR InterPro: IPR000954; Aminotran_3.
 DR InterPro: IPR004637; Dat.
 DR Pfam: PF00202; aminotran_3; 1.
 DR TIGRFAMS: TIGR00709; dat; 1.
 DR PROSITE: PS00600; AA_TRANSFER_CLASS_3; FALSE_NEG.
 DR TRANSFERASE; Aminotransferase; Pyridoxal phosphate.
 DR BINDING 267 267 PYRIDOXAL PHOSPHATE (POTENTIAL).
 DR SEQUENCE 423 AA; 46200 MW; 735C6BCF5A88288C CRC64;
 DR -----
 DR Query Match 61.1%; Score 33; DB 1; Length 423;
 DR Best Local Similarity 58.3%; Pred. No. 32;
 DR Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;
 DR
 DR QY 1 EEVW--PXGMDY 10
 DR |||: | | | |
 DR DB 91 EEVILKPRGLDY 102
 DR -----
 DR RESULT 18
 DR ECE2_HUMAN STANDARD; PRT; 787 AA.
 DR ID ECE2_HUMAN
 DR AC O60344; Q96NX4; Q96NX3;
 DR DT 30-MAY-2000 (Rel. 39, Created)
 DR DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DR DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DR DE Endothelin-converting enzyme 2 (EC 3.4.24.71) (ECE-2).
 DR GN ECE2 OR KIAA0604.
 DR OS Homo sapiens (Human).
 DR OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DR OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 DR NCBI_TaxID=9606;
 DR [1]
 DR SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
 DR Lorenzo M.-N., Khan R.Y., Wang Y., Tai S.C., Chan G.C., Cheung A.H.,
 DR Marsden P.A.;
 DR "Human endothelin converting enzyme-2 (ECE2): characterization of mRNA
 DR species and chromosomal localization.";
 DR Biochim. Biophys. Acta 0:0-0(2002).
 DR [2]
 DR SEQUENCE FROM N.A. (ISOFORM B).
 DR TISSUE=Brain;
 DR MEDLINE=98290545; PubMed=9628581;
 DR Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
 DR Nomura N., Ohara O.;
 DR "Prediction of the coding sequences of unidentified human genes. IX.
 DR The complete sequences of 100 new cDNA clones from brain which can
 DR code for large proteins in vitro.";
 DR DNA Res. 5:31-39(1998).
 CC -1- FUNCTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1 (BY
 CC SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
 CC Trp-1-Val-22 bond in the precursor.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 3 isoforms; ECE-2A (shown here), ECE-2B and
 CC ECE-2C; are produced by alternative splicing.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13.
 CC -----
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 CC -----
 CC EMBL: AF428263; AAL30386.1; -
 CC EMBL: AF428264; AAL30387.1; -
 CC EMBL: AF192531; AAG28399.1; -
 CC EMBL: AB011176; BAA25530.1; -
 CC HSSP: P08473; IDMT.
 CC MEROPS: M13.003; -
 CC InterPro: IPR000718; Peptidase_M13.
 CC InterPro: IPR000130; Zn_MTpeptdse.

FT CARBOHYD 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 322 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 305 TAGANTDKLEVLNVTDFEDAGEXTCLAGNSIGFSGSHS
 FT AWLVVLP -> SWISENVEADARLRLANVSERDGSGEYLCRA
 FT TNFIGNVAEKAFWLKRVHGPQA (IN ISOFORM 2).
 FT P -> L (IN REF. 2).
 FT CONFLICT 684 MISSING (IN REF. 2).
 FT CONFLICT 687 MISSING (IN REF. 2).
 SQ SEQUENCE 801 AA; 87758 MW; 68BC110212691705 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 801;
 Best Local Similarity 85.7%; Pred. No. 64;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGMGMS 11
 | | | | |
 Db 566 PGMGMS 572

RESULT 20
 CEK2_CHICK STANDARD; PRT; 806 AA.
 ID CEK2_CHICK STANDARD; PRT; 806 AA.
 AC P18450;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine kinase receptor CEK2 precursor (EC 2.7.1.112).
 GN CEK2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90332672; PubMed=2165604;
 RA Pasquale E.B.;
 RT "A distinctive family of embryonic protein-tyrosine kinase
 receptors.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:5812-5816(1990).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
 tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR
 FAMILY.
 CC -1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC
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 CC
 CC EMBL; M35195; AAA48664.1; -
 DR PIR; A35963; A35963.
 DR HSP; P11362; 1FKG.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003598; Ig_c2.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00047; Ig; 3.
 DR Pfam; PF00069; pkinase; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk_pkinase; 1.
 DR SMART; SM00408; IGG2; 3.
 DR SMART; SM00219; TYRK; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
 KW Receptor; Glycoprotein; Tyrosine-protein kinase; ATP-binding;
 KW Transferase; Phosphorylation; Transmembrane; Immunoglobulin domain;
 KW Repeat; Signal.

FT SIGNAL 1 19
 FT CHAIN 20 806
 FT DOMAIN 20 364
 FT TRANSMEM 365 389
 FT DOMAIN 390 806
 FT DOMAIN 54 114
 FT DOMAIN 163 229
 FT DOMAIN 262 340
 FT DOMAIN 131 141
 FT DOMAIN 466 755
 FT NP_BIND 472 480
 FT BINDING 502 502
 FT ACT_SITE 611 611
 FT MOD_RES 642 642
 FT DISULFID 61 107
 FT DISULFID 170 222
 FT DISULFID 269 333
 FT CARBOHYD 83 83
 FT CARBOHYD 96 96
 FT CARBOHYD 118 118
 FT CARBOHYD 219 219
 FT CARBOHYD 256 256
 FT CARBOHYD 288 288
 FT CARBOHYD 309 309
 FT CARBOHYD 322 322
 SQ SEQUENCE 806 AA; 89730 MW; B38B3C6D5F2314B6 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 806;
 Best Local Similarity 85.7%; Pred. No. 64;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGMGMS 11
 | | | | |
 Db 566 PGMGMS 572

RESULT 21
 SULH_SCHPO STANDARD; PRT; 877 AA.
 ID SULH_SCHPO STANDARD; PRT; 877 AA.
 AC 074377;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Probable sulfate permease C3H7.02.
 GN SPBC3H7.02.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Church C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Furnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Arruti I., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
RT "the genome sequence of Schizosaccharomyces pombe.";
CC Nature 415:871-880(2002).
CC -1- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS.
CC -1- SIMILARITY: CONTAINS 1 STAS DOMAIN.
CC -----
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CC -----
DR EMBL; AL031261; CAA20298.1; -
DR InterPro: IPR002645; STAS.
DR Pfam: PF00916; Sulfate_transp; 1.
DR Pfam: PF01740; STAS; 1.
DR TIGRFAMs: TIGR00815; sulp; 1.
DR PROSITE: PS01130; SLC26A; 1.
DR PROSITE: PS50801; STAS; 1.
KW Transport; Transmembrane.
FT TRANSMEM 133 153 POTENTIAL.
FT TRANSMEM 161 181 POTENTIAL.
FT TRANSMEM 186 206 POTENTIAL.
FT TRANSMEM 221 241 POTENTIAL.
FT TRANSMEM 243 263 POTENTIAL.
FT TRANSMEM 292 312 POTENTIAL.
FT TRANSMEM 329 349 POTENTIAL.
FT TRANSMEM 384 404 POTENTIAL.
FT TRANSMEM 424 444 POTENTIAL.
FT TRANSMEM 461 481 POTENTIAL.
FT TRANSMEM 484 504 POTENTIAL.
FT TRANSMEM 518 538 POTENTIAL.
FT TRANSMEM 543 563 POTENTIAL.
FT DOMAIN 594 747 STAS.
SQ SEQUENCE 877 AA; 96373 MW; 56995A8493371E43 CRC64;
Query Match 61.1%; Score 33; DB 1; Length 877;
Best Local Similarity 66.7%; Pred. No. 70;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 VVPXGMDYS 11
D 148 VVPQGSYA 156
RESULT 22
ENV_SFV3L STANDARD; PRT; 982 AA.
AC P27399;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ENV polyprotein (Coat polyprotein).
GN ENV.
OS Simian foamy virus (type 3 / strain LK3) (SFV-3).
OC Viruses; Retroid viruses; Retroviridae; Spumavirus.
OX NCBI_TaxID=11644;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92124734; PubMed=1310187;
RA Renne R., Friedl E., Schweizer M., Fleps U., Turek R.,
RA Neumann-Haefelin D.;
RT "Genomic organization and expression of simian foamy virus type 3

(SFV-3).";
RL Virology 186:597-608(1992).
CC -----
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CC -----
DR EMBL; M74895; AAA47798.1; ALT_INIT.
DR PIR; C40820; VCLJLK.
DR InterPro: IPR005070; Foamy_virus_ENV; 1.
DR Pfam: PF03408; Foamy_virus_ENV; 1.
KW Coat protein; Transmembrane; Glycoprotein.
FT TRANSMEM 68 88 I (POTENTIAL).
FT TRANSMEM 95 975 II (POTENTIAL).
FT CARBOHYD 17 17 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 25 25 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 346 346 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 404 404 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 412 412 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 484 484 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 522 522 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 551 551 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 776 776 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 802 802 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 827 827 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 982 AA; 113313 MW; 721F2F8929D604FF CRC64;
Query Match 61.1%; Score 33; DB 1; Length 982;
Best Local Similarity 66.7%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 EEVVPXGMD 9
D 44 EEVPTPRMD 52
RESULT 23
RPOC_VIBCH STANDARD; PRT; 1401 AA.
AC Q9KV29;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
DE beta' chain) (RNA polymerase beta' subunit).
GN RPOC OR VC0329.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION

CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES (By similarity).
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA](N).
CC -!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN (By similarity).
CC -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC
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CC
CC EMBL: AE004121; AAF93502.1; -.
CC DR HSP: O9KW06; 1HQW.
CC DR TIGR: VC0329; -.
CC DR InterPro: IPR000722; RNA_pol_A.
CC DR InterPro: IPR002879; RNA_pol_A2.
CC DR Pfam: PF00623; RNA_pol_A; 1.
CC DR Pfam: PF01854; RNA_pol_A2; 2.
CC DR Transferase: DNA-directed RNA polymerase; Transcription;
CC KW Complete proteome
CC SQ SEQUENCE 1401 AA; 155021 MW; DFDB0F2B5514504F CRC64;
CC
CC Query Match 61.1%; Score 33; DB 1; Length 1401;
CC Best Local Similarity 50.0%; Pred. No. 1.2e+02;
CC Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
CC
CC QY 2 EVVPGMDYS 11
CC DB 581 QIVPKGLPYS 590
CC
CC
CC RESULT 24
CC ZEPL_HUMAN STANDARD; PRT; 2717 AA.
CC ID ZEPL_HUMAN
CC AC P15822;
CC DT 01-APR-1990 (Rel. 14, Created)
CC DT 01-APR-1990 (Rel. 14, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE Zinc finger protein 40 (human immunodeficiency virus type I enhancer-
CC binding protein 1) (HIV-EPI) (Major histocompatibility complex binding
CC protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
CC (PRDII-BF1).
CC GN HIVP1 OR ZNF40.
CC OS Homo sapiens (Human).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC OX NCBI_TaxID=9606;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=90169514; PubMed=2106471;
CC RA Fan C.M., Maniatis T.;
CC RT "A DNA-binding protein containing two widely separated zinc finger
CC motifs that recognize the same DNA sequence.";
CC RL Genes Dev. 4:29-42(1990).
CC RN [2]
CC RP STRUCTURE BY NMR OF 2113-2142.
CC RX MEDLINE=91064333; PubMed=2248949;
CC RA Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
CC Gronenborn A.M.;
CC RT "High-resolution three-dimensional structure of a single zinc finger
CC from a human enhancer binding protein in solution.";
CC RL Biochemistry 29:9324-9334(1990).
CC RN [3]
CC RP STRUCTURE BY NMR OF 2087-2142.
CC RX MEDLINE=92232684; PubMed=1567844;
CC RA Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E.,
CC Gronenborn A.M.;

RT "High-resolution solution structure of the double Cys2His2 zinc
RT finger from the human enhancer binding protein MBP-1.";
RL Biochemistry 31:3907-3917(1992).
CC -!- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE
CC '5'-GGGAGTTTC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF
CC NUMEROUS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CMV, OR HIV1.
CC IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS
CC OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I
CC MHC, INTERLEUKIN-2 RECEPTOR, AND INTERFERON-BETA GENES. IT MAY ACT
CC IN T-CELL ACTIVATION.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- INDUCTION: BY MITOGEN AND PHORBOL ESTER.
CC -!- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY
CC SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
CC ZINC-FINGER IN-BETWEEN.
CC -!- SIMILARITY: STRONG, TO HIVP2.
CC
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CC
CC EMBL: X51435; CAA35798.1; -.
CC DR PIR: A34203; A34203
CC DR PDB: 3ZNF; 15-JAN-92.
CC DR PDB: 4ZNF; 15-JAN-92.
CC DR PDB: 1BBO; 31-OCT-93.
CC DR TRANSFAC: T00497; -.
CC DR Genew: HGNC:4920; HIVP1.
CC DR MIM: 194540; -.
CC DR InterPro: IPR000822; Znf_C2H2.
CC DR Pfam: PF00096; Zf-C2H2; 5.
CC DR PRINTS: PR00048; ZINC_FINGER.
CC DR SMART: SM00355; Znf_C2H2; 4.
CC DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
CC DR PROSITE: PS50157; ZINC_FINGER_C2H2_2; 4.
CC KW Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;
CC Nuclear protein; Repeat; 3D-structure.
CC FT DOMAIN 406 456 ZINC FINGERS.
CC FT ZN_FING 406 428 C2H2-TYPE.
CC FT ZN_FING 434 456 C2H2-TYPE.
CC FT DOMAIN 803 806 POLY-SER.
CC FT ZN_FING 958 981 C2HC-TYPE (POTENTIAL).
CC FT DOMAIN 2087 2109 ZINC FINGERS.
CC FT ZN_FING 2115 2139 C2H2-TYPE.
CC FT ZN_FING 2115 2139 C2H2-TYPE.
CC FT STRAND 2088 2088
CC FT TURN 2090 2092
CC FT STRAND 2095 2095
CC FT HELIX 2099 2108
CC FT TURN 2109 2109
CC FT STRAND 2115 2116
CC FT STRAND 2123 2124
CC FT HELIX 2127 2135
CC SQ SEQUENCE 2717 AA; 297217 MW; D45D3CA951FEA561 CRC64;
CC
CC Query Match 61.1%; Score 33; DB 1; Length 2717;
CC Best Local Similarity 66.7%; Pred. No. 2.3e+02;
CC Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
CC
CC QY 3 VVPGMDYS 11
CC DB 2405 VVPAGLTYS 2413
CC
CC RESULT 25
CC ET2A_XENLA STANDARD; PRT; 472 AA.
CC ID ET2A_XENLA
CC AC P19102;
CC DT 01-NOV-1990 (Rel. 16, Created)

01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
C-ETS-2A protein.
GN ETS2A OR ETS-2A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=92158632; PubMed=1741266;
RA Burdett L.A., Qi S.W., Chen Z.Q., Lautenberger J.A., Papas T.S.;
RT "Characterization of the cDNA sequences of two xenopus ets-2 proto-
oncogenes";
RL Nucleic Acids Res. 20:371-371(1992).
RN [2]
RN SEQUENCE OF 121-472 FROM N.A.
RP TISSUE=Oocyte;
RX MEDLINE=90356411; PubMed=2201951;
RA Wolff C.M., Stiegler P., Baltzinger M., Meyer D., Ghysdael J.,
RA Stehelin D., Befort N., Remy P.;
RT "Isolation of two different c-ets-2 proto-oncogenes in xenopus
laevis";
RL Nucleic Acids Res. 18:4603-4604(1990).
RN [3]
RN SEQUENCE OF 121-472 FROM N.A.
RX MEDLINE=92088972; PubMed=1751411;
RA Wolff C.M., Stiegler P., Baltzinger M., Meyer D., Ghysdael J.,
RA Stehelin D., Befort N., Remy P.;
RT "Cloning, sequencing, and expression of two Xenopus laevis c-ets-2
proto-oncogenes";
RL Cell Growth Differ. 2:447-456(1991).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: BELONGS TO THE ETS FAMILY.
CC -!- SIMILARITY: CONTAINS 1 POINTED (PNT) DOMAIN.
CC -----
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CC -----
DR EMBL; M81683; AAA49705.1; -;
DR EMBL; X51826; CAA36124.1; -;
DR PIR; S10994; S10994.
DR PIR; S28824; S28824.
DR HSP; P14921; 2STT.
DR TRANSFAC; T02041; -;
DR InterPro; IPR000418; Ets.
DR InterPro; IPR002341; HSF_ETS.
DR InterPro; IPR003118; SAM_PNT.
DR Pfam; PF00178; Ets; 1.
DR Pfam; PF02198; SAM_PNT; 1.
DR PRINTS; PR00454; ETSDOMAIN.
DR SMART; SM00413; ETS; 1.
DR SMART; SM00251; SAM_PNT; 1.
DR PROSITE; PS00345; ETS_DOMAIN_1; 1.
DR PROSITE; PS00346; ETS_DOMAIN_2; 1.
DR PROSITE; PS50061; ETS_DOMAIN_3; 1.
KW DNA-binding; Nuclear protein.
FT DOMAIN 87 170 POINTED.
FT DNA_BIND 366 446 ETS-DOMAIN.
SQ SEQUENCE 472 AA; 53894 MW; E0E808B5E6BF11 CRC64;

Query Match 60.2%; Score 32.5; DB 1; Length 472;
Best Local Similarity 58.3%; Pred. No. 46;
Matches 7; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 EEVPEXGMD-YS 11
|: ||| |||

Db 49 EQAVPTGLDSYS 60

Search completed: June 10, 2003, 13:40:21
Job time : 4.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:30:25 ; Search time-25.7857 seconds
(without alignments)
87.898 Million cell updates/sec

Title: US-09-909-164-12
Perfect score: 54
Sequence: 1 EHVVPXGMDYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : SPTREMBL21.*

- 1: sp.archaea.*
- 2: sp.bacteria.*
- 3: sp.fungi.*
- 4: sp.human.*
- 5: sp.invertebrate.*
- 6: sp.mammal.*
- 7: sp.mhc.*
- 8: sp.organelle.*
- 9: sp.phase.*
- 10: sp.plant.*
- 11: sp.rodent.*
- 12: sp.virus.*
- 13: sp.vertibrate.*
- 14: sp.unclassified.*
- 15: sp.rvirus.*
- 16: sp.bacteriap.*
- 17: sp.archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	74.1	156	3	Q12479 saccharomyc
2	38	70.4	363	17	Q30260 archaeoglob
3	38	70.4	1063	16	Q8RG86 fusobacteri
4	36	66.7	341	10	Q22081 citrus unsh
5	36	66.7	348	10	Q22096 citrus unsh
6	36	66.7	452	10	Q8W568 arabidopsis
7	36	66.7	460	10	Q9C9T7 arabidopsis
8	36	66.7	1047	10	P93782 saccharum o
9	36	66.7	1083	10	Q9SN30 arabidopsis
10	36	66.7	1084	10	Q43010 oryza sativ
11	36	66.7	1100	10	Q8S064 oryza sativ
12	35	64.8	219	5	Q9GQ04 eriocheir s
13	35	64.8	253	16	Q8XPA8 clostridium
14	35	64.8	298	2	O52367 rhizobium t
15	35	64.8	425	5	Q9XVK4 caenorhabdi
16	35	64.8	433	16	Q9A382 caulobacter

RESULT 1

ID	Q12479	PRELIMINARY;	PRT;	156 AA.
AC	Q12479;	(TREMBLrel. 01, Created)		
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	ORF YOR013W.			
GN	YOR013W.			

ALIGNMENTS

17	35	64.8	440	17	Q9YFI3	Q9yfi3 aeropyrum p
18	35	64.8	511	2	O52680	O52680 escherichia
19	35	64.8	517	16	O8XZL5	O8xz15 ralstonia s
20	35	64.8	745	5	Q9SP46	Q9sp46 carcinus ma
21	35	64.8	1031	5	Q9U6A3	Q9u6a3 callinectes
22	35	64.8	1150	5	O17704	O17704 caenorhabdl
23	35	64.8	1410	2	O52673	O52673 escherichia
24	35	64.8	1420	2	O52666	O52666 escherichia
25	35	64.8	1474	17	O27146	O27146 methanobact
26	35	64.8	1828	16	Q98K29	Q98k29 rhizobium l
27	35	64.8	2778	5	Q9V9T6	Q9v9t6 drosophila
28	34	63.9	748	4	O8TBJ7	O8tbj7 homo sapien
29	34	63.0	143	5	Q9VSY8	Q9vsy8 drosophila
30	34	63.0	154	10	Q9SBB8	Q9sbb8 oryza sativ
31	34	63.0	215	16	O8RG15	O8rg15 thermoanaer
32	34	63.0	290	16	O8U7J0	O8u7j0 agrobacteri
33	34	63.0	296	17	Q9YET8	Q9yet8 aeropyrum p
34	34	63.0	357	17	O29920	O29920 archaeoglob
35	34	63.0	366	17	O29451	O29451 archaeoglob
36	34	63.0	387	16	Q98FX1	Q98fx1 rhizobium l
37	34	63.0	543	3	O8TFF4	O8tff4 trichoderma
38	34	63.0	558	16	Q8R8Z2	Q8r8z2 thermoanaer
39	34	63.0	565	16	Q9CIN1	Q9cin1 lactococcus
40	34	63.0	587	16	Q9JZP8	Q9jzp8 neisseria m
41	34	63.0	906	10	Q9ZSY4	Q9zsy4 arabidopsis
42	34	63.0	908	10	Q9FJK8	Q9fjk8 arabidopsis
43	34	63.0	908	10	O8W4J9	O8w4j9 arabidopsis
44	34	63.0	908	10	Q9ZSY3	Q9zsy3 arabidopsis
45	34	63.0	909	10	Q9MSA1	Q9msa1 arabidopsis
46	34	63.0	1062	2	P95422	P95422 pseudomonas
47	34	63.0	1062	1	Q910Y8	Q910y8 pseudomonas
48	34	63.0	1062	1	O74056	O74056 cenarchaeum
49	33	61.1	78	6	Q9XST4	Q9xst4 canis famil
50	33	61.1	97	17	Q97VR9	Q97vr9 sulfolobus
51	33	61.1	128	17	Q97US8	Q97us8 sulfolobus
52	33	61.1	172	13	Q02528	Q02528 oryzias lat
53	33	61.1	175	10	O8VY88	O8vy88 arabidopsis
54	33	61.1	183	2	Q9S1I0	Q9s1i0 sweet potat
55	33	61.1	184	17	Q97XJ2	Q97xj2 sulfolobus
56	33	61.1	193	5	Q8SWL4	Q8swl4 encephalito
57	33	61.1	209	13	Q9DE16	Q9de16 brachydania
58	33	61.1	210	10	O6S890	O6s890 cyclotella
59	33	61.1	217	4	O00404	O00404 homo sapien
60	33	61.1	225	10	Q40129	Q40129 lycopersico
61	33	61.1	230	17	Q9P9L6	Q9p9l6 pyrobaculum
62	33	61.1	247	16	O92U66	O92u66 rhizobium m
63	33	61.1	257	10	Q9C6J0	Q9c6j0 arabidopsis
64	33	61.1	262	17	Q97YB8	Q97yb8 sulfolobus
65	33	61.1	267	17	Q97Y57	Q97y57 sulfolobus
66	33	61.1	299	4	Q9UEE9	Q9uee9 homo sapien
67	33	61.1	299	17	Q97TV4	Q97tv4 sulfolobus
68	33	61.1	299	17	Q9UWN4	Q9uwn4 sulfolobus
69	33	61.1	307	17	Q9HP60	Q9hp60 halobacteri
70	33	61.1	396	17	Q8TIT9	Q8tit9 methanosarc
71	33	61.1	441	17	Q9HIW6	Q9hiw6 thermoplasma
72	33	61.1	556	4	O43733	O43733 homo sapien
73	33	61.1	577	15	Q9QBR8	Q9qbr8 simian foam
74	33	61.1	577	15	Q9QBR7	Q9qbr7 simian foam
75	33	61.1	577	15	Q9QBR6	Q9qbr6 simian foam

OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA De haan M., Grivell L.A., Maarse A.C.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA STRAIN-FY1679;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA STRAIN-FY1679;
 RL MEDLINE-94019318; PubMed-8413243;
 RA Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlenny G.,
 RT Sherman F.;
 RT "CYC2 encodes a factor involved in mitochondrial import of yeast
 cytochrome c.";
 RL Mol. Cell. Biol. 13:6442-6451(1993).
 RN [5]
 RP SEQUENCE FROM N.A.
 RA STRAIN-FY1679;
 RL MEDLINE-94169519; PubMed-7764548;
 RA Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
 RT "Molecular cloning of a gene, DHS1, which complements a drug-
 hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
 RL Biosci. Biotechnol. Biochem. 58:391-395(1994).
 DR EMBL; Z74920; CAA99201.1; -;
 DR EMBL; X87331; CAA60762.1; -;
 DR SGD; S0005539; YOR013W.
 SQ SEQUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;
 Query Match 74.1%; Score 40; DB 3; Length 156;
 Best Local Similarity 77.8%; Pred. No. 1.7;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 EVVPGMGNDY 10
 Db ||| ||||
 50 EVNPLGNDY 58
 RESULT 2
 O30260
 ID O30260 PRELIMINARY; PRT; 363 AA.
 AC O30260;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein AF2411.
 GN AF2411.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE-98049343; PubMed-9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kervlavage A.R., Graham D.E., Kyrpides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,

RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 DR EMBL; AE001109; AAB91255.1; -;
 DR TIGR; AF2411; -;
 DR InterPro; IPR002103; Bac_luciferase.
 DR Pfam; PF00296; bac_luciferase; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 363 AA; 41736 MW; 0E976EAE788F4803 CRC64;
 Query Match 70.4%; Score 38; DB 17; Length 363;
 Best Local Similarity 54.5%; Pred. No. 12;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EVVPGMGNDY 11
 Db |::| |::|
 120 ENIVPYGIDFS 130
 RESULT 3
 O8RG86
 ID O8RG86 PRELIMINARY; PRT; 1063 AA.
 AC O8RG86;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Carbamoyl-phosphate synthase large chain (EC 6.3.5.5).
 GN FN0422.
 OS Fusobacterium nucleatum (subsp. nucleatum).
 OC Bacteria; Fusobacteria; Fusobacterium.
 OX NCBI_TaxID=76856;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 25586;
 RX MEDLINE-21886394; PubMed-11889109;
 RA Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
 RA Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
 RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
 RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
 RA Fongstein M., Kyrpides N., Overbeek R.;
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium
 nucleatum strain ATCC 25586.";
 RL J. Bacteriol. 184:2005-2018(2002).
 DR EMBL; AF010554; AAL94625.1; -;
 KW Ligase; Complete proteome.
 SQ SEQUENCE 1063 AA; 118008 MW; 39700E10B7CCE411 CRC64;
 Query Match 70.4%; Score 38; DB 16; Length 1063;
 Best Local Similarity 60.0%; Pred. No. 39;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 EVVPGMGNDY 11
 Db |::| |::|
 195 EIVPGLNYS 204
 RESULT 4
 O22081
 ID O22081 PRELIMINARY; PRT; 341 AA.
 AC O22081;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Sucrose-phosphate synthase (Fragment).
 GN CIMSFS2.
 OS Citrus unshiu (Satsuma orange).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Sapindales; Rutaceae; Citrus.
 OX NCBI_TaxID=55188;

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[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=CV. MIYAGAWA-WASE; TISSUE=JUICE SACS AND SEGMENT EPIDERMIS;
RX MEDLINE=96439842; PubMed=8842155;
RA Komatsu A., Takanokura Y., Omura M., Akihama T.;
RT "Cloning and molecular analysis of cDNA encoding three sucrose
RT phosphate synthase isoforms from a citrus fruit (Citrus unshiu
RT Marc.).";
RL Mol. Gen. Genet. 252:346-351(1996).
[2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=CV. MIYAGAWA-WASE; TISSUE=JUICE SACS AND SEGMENT EPIDERMIS;
RA Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;
RT "Differential expression of three sucrose-phosphate synthase isoforms
RT during sucrose accumulation in citrus fruits (Citrus unshiu Marc.).";
RL Plant Sci. 140:169-178(1999).
DR EMBL: AB006319; BAA23215.1; -.
FT NON_TER 341 341
FT SEQUENCE 341 AA; 38136 MW; 61417A69C4560777 CRC64;
Query Match 66.7%; Score 36; DB 10; Length 341;
Best Local Similarity 66.7%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 VVPXGMDYS 11
Db 228 VIPPGMDFS 236

RESULT 5
OZ2096 PRELIMINARY; PRT; 348 AA.
AC OZ2096;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Sucrose-phosphate synthase (Fragment).
GN CITSPS3.
OS Citrus unshiu (Satsuma orange).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Sapindales; Rutaceae; Citrus.
OX NCBI_TaxID=55188;

SEQUENCE FROM N.A.
RC TISSUE=JUICE SACS AND SEGMENT EPIDERMIS;
RX MEDLINE=96439842; PubMed=8842155;
RA Komatsu A., Takanokura Y., Omura M., Akihama T.;
RT "Cloning and molecular analysis of cDNA encoding three sucrose
RT phosphate synthase isoforms from a citrus fruit (Citrus unshiu
RT Marc.).";
RL Mol. Gen. Genet. 252:346-351(1996).
[2]
RN RP SEQUENCE FROM N.A.
RC TISSUE=JUICE SACS AND SEGMENT EPIDERMIS;
RA Komatsu A., Takanokura Y., Moriguchi T., Omura M., Akihama T.;
RT "Differential expression of three sucrose-phosphate synthase isoforms
RT during sucrose accumulation in citrus fruits (Citrus unshiu Marc.).";
RL Plant Sci. 140:169-178(1999).
DR EMBL: AB006660; BAA22071.1; -.
FT NON_TER 348 348
FT SEQUENCE 348 AA; 38556 MW; EELC21EBA6FF5C5E CRC64;
Query Match 66.7%; Score 36; DB 10; Length 348;
Best Local Similarity 66.7%; Pred. No. 30;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 VVPXGMDYS 11
Db 234 VIPPGMDFS 242

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RESULT 6
Q8W568 PRELIMINARY; PRT; 452 AA.
ID Q8W568;
AC Q8W568;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Atlg73750/F25P22.17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
RN RP SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF419606; AAL31938.1; -.
DR InterPro: IPR002471; Prol_endopep_ser.
DR InterPro: IPR00379; Ser_estrns_site.
DR PROSITE: PS00708; PRO-ENDOPEP_SER; UNKNOWN_1.
SQ SEQUENCE 452 AA; 49682 MW; A159955B21742C4A CRC64;
Query Match 66.7%; Score 36; DB 10; Length 452;
Best Local Similarity 70.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 EEVVPXGMDY 10
Db 210 EEDVPSAMDY 219

RESULT 7
Q9C9T7 PRELIMINARY; PRT; 460 AA.
ID Q9C9T7;
AC Q9C9T7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 50.6 kDa protein.
GN F25P22.17.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huitzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.-L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Li X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Millitscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

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RESULT 11
08S064

ID Q8S064 PRELIMINARY; PRT; 1100 AA.
 AC Q8S064;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Putative sucrose-phosphate synthase.
 GN P0678F11.14.
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 clone:P0678F11.14";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP003437; BAB86107.1; -;
 SQ SEQUENCE 1100 AA; 121170 MW; 084F4604BA389CAD CRC64;
 Query Match 66.7%; Score 36; DB 10; Length 1100;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 VVPXGMDYS 11
 DB 469 VIPPGMDFS 477

RESULT 12
 Q9GQ04 PRELIMINARY; PRT; 219 AA.
 ID Q9GQ04;
 AC Q9GQ04;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE Na+/K+/2Cl-cotransporter (Fragment).
 OS Eriocheir sinensis (Chinese mitten crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubranchyura; Grapsoidae; Varunidae; Eriocheir.
 OX NCBI_TaxID=95602;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=GILL;
 RA Wehrhau D., Towle D.W.;
 RT "Na+/H+-exchanger and Na+/K+/2Cl- -cotransporter are expressed in
 RT gills of the euryhaline Chinese crab Eriocheir sinensis.";
 RL Comp. Biochem. Physiol. 126:S158-S158(2000).
 DR EMBL: AF301160; AAG39938.1; -;
 FT NON_TER 1
 FT NON_TER 219
 SQ SEQUENCE 219 AA; 24159 MW; 599442DA26F0D3F1 CRC64;
 Query Match 64.8%; Score 35; DB 5; Length 219;
 Best Local Similarity 75.08%; Pred. No. 29;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 4 VPXGMDYS 11
 DB 107 VPOGLDYS 114

RESULT 13
 Q8XPA8 PRELIMINARY; PRT; 253 AA.
 ID Q8XPA8
 AC Q8XPA8;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical protein CPE0057.

GN CPE0057.
 OS Clostridium perfringens.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
 OC Clostridiales; Clostridiaceae; Clostridium.
 OX NCBI_TaxID=1302;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=13 / TYPE A;
 RX PubMed=11792842;
 RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yanashita A.,
 RA Shiba T., Ogasawara N., Hattori M., Kunara S., Hayashi H.;
 RT "Complete genome sequence of Clostridium perfringens, an anaerobic
 RT flesh-eater";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
 DR EMBL: AP003185; BAB79763.1; -;
 DR InterPro; IPR000205; NAD_binding.
 DR InterPro; IPR000594; Thif_domain.
 DR Pfam; PF00899; Thif; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 253 AA; 27714 MW; 814DF79D3E0D7486 CRC64;
 Query Match 64.8%; Score 35; DB 16; Length 253;
 Best Local Similarity 50.0%; Pred. No. 34;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPGMDY 10
 DB 108 EIIIPDDVDY 117

RESULT 14
 O52367 PRELIMINARY; PRT; 298 AA.
 ID O52367;
 AC O52367;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Aryl-alcohol dehydrogenase homolog (Fragment).
 GN XYLBI.
 OS Rhizobium tropici.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=398;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CFN299;
 RA Rosenblueth M., Hynes M.F., Martinez-Romero E.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- COFACTOR: ZINC (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
 CC FAMILY.
 DR EMBL: AF036920; AAC04779.1; -;
 DR HSSP; P07846; ISDG.
 DR InterPro; IPR002328; ADH_zinc.
 DR InterPro; IPR002085; Adh_zn_family.
 DR InterPro; IPR000205; NAD_binding.
 DR Pfam; PF00107; adh_zinc; 1.
 DR PROSITE; PS00059; ADH_ZINC; 1.
 KW Oxidoreductase; Plasmid; Zinc.
 FT NON_TER 298
 SQ SEQUENCE 298 AA; 31092 MW; 49B2F8117C33AE87 CRC64;
 Query Match 64.8%; Score 35; DB 2; Length 298;
 Best Local Similarity 50.0%; Pred. No. 41;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 EVVVPGMDYS 11
 DB 250 EIIPEGADFS 259

RESULT 15

Q9XVK4
ID Q9XVK4 PRELIMINARY; PRT; 425 AA.
AC Q9XVK4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE R10D12.10 protein.
GN R10D12.10.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RA SEQUENCE FROM N.A.
RP Percy C.M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-99069613; PubMed-9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL: Z81109; CAB03241.1;
DR InterPro: IPR000719; Euk_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Transferrase.
KW
SQ SEQUENCE 425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;

Query Match 64.8%; Score 35; DB 5; Length 425;
Best Local Similarity 50.0%; Pred. No. 61;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
Db 335 EQIVPGLOY 344
:::|:|

RESULT 16

Q9A382
ID Q9A382 PRELIMINARY; PRT; 433 AA.
AC Q9A382;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Peptidoglycan-binding protein, putative.
GN CC3322.
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
OC Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RA SEQUENCE FROM N.A.
RX STRAIN-ATCC 19089 / CB15;
RX MEDLINE-21173698; PubMed-11259647;
RA Nieman W.C.; Feldblyum T.V.; Laub M.T.; Paulsen I.T.; Nelson K.E.;
RA Eisen J.; Heidelberg J.F.; Alley M.R.K.; Ohta N.; Maddock J.R.;
RA Potocka I.; Nelson W.C.; Newton A.; Stephens C.; Phadke N.D.; Ely B.;
RA DeBoy R.T.; Dodson R.J.; Durkin A.S.; Gwinn M.L.; Haft D.H.;
RA Kolonay J.F.; Smit J.; Craven M.B.; Khouri H.; Shetty J.; Berry K.;
RA Uterback T.; Tran K.; Wolf A.; Vamathevan J.; Ermolaeva M.; White O.;
RA Salzberg S.L.; Venter J.C.; Shapiro L.; Fraser C.M.;
RT "Complete genome sequence of Caulobacter crescentus."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
DR EMBL: AE005994; AAK25284.1;
DR HSSP: P41052; 1LTM.
DR TIGR: CC3322;
DR InterPro: IPR002477; PG_binding.
DR Pfam: PF01471; PG_binding_1;
KW Complete proteome.
SQ SEQUENCE 433 AA; 46169 MW; F7DD18B9F4CA10A7 CRC64;

Query Match 64.8%; Score 35; DB 16; Length 433;
Best Local Similarity 54.5%; Pred. No. 62;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
Db 266 EVILPGFDYS 276
:::|:|

RESULT 17

Q9YFI3
ID Q9YFI3 PRELIMINARY; PRT; 440 AA.
AC Q9YFI3;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE 440AA long hypothetical alkaline protease.
GN APEQ263.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococcaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RA SEQUENCE FROM N.A.
RP STRAIN=K1;
RX MEDLINE-99310339; PubMed-10382966;
RA Kavarabayasi Y.; Hino Y.; Horikawa H.; Yamazaki S.; Haikawa Y.;
RA Jin-no K.; Takahashi M.; Sekine M.; Baba S.-I.; Ankai A.; Kosugi H.;
RA Hosooyama A.; Fukui S.; Nagai Y.; Nishijima K.; Nakazawa H.;
RA Takamiya M.; Masuda S.; Funahashi T.; Tanaka T.; Kudoh Y.;
RA Yamazaki J.; Kishida N.; Oguchi A.; Aoki K.-I.; Kubota K.;
RA Nakamura Y.; Nomura N.; Sako Y.; Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
Crenarchaeon, Aeropyrum pernix K1."
RL DNA Res. 6:83-101(1999).
DR EMBL: AP000058; BAA79178.1;
DR HSSP: P00782; 2SET.
DR InterPro: IPR00209; Peptidase_S8.
DR Pfam: PF00082; Peptidase_S8; 1.
DR PRINTS: PR00723; SUBTILISIN.
DR PROSITE: PS00136; SUBTILASE_ASP; 1.
DR PROSITE: PS00137; SUBTILASE_HIS; 1.
DR PROSITE: PS00138; SUBTILASE_SER; 1.
KW Protease; Complete proteome.
SQ SEQUENCE 440 AA; 44680 MW; E43E6E2174B6F07E CRC64;

Query Match 64.8%; Score 35; DB 17; Length 440;
Best Local Similarity 66.7%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EVVPXGMDY 10
Db 120 EVLPWGVY 128
:::|:|

RESULT 18

O52680
ID O52680 PRELIMINARY; PRT; 511 AA.
AC O52680; O47289;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Core protein (Fragment).
GN RHSG.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RA SEQUENCE FROM N.A.
RC STRAIN-ECOR-50;
RW Wang Y.-D.; Zhao S.; Hill C.W.;

RT "Rhs elements comprise three subfamilies";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBDJ databases.
 FR EMBL; AF044506; AAC62388.1; -;
 DT NON_TER 511
 SQ SEQUENCE 511 AA; 55877 MW; C85402569450DBFF CRC64;

Query Match 64.8%; Score 35; DB 2; Length 511;
 Best Local Similarity 60.0%; Pred. No. 75;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
 ||| |||
 Db 381 EQVNPGLDY 390

RESULT 19

Q8XZLS PRELIMINARY; PRT; 517 AA.
 ID Q8XZLS;
 AC Q8XZLS;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Probable SUBSTATE-binding periplasmic (PBP) ABC transporter protein.
 DE RSC1380 OR RS04663.
 GN RSC1380
 OS Ralstonia solanacearum (Pseudomonas solanacearum).
 OC Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
 OC Ralstonia.
 OX NCBI_TaxID=305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-GMI1000;
 RX MEDLINE-21681879; PubMed-11823852;
 RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Canus J.C., Cattolico L., Chandler M., Choise N., Claudel-Renard C., Cunac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Signier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
 RA "Genome sequence of the plant pathogen Ralstonia solanacearum";
 RT Nature 415:497-502(2002).
 RL EMBL; AL640664; CAD15082.1; -;
 DR InterPro: IPR000914; SBP_bac_5.
 DR Pfam: PF00496; SBP_bac_5; 1.
 KW Complete proteome.
 SQ SEQUENCE 517 AA; 57349 MW; 861EE836F645F2DA CRC64;

Query Match 64.8%; Score 35; DB 16; Length 517;
 Best Local Similarity 66.7%; Pred. No. 76;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
 ||| |||
 Db 316 VVPQGVDA 324

RESULT 20

Q95P46 PRELIMINARY; PRT; 745 AA.
 ID Q95P46;
 AC Q95P46;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Na+/K+/2Cl-cotransporter (Fragment).
 DE Carcinus maenas (Common shore crab) (Green crab).
 OS Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunioidea; Portunidae; Carcinus.
 OX NCBI_TaxID=6759;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-GILL;
 RA Weihrach D., Towle D.W.;

RT "Sequence and expression analysis of the Na+/K+/2Cl- cotransporter in the euryhaline crabs Callinectes sapidus and Carcinus maenas";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBDJ databases.
 FR EMBL; AY035548; AAK62044.1; -;
 DT InterPro: IPR002293; AA/rel_primeasel.
 DR InterPro: IPR004841; Permease.
 DR Pfam: PF00324; aa_permeases; 1.
 FT NON_TER 745
 FT NON_TER 745
 SQ SEQUENCE 745 AA; 81249 MW; 08AE2D3E1F70C7BE CRC64;

Query Match 64.8%; Score 35; DB 5; Length 745;
 Best Local Similarity 75.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VVPXGMDYS 11
 ||| |||
 Db 625 VPOGLDYS 632

RESULT 21

Q9U6A3 PRELIMINARY; PRT; 1031 AA.
 ID Q9U6A3;
 AC Q9U6A3;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Na+/K+/2Cl-cotransporter.
 GN NKCC.
 OS Callinectes sapidus (Blue crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Eubrachyura; Portunioidea; Portunidae; Callinectes.
 OX NCBI_TaxID=6763;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-GILL;
 RC Towle D.W.;
 RA "Cloning and sequencing a Na+/K+/2Cl- cotransporter from gills of the euryhaline blue crab Callinectes sapidus";
 RT Am. Zoologist 38:114A-114A(1998).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE-GILL;
 RA Towle D.W., Weihrach D.;
 RA Submitted (SEP-1999) to the EMBL/GenBank/DBDJ databases.
 DR EMBL; AF190129; AAF05702.1; -;
 DR InterPro: IPR002293; AA/rel_primeasel.
 DR InterPro: IPR004842; KCL_cotransport.
 DR InterPro: IPR002443; NaKCL_transporter.
 DR PRINTS: PR01207; NAKCLTRNSPRT.
 DR TIGRFAMS: TIGR00930; 2a30; 1.
 SQ SEQUENCE 1031 AA; 113699 MW; F67773021AB05D71 CRC64;

Query Match 64.8%; Score 35; DB 5; Length 1031;
 Best Local Similarity 75.0%; Pred. No. 1.7e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VVPXGMDYS 11
 ||| |||
 Db 737 VPOGLDYS 744

RESULT 22

Q17704 PRELIMINARY; PRT; 1150 AA.
 ID Q17704;
 AC Q17704; O17976;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE C53A5.2 protein.
 GN C53A5.2.
 OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Mortimore B.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kershaw J., Kirsten J., Laister L., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
 RA Smalton N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstein L., Wilkinson-Sproat J., Wohldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RN Nature 368:32-38(1994).
 RL [3]
 RP SEQUENCE FROM N.A.
 RA Matthews L.;
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z81486; CAB03994.1; -;
 DR EMBL; Z78015; CAB03994.1; JOINED.
 DR EMBL; Z78015; CAB01437.1; -;
 DR EMBL; Z81486; CAB01437.1; JOINED.
 DR InterPro; IPR001201; PAP_25A_core.
 DR InterPro; IPR000051; SAM_Bind.
 DR InterPro; IPR003402; Unk_Met10.
 DR Pfam; PF02475; Met_10; 1.
 SQ SEQUENCE 1150 AA; 133001 MW; BA130A251C1A12F8 CRC64;

Query Match 64.8%; Score 35; DB 5; Length 1150;
 Best Local Similarity 66.7%; Pred. NO. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVFXGMDYS 11
 :|:|:|:
 Db 562 VLPVGIDYS 570

RESULT 23
 O52673
 ID 052673 PRELIMINARY; PRT; 1410 AA.
 AC 052673;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Core protein.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EC11;
 RX MEDLINE=98361897; PubMed=9696756;
 RA Wang Y.D., Zhao S., Hill C.W.;
 RT "Rhs elements comprise three subfamilies which diverged prior to
 RT acquisition by Escherichia coli.";
 RL J. Bacteriol. 180:4102-4110(1998).
 DR EMBL; AF044503; AAC32478.1; -;
 DR InterPro; IPR001826; Rhs.
 DR Pfam; PF03527; Rhs; 1.
 DR PRINTS; PR00394; RhsPROTEIN.
 SQ SEQUENCE 1410 AA; 158739 MW; 39ECB9F8C97FCB15 CRC64;

Query Match 64.8%; Score 35; DB 2; Length 1410;

Best Local Similarity 60.0%; Pred. NO. 2.4e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
 :|:|:|:|:
 Db 382 EQVNPGLDY 391

RESULT 24
 O52666
 ID 052666 PRELIMINARY; PRT; 1420 AA.
 AC 052666;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Core protein.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EC45;
 RX MEDLINE=98361897; PubMed=9696756;
 RA Wang Y.D., Zhao S., Hill C.W.;
 RT "Rhs elements comprise three subfamilies which diverged prior to
 RT acquisition by Escherichia coli.";
 RL J. Bacteriol. 180:4102-4110(1998).
 DR EMBL; AF044503; AAC32478.1; -;
 DR InterPro; IPR001826; Rhs.
 DR InterPro; IPR000130; Zn_MTPetdse.
 DR Pfam; PF03527; Rhs; 1.
 DR PRINTS; PR00394; RhsPROTEIN.
 DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN_1.
 SQ SEQUENCE 1420 AA; 159215 MW; E7851E4D48740621 CRC64;

Query Match 64.8%; Score 35; DB 2; Length 1420;
 Best Local Similarity 60.0%; Pred. NO. 2.4e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
 :|:|:|:|:
 Db 381 EQVNPGLDY 390

RESULT 25
 O27146
 ID 027146 PRELIMINARY; PRT; 1474 AA.
 AC 027146;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative membrane protein.
 GN MTH1074.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DELTA H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., DeLoughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Wani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RT "Complete genome sequence of Methanobacterium thermoautotrophicum
 RT deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 DR EMBL; AE000878; AAB85563.1; -;

DR InterPro; IPR001434; DUF11.
 DR Pfam; PF01345; DUF11; 9.
 KW Complete proteome.
 SQ SEQUENCE 1474 AA; 153713 MW; 11D4D27BD86255F0 CRC64;
 Query Match 64.8%; Score 35; DB 17; Length 1474;
 Best Local Similarity 55.6%; Pred. No. 2.5e+02;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 EVVPXGMDY 10
 Db 1238 DVLPAGLDY 1246

Search completed: June 10, 2003, 13:46:33
 Job time : 25.7857 secs

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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:24:45 ; Search time 31.3571 Seconds
(without alignments)
46.744 Million cell updates/sec

Title: US-09-909-164-13
Perfect score: 54
Sequence: 1 EEVVPXGMDYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	52	96.3	11	23	ABB80524
2	52	96.3	11	23	ABB80528
3	52	96.3	11	23	ABB80529
4	52	96.3	11	23	ABB80561
5	52	96.3	11	23	ABB80562
6	47	87.0	11	23	ABB80538
7	47	87.0	11	23	ABB80542
8	47	87.0	11	23	ABB80543
9	46	85.2	11	23	ABB80521
10	46	85.2	11	23	ABB80522
					Hepatitis C virus
					Hepatitis C virus
					Hepatitis C virus
					Hepatitis C virus
					Hepatitis C virus
					Hepatitis C virus
					Hepatitis C virus
					Hepatitis C virus
					Hepatitis C virus
					Hepatitis C virus

RESULT 1
ABB80524
ID ABB80524 standard; peptide; 11 AA.

11	46	85.2	11	23	ABB80525	Hepatitis C virus
12	46	85.2	11	23	ABB80526	Hepatitis C virus
13	46	85.2	11	23	ABB80547	Hepatitis C virus
14	46	85.2	11	23	ABB80548	Hepatitis C virus
15	46	85.2	11	23	ABB80551	Hepatitis C virus
16	46	85.2	11	23	ABB80556	Hepatitis C virus
17	46	85.2	11	23	ABB80557	Hepatitis C virus
18	46	85.2	11	23	ABB80559	Hepatitis C virus
19	46	85.2	11	23	ABB80563	Hepatitis C virus
20	46	85.2	11	23	ABB80564	Hepatitis C virus
21	46	85.2	11	23	ABB80565	Hepatitis C virus
22	46	85.2	11	23	ABB80566	Hepatitis C virus
23	46	85.2	11	23	ABB80567	Hepatitis C virus
24	46	85.2	11	23	ABB80568	Hepatitis C virus
25	45	83.3	11	23	ABB80523	Hepatitis C virus
26	45	83.3	11	23	ABB80527	Hepatitis C virus
27	45	83.3	11	23	ABB80538	Hepatitis C virus
28	45	83.3	11	23	ABB80560	Hepatitis C virus
29	44	81.5	11	23	ABB80533	Hepatitis C virus
30	44	81.5	11	23	ABB80534	Hepatitis C virus
31	41	75.9	11	23	ABB80535	Hepatitis C virus
32	41	75.9	11	23	ABB80536	Hepatitis C virus
33	41	75.9	11	23	ABB80539	Hepatitis C virus
34	41	75.9	11	23	ABB80540	Hepatitis C virus
35	40	74.1	11	23	ABB80537	Hepatitis C virus
36	40	74.1	11	23	ABB80541	Hepatitis C virus
37	40	74.1	11	23	ABB80544	Hepatitis C virus
38	40	74.1	11	23	ABB80545	Hepatitis C virus
39	40	74.1	11	23	ABB80549	Hepatitis C virus
40	40	74.1	11	23	ABB80552	Hepatitis C virus
41	40	74.1	11	23	ABB80553	Hepatitis C virus
42	39	72.2	11	23	ABB80546	Hepatitis C virus
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44	39	72.2	11	23	ABB80554	Hepatitis C virus
45	39	72.2	11	23	ABB80555	Hepatitis C virus
46	38	70.4	11	23	ABB80530	Hepatitis C virus
47	37	68.5	11	23	ABB80532	Hepatitis C virus
48	37	68.5	11	23	ABB80533	Hepatitis C virus
49	36	66.7	20	20	AAU76810	Hepatitis C virus
50	36	66.7	341	22	AAE00907	Citrus partial suc
51	36	66.7	348	22	AAE00908	Citrus partial suc
52	36	66.7	460	23	ABY1579	Herbicidally activ
53	36	66.7	1022	22	ABG03621	Novel human diagno
54	36	66.7	1022	22	ABG05826	Novel human diagno
55	36	66.7	1022	22	ABG08173	Novel human diagno
56	36	66.7	1068	13	AAZ20198	Sucrose phosphate
57	36	66.7	1068	13	AAZ27931	SFS protein. Zea
58	36	66.7	1068	18	AAW38266	Maize sucrose phos
59	36	66.7	1068	18	AAW09869	Sucrose phosphate
60	36	66.7	1071	15	AAW60796	Rice sucrose phosp
61	36	66.7	1083	23	ABY92875	Herbicidally activ
62	35	64.8	2778	22	ABY58683	Drosophila melanog
63	34.5	63.0	748	22	AAW40225	Human polypeptide
64	34	63.0	140	16	AAW42332	Mab L243 VH region
65	34	63.0	140	16	AAW42335	Humanized antibody
66	34	63.0	140	16	AAW42365	CDR-grafted L243-g
67	34	63.0	140	16	AAW42377	MHC-II Mab L243 he
68	34	63.0	143	22	ABY60256	Drosophila melanog
69	34	63.0	150	21	AAW28379	Arabidopsis thalia
70	34	63.0	150	22	AAW87623	Bovine mammary tis
71	34	63.0	222	22	AAU03629	Group B Streptococ
72	34	63.0	222	23	ABP26468	Streptococcus poly
73	34	63.0	565	23	ABY53631	Lactococcus lactis
74	34	63.0	587	21	AAW74287	Neisseria meningit
75	34	63.0	1062	22	AAU33615	Pseudomonas aerugi

ALIGNMENTS

XX AC ABB80524;
 XX DT 08-OCT-2002 (first entry)
 XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
 XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX OS virucide.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT WO200208251-A2.
 FT 31-JAN-2002.
 FT 19-JUL-2001; 2001WO-US23169.
 FT 21-JUL-2000; 2000US-220101P.
 FT (CORV-) CORVAS INT INC.
 FT Lim-wilby M, Levy OE, Brunck TK;
 FT WPI; 2002-361643/39.
 FT Novel peptide compound having hepatitis C virus protease inhibitory
 FT activity useful for treating disorders associated with hepatitis C
 FT virus protease -
 FT Claim 17; Page 64; 69pp; English.
 FT The sequence represents a peptide compound of the invention having
 FT hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 FT invention are alpha-ketoamide peptide analogues. The peptides have
 FT virucide activity, and are useful for treating and in the manufacture of
 FT a medicament to treat disorders associated with HCV protease. A
 FT pharmaceutical composition comprising the peptide as an active ingredient
 FT is useful for treating disorders associated with hepatitis C virus.
 XX PS Claim 17; Page 64; 69pp; English.
 XX CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX SQ Sequence 11 AA;
 Query Match 96.3%; Score 52; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEVVPXGMDYS 11
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 DB 1 EEVVPXGMDYS 11
 RESULT 2
 ABB80528
 ID ABB80528 standard; peptide; 11 AA.
 XX AC ABB80528;
 XX DT 08-OCT-2002 (first entry)
 XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
 XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;

KW virucide.
 XX Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 8 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT WO200208251-A2.
 FT 31-JAN-2002.
 FT 19-JUL-2001; 2001WO-US23169.
 FT 21-JUL-2000; 2000US-220101P.
 FT (CORV-) CORVAS INT INC.
 FT Lim-wilby M, Levy OE, Brunck TK;
 FT WPI; 2002-361643/39.
 FT Novel peptide compound having hepatitis C virus protease inhibitory
 FT activity useful for treating disorders associated with hepatitis C
 FT virus protease -
 FT Claim 17; Page 64; 69pp; English.
 FT The sequence represents a peptide compound of the invention having
 FT hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 FT invention are alpha-ketoamide peptide analogues. The peptides have
 FT virucide activity, and are useful for treating and in the manufacture of
 FT a medicament to treat disorders associated with HCV protease. A
 FT pharmaceutical composition comprising the peptide as an active ingredient
 FT is useful for treating disorders associated with hepatitis C virus.
 XX PS Claim 17; Page 64; 69pp; English.
 XX CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX SQ Sequence 11 AA;
 Query Match 96.3%; Score 52; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEVVPXGMDYS 11
 |||||
 DB 1 EEVVPXGMDYS 11
 RESULT 3
 ABB80529
 ID ABB80529 standard; peptide; 11 AA.
 XX AC ABB80529;
 XX DT 08-OCT-2002 (first entry)
 XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9.
 XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX OS virucide.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"

FT FT /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT FT residue 7"
 FT FT
 FT FT Misc-difference 8
 FT FT /note= "D-form residue"
 FT FT Misc-difference 9
 FT FT /note= "D-form residue"
 FT FT Modified-site 11
 FT FT /note= "C-terminal amide"
 FT FT
 XX WO200208251-A2.
 PN XX
 XX 31-JAN-2002.
 XX XX
 XX 19-JUL-2001; 2001WO-US23169.
 XX XX
 XX 21-JUL-2000; 2000US-220101P.
 XX XX
 XX (CORV-) CORVAS INT INC.
 XX XX
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX XX
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease -
 PT
 XX Claim 17; Page 64; 69pp; English.
 XX
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 96.3%; Score 52; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEVVPXGMDYS 11
 DB 1 EEVVPXGMDYS 11
 RESULT 4
 ABB80561
 ID ABB80561 standard; peptide; 11 AA.
 XX AC ABB80561;
 XX
 XX 08-OCT-2002 (first entry)
 XX
 XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
 XX
 XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 8 /note= "D-form residue"
 FT Modified-site 8 /note= "Oxymethionine"
 FT
 FT

FT Modified-site 11 /note= "C-terminal amide"
 FT
 XX WO200208251-A2.
 PN XX
 XX 31-JAN-2002.
 XX XX
 XX 19-JUL-2001; 2001WO-US23169.
 XX XX
 XX 21-JUL-2000; 2000US-220101P.
 XX XX
 XX (CORV-) CORVAS INT INC.
 XX XX
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX XX
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease -
 PT
 XX Claim 17; Page 65; 69pp; English.
 XX
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX
 XX Sequence 11 AA;
 SQ
 Query Match 96.3%; Score 52; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEVVPXGMDYS 11
 DB 1 EEVVPXGMDYS 11
 RESULT 5
 ABB80562
 ID ABB80562 standard; peptide; 11 AA.
 XX AC ABB80562;
 XX
 XX 08-OCT-2002 (first entry)
 XX
 XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42.
 DE
 XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 8 /note= "D-form residue"
 FT Modified-site 8 /note= "Oxymethionine"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT
 XX WO200208251-A2.
 PN

XX PD 31-JAN-2002.
 XX PF 19-JUL-2001; 2001WO-US23169.
 XX PR 21-JUL-2000; 2000US-220101P.
 XX PA (CORV-) CORVAS INT INC.
 XX PI Lim-wilby M, Levy OE, Brunck TK;
 XX PS WPI; 2002-361643/39.
 XX DR Novel peptide compound having hepatitis C virus protease inhibitory
 XX PT activity useful for treating disorders associated with hepatitis C
 XX PT virus protease
 XX PS Claim 17; Page 65; 69pp; English.
 XX CC The sequence represents a peptide compound of the invention having
 XX CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 XX CC invention are alpha-ketoamide peptide analogues. The peptides have
 XX CC virucide activity, and are useful for treating and in the manufacture of
 XX CC a medicament to treat disorders associated with HCV protease. A
 XX CC pharmaceutical composition comprising the peptide as an active ingredient
 XX CC is useful for treating disorders associated with hepatitis C virus.
 XX SQ Sequence 11 AA;
 Query Match 96.3%; Score 52; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0015;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EEVVPXGMDYS 11
 Db 1 EEVVPXGMDYS 11
 RESULT 6
 ABB80538
 ID ABB80538 standard; peptide; 11 AA.
 AC ABB80538;
 XX 08-OCT-2002 (first entry)
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #18.
 XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 KW Synthetic.
 OS Key Location/Qualifiers
 XX Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "D-form residue"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT WO200208251-A2.
 PN 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 XX PF 21-JUL-2000; 2000US-220101P.
 XX PR (CORV-) CORVAS INT INC.
 XX PI Lim-wilby M, Levy OE, Brunck TK;
 XX PS WPI; 2002-361643/39.
 XX DR Novel peptide compound having hepatitis C virus protease inhibitory
 XX PT activity useful for treating disorders associated with hepatitis C
 XX PT virus protease

XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 XX PT activity useful for treating disorders associated with hepatitis C
 XX PT virus protease
 XX PS Claim 17; Page 64; 69pp; English.
 XX CC The sequence represents a peptide compound of the invention having
 XX CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 XX CC invention are alpha-ketoamide peptide analogues. The peptides have
 XX CC virucide activity, and are useful for treating and in the manufacture of
 XX CC a medicament to treat disorders associated with HCV protease. A
 XX CC pharmaceutical composition comprising the peptide as an active ingredient
 XX CC is useful for treating disorders associated with hepatitis C virus.
 XX SQ Sequence 11 AA;
 Query Match 87.0%; Score 47; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.014;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 EEVVPXGMDYS 11
 Db 1 EEVVPXGMDYS 11
 RESULT 7
 ABB80542
 ID ABB80542 standard; peptide; 11 AA.
 AC ABB80542;
 XX 08-OCT-2002 (first entry)
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #22.
 XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 KW Synthetic.
 OS Key Location/Qualifiers
 XX Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 8 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT WO200208251-A2.
 PN 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 XX PF 21-JUL-2000; 2000US-220101P.
 XX PR (CORV-) CORVAS INT INC.
 XX PA Lim-wilby M, Levy OE, Brunck TK;
 XX PS WPI; 2002-361643/39.
 XX DR Novel peptide compound having hepatitis C virus protease inhibitory
 XX PT activity useful for treating disorders associated with hepatitis C
 XX PT virus protease

XX

PS Claim 17; Page 65; 69pp; English.

XX

CC The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.

XX

SQ Sequence 11 AA;

Query Match 87.0%; Score 47; DB 23; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.014; Length 11;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1 EEVVPXGMDYS 11

|||||

Db

1 EEVVPXGQDYS 11

RESULT 8

ABB0543

ID ABB0543 standard; peptide; 11 AA.

AC

ABB0543;

XX

DT 08-OCT-2002 (first entry)

XX

DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #23.

XX

KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT

Modified-site 1 /note= "N-terminal acetyl"

FT

Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"

FT

Misc-difference 8 /note= "D-form residue"

FT

Misc-difference 9 /note= "D-form residue"

FT

Modified-site 11 /note= "C-terminal amide"

FT

WO200208251-A2.

XX

31-JAN-2002.

XX

19-JUL-2001; 2001WO-US23169.

XX

21-JUL-2000; 2000US-220101P.

XX

(CORV-) CORVAS INT INC.

XX

Lim-wilby M, Levy OE, Brunck TK;

XX

WPI; 2002-361643/39.

XX

Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease

XX

Claim 17; Page 65; 69pp; English.

PS

CC The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have

XX

CC

virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.

XX

SQ Sequence 11 AA;

Query Match 87.0%; Score 47; DB 23; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.014; Length 11;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY

1 EEVVPXGMDYS 11

|||||

Db

1 EEVVPXGQDYS 11

RESULT 9

ABB0521

ID ABB0521 standard; peptide; 11 AA.

XX

AC ABB0521;

XX

DT 08-OCT-2002 (first entry)

XX

DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1.

XX

KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT

Modified-site 1 /note= "N-terminal acetyl"

FT

Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"

FT

Modified-site 11 /note= "C-terminal amide"

FT

WO200208251-A2.

XX

31-JAN-2002.

XX

19-JUL-2001; 2001WO-US23169.

XX

21-JUL-2000; 2000US-220101P.

XX

(CORV-) CORVAS INT INC.

XX

Lim-wilby M, Levy OE, Brunck TK;

XX

WPI; 2002-361643/39.

XX

Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease

XX

Claim 17; Page 64; 69pp; English.

PS

CC The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.

XX

SQ Sequence 11 AA;

Query Match 85.2%; Score 46; DB 23; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.022; Length 11;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EEVVPXGMDYS 11
 DB 1 EEVVPXGMSYS 11

RESULT 10

ABB80522
 ID ABB80522 standard; peptide; 11 AA.

XX AC ABB80522;
 XX DT 08-OCT-2002 (first entry)
 XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
 XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX KW virucide.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl"
 FT Modified-site 6
 FT /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 9
 FT /note= "D-form residue"
 FT Modified-site 11
 FT /note= "C-terminal amide"
 XX WO200208251-A2.
 XX 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 XX 21-JUL-2000; 2000US-220101P.
 XX (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.

Novel peptide compound having hepatitis C virus protease inhibitory
 activity useful for treating disorders associated with hepatitis C
 virus protease

Claim 17; Page 64; 69pp; English.

The sequence represents a peptide compound of the invention having
 hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 invention are alpha-ketoamide peptide analogues. The peptides have
 virucide activity, and are useful for treating and in the manufacture of
 a medicament to treat disorders associated with HCV protease. A
 pharmaceutical composition comprising the peptide as an active ingredient
 is useful for treating disorders associated with hepatitis C virus.

Sequence 11 AA;

Query Match 85.2%; Score 46; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.022;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EEVVPXGMDYS 11
 DB 1 EEVVPXGMSYS 11

RESULT 11

ABB80525

ID ABB80525 standard; peptide; 11 AA.

XX AC ABB80525;
 XX DT 08-OCT-2002 (first entry)

XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5.
 XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX KW virucide.
 XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl"
 FT Modified-site 6
 FT /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 8
 FT /note= "D-form residue"
 FT Modified-site 11
 FT /note= "C-terminal amide"

XX WO200208251-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

Novel peptide compound having hepatitis C virus protease inhibitory
 activity useful for treating disorders associated with hepatitis C
 virus protease

Claim 17; Page 64; 69pp; English.

The sequence represents a peptide compound of the invention having
 hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 invention are alpha-ketoamide peptide analogues. The peptides have
 virucide activity, and are useful for treating and in the manufacture of
 a medicament to treat disorders associated with HCV protease. A
 pharmaceutical composition comprising the peptide as an active ingredient
 is useful for treating disorders associated with hepatitis C virus.

Sequence 11 AA;

Query Match 85.2%; Score 46; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.022;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EEVVPXGMDYS 11
 DB 1 EEVVPXGMSYS 11

RESULT 12

ABB80526

ID ABB80526 standard; peptide; 11 AA.

XX AC ABB80526;

XX DT 08-OCT-2002 (first entry)

XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6.

KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT
 FT Misc-difference 8 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT
 XX WO200208251-A2.
 PN 31-JAN-2002.
 XX
 FT 19-JUL-2001; 2001WO-US23169.
 FT 21-JUL-2000; 2000US-220101P.
 FT (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease
 XX
 PS Claim 17; Page 64; 69pp; English.
 XX
 CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX
 PS Sequence 11 AA;
 XX
 CC Query Match 85.2%; Score 46; DB 23; Length 11;
 CC Best Local Similarity 90.9%; Pred. No. 0.022;
 CC Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 EEVVPXGMDYS 11
 Dd ||||| ||
 1 EEVVPXGMSYS 11
 RESULT 13
 ABB80547
 ID ABB80547 standard; peptide; 11 AA.
 XX
 AC ABB80547;
 XX
 DT 08-OCT-2002 (first entry)
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #27.
 XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX Synthetic.
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT
 FT Misc-difference 8 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT
 XX WO200208251-A2.
 PN 31-JAN-2002.
 XX
 FT 19-JUL-2001; 2001WO-US23169.
 FT 21-JUL-2000; 2000US-220101P.
 FT (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease
 XX
 PS Claim 17; Page 64; 69pp; English.
 XX
 CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.

FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Modified-site 11 /note= "C-terminal amide"
 FT
 XX WO200208251-A2.
 PN 31-JAN-2002.
 XX
 FT 19-JUL-2001; 2001WO-US23169.
 FT 21-JUL-2000; 2000US-220101P.
 FT (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease
 XX
 PS Claim 17; Page 65; 69pp; English.
 XX
 CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX
 PS Sequence 11 AA;
 XX
 CC Query Match 85.2%; Score 46; DB 23; Length 11;
 CC Best Local Similarity 90.9%; Pred. No. 0.022;
 CC Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 EEVVPXGMDYS 11
 Dd ||||| ||
 1 EEVVPXGTDYS 11
 RESULT 14
 ABB80548
 ID ABB80548 standard; peptide; 11 AA.
 XX
 AC ABB80548;
 XX
 DT 08-OCT-2002 (first entry)
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #28.
 XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT
 XX WO200208251-A2.
 PN 31-JAN-2002.
 XX
 FT 19-JUL-2001; 2001WO-US23169.
 FT 21-JUL-2000; 2000US-220101P.
 FT (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease
 XX
 PS Claim 17; Page 65; 69pp; English.
 XX
 CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.

PN WO200208251-A2.
 XX 31-JAN-2002.
 PD 19-JUL-2001; 2001WO-US23169.
 XX 21-JUL-2000; 2000US-220101P.
 PR (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 PI WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 XX activity useful for treating disorders associated with hepatitis C
 XX virus protease.
 XX Claim 17; Page 65; 69pp; English.
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX Sequence 11 AA;
 SQ Query Match 85.2%; Score 46; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.022;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGMDYS 11
 DB ||||| |||
 1 EEVVPXGTDYS 11

RESULT 15
 ABB80551
 ID ABB80551 standard; peptide; 11 AA.
 AC ABB80551;
 XX 08-OCT-2002 (first entry)
 DT Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #31.
 DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 KW Synthetic.
 OS Key Location/Qualifiers
 FH Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT WO200208251-A2.
 PN 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 PD 21-JUL-2000; 2000US-220101P.
 XX (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 PI WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 XX activity useful for treating disorders associated with hepatitis C
 XX virus protease.

PA (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 DR Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease.
 XX Claim 17; Page 65; 69pp; English.
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX Sequence 11 AA;
 SQ Query Match 85.2%; Score 46; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.022;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGMDYS 11
 DB ||||| |||
 1 EEVVPXGTDYS 11

RESULT 16
 ABB80556
 ID ABB80556 standard; peptide; 11 AA.
 AC ABB80556;
 XX 08-OCT-2002 (first entry)
 DT Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #36.
 DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 KW Synthetic.
 OS Key Location/Qualifiers
 FH Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 8 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT WO200208251-A2.
 PN 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 PD 21-JUL-2000; 2000US-220101P.
 XX (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 PI WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 XX activity useful for treating disorders associated with hepatitis C
 XX virus protease.

PT virus protease .
 XX Claim 17; Page 65; 69pp; English.
 XX
 CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX
 SQ Sequence 11 AA;
 Query Match 85.2%; Score 46; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.022;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGMDYS 11
 DB 1 EEVVPXGSDYS 11
 RESULT 17
 ABB80557
 ID ABB80557 standard; peptide; 11 AA.
 XX
 AC ABB80557;
 XX
 DT 08-OCT-2002 (first entry)
 XX
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #37.
 XX
 KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 8 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 XX
 PN WO200208251-A2.
 XX
 XX 31-JAN-2002.
 XX
 XX 19-JUL-2001; 2001WO-US23169.
 XX
 XX 21-JUL-2000; 2000US-220101P.
 XX
 XX (CORV-) CORVAS INT INC.
 XX
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 XX activity useful for treating disorders associated with hepatitis C
 XX virus protease .
 XX
 XX Claim 17; Page 65; 69pp; English.
 XX
 CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.

CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX
 SQ Sequence 11 AA;
 Query Match 85.2%; Score 46; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.022;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGMDYS 11
 DB 1 EEVVPXGSDYS 11
 RESULT 18
 ABB80559
 ID ABB80559 standard; peptide; 11 AA.
 XX
 AC ABB80559;
 XX
 DT 08-OCT-2002 (first entry)
 XX
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #39.
 XX
 KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 8 /note= "D-form residue"
 FT Modified-site 8 /note= "Oxymethionine"
 FT Modified-site 11 /note= "C-terminal amide"
 XX
 PN WO200208251-A2.
 XX
 XX 31-JAN-2002.
 XX
 XX 19-JUL-2001; 2001WO-US23169.
 XX
 XX 21-JUL-2000; 2000US-220101P.
 XX
 XX (CORV-) CORVAS INT INC.
 XX
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 XX activity useful for treating disorders associated with hepatitis C
 XX virus protease .
 XX
 XX Claim 17; Page 65; 69pp; English.
 XX
 CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.

SQ Sequence 11 AA;

Query Match 85.2%; Score 46; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.022;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
|||||||
Db 1 EEVVPXGMSYS 11

RESULT 19

ABB80563
ID ABB80563 standard; peptide; 11 AA.

XX AC ABB80563;

XX DT 08-OCT-2002 (first entry)

XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #43.

XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.

XX KW virucide.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 1

XX FT /note= "N-terminal acetyl"

XX FT Modified-site 6

XX FT /note= "Valyl carbonyl forming keto-amide linkage with
residue 7"

XX FT Modified-site 11

XX FT /note= "C-terminal amide"

XX XX WO200208251-A2.

XX PN 31-JAN-2002.

XX PD 19-JUL-2001; 2001WO-US23169.

XX PF 21-JUL-2000; 2000US-220101P.

XX PR (CORV-) CORVAS INT INC.

XX PA Lim-wilby M, Levy OE, Brunck TK;

XX PI WPI; 2002-361643/39.

XX DR Novel peptide compound having hepatitis C virus protease inhibitory
activity useful for treating disorders associated with hepatitis C
virus protease

XX PT Claim 17; Page 65; 69pp; English.

XX PS The sequence represents a peptide compound of the invention having
hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
invention are alpha-ketoamide peptide analogues. The peptides have
virucide activity, and are useful for treating and in the manufacture of
a medicament to treat disorders associated with HCV protease. A
pharmaceutical composition comprising the peptide as an active ingredient
is useful for treating disorders associated with hepatitis C virus.

XX CC Query Match 85.2%; Score 46; DB 23; Length 11;

XX CC Best Local Similarity 90.9%; Pred. No. 0.022;

XX CC Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11

|||||||

Db 1 EEVVPXGMSYS 11

Query Match

Best Local Similarity 90.9%; Pred. No. 0.022;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11

|||||||

Db 1 EEVVPXGMSYS 11

RESULT 21

ABB80565

ID ABB80565 standard; peptide; 11 AA.

XX AC ABB80565;

XX DT 08-OCT-2002 (first entry)

XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #45.

RESULT 20

ABB80564

ID ABB80564 standard; peptide; 11 AA.

XX AC ABB80564;

XX DT 08-OCT-2002 (first entry)

XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44.

XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.

XX KW virucide.

XX OS Synthetic.

XX FH Key Location/Qualifiers

XX FT Modified-site 1

XX FT /note= "N-terminal acetyl"

XX FT Modified-site 6

XX FT /note= "Leucyl carbonyl forming keto-amide linkage with
residue 7"

XX FT Modified-site 11

XX FT /note= "C-terminal amide"

XX XX WO200208251-A2.

XX PN 31-JAN-2002.

XX PD 19-JUL-2001; 2001WO-US23169.

XX PF 21-JUL-2000; 2000US-220101P.

XX PR (CORV-) CORVAS INT INC.

XX PA Lim-wilby M, Levy OE, Brunck TK;

XX PI WPI; 2002-361643/39.

XX DR Novel peptide compound having hepatitis C virus protease inhibitory
activity useful for treating disorders associated with hepatitis C
virus protease

XX PT Claim 17; Page 65; 69pp; English.

XX PS The sequence represents a peptide compound of the invention having
hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
invention are alpha-ketoamide peptide analogues. The peptides have
virucide activity, and are useful for treating and in the manufacture of
a medicament to treat disorders associated with HCV protease. A
pharmaceutical composition comprising the peptide as an active ingredient
is useful for treating disorders associated with hepatitis C virus.

XX CC Query Match 85.2%; Score 46; DB 23; Length 11;

XX CC Best Local Similarity 90.9%; Pred. No. 0.022;

XX CC Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11

|||||||

Db 1 EEVVPXGMSYS 11

XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX
 XX Synthetic.
 XX
 XX Location/Qualifiers
 FH Modified-site 1
 FT /note= "N-terminal acetyl"
 FT 6
 FT Modified-site
 FT /note= "Norleucyl carbonyl forming keto-amide linkage
 FT with residue 7"
 FT
 FT Modified-site 11
 FT /note= "C-terminal amide"
 FT
 XX WO200208251-A2.
 XX
 XX 31-JAN-2002.
 XX
 XX 19-JUL-2001; 2001WO-US23169.
 PF
 XX 21-JUL-2000; 2000US-220101P.
 XX
 XX (CORV-) CORVAS INT INC.
 XX
 XX Lim-wilby M, Levy OE, Brunck TK;
 PI
 XX WPI; 2002-361643/39.
 DR
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease
 PT
 XX
 PS Claim 17; Page 65; 69pp; English.
 XX
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX
 XX Sequence 11 AA;
 PS
 Query Match 85.2%; Score 46; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.022;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGMDYS 11
 DB 1 EEVVPXGMSYS 11
 XX
 RESULT 22
 ABB80566
 ID ABB80566 standard; peptide; 11 AA.
 XX
 AC ABB80566;
 XX
 XX 08-OCT-2002 (first entry)
 DT
 XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46.
 DE
 XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 KW
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "N-terminal acetyl"
 FT 6
 FT Modified-site
 FT /note= "N-terminal acetyl"

FT /note= "2-aminoisobutryl carbonyl residue forming a
 FT keto-amide linkage with residue 7"
 FT Modified-site 11
 FT /note= "C-terminal amide"
 XX
 XX WO200208251-A2.
 XX
 XX 31-JAN-2002.
 XX
 XX 19-JUL-2001; 2001WO-US23169.
 PF
 XX 21-JUL-2000; 2000US-220101P.
 XX
 XX (CORV-) CORVAS INT INC.
 XX
 XX Lim-wilby M, Levy OE, Brunck TK;
 PI
 XX WPI; 2002-361643/39.
 DR
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease
 PT
 XX
 PS Claim 17; Page 65; 69pp; English.
 XX
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX
 XX Sequence 11 AA;
 PS
 Query Match 85.2%; Score 46; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.022;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGMDYS 11
 DB 1 EEVVPXGMSYS 11
 XX
 RESULT 23
 ABB80567
 ID ABB80567 standard; peptide; 11 AA.
 XX
 AC ABB80567;
 XX
 XX 08-OCT-2002 (first entry)
 DT
 XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #47.
 DE
 XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 KW
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /note= "N-terminal acetyl"
 FT 6
 FT Modified-site
 FT /note= "(s,s)allothreonyl carbonyl residue forming a
 FT keto-amide linkage with residue 7"
 FT
 FT Modified-site 11
 FT /note= "C-terminal amide"
 FT
 XX WO200208251-A2.
 XX
 XX 31-JAN-2002.
 XX
 XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.
 XX (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease
 XX
 XX Claim 17; Page 65; 69pp; English.
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX
 XX SQ Sequence 11 AA;
 XX
 XX Query Match 85.2%; Score 46; DB 23; Length 11;
 XX Best Local Similarity 90.9%; Pred. No. 0.022;
 XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGMDYS 11
 DB ||||| ||
 1 EEVVPXGMSYS 11
 RESULT 24
 ABB80568
 ID ABB80568 standard; peptide; 11 AA.
 XX ABB80568;
 XX 08-OCT-2002 (first entry)
 XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #48.
 DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX virucide.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Alpha-propionyl-glycyl-carbonyl residue forming
 FT a keto-amide linkage with residue 7"
 FT Modified-site 11 /note= "C-terminal amide"
 FT WO200208251-A2.
 XX 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 XX 21-JUL-2000; 2000US-220101P.
 XX (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory

PT activity useful for treating disorders associated with hepatitis C
 PT virus protease
 XX Claim 17; Page 65; 69pp; English.
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX
 XX SQ Sequence 11 AA;
 XX
 XX Query Match 85.2%; Score 46; DB 23; Length 11;
 XX Best Local Similarity 90.9%; Pred. No. 0.022;
 XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGMDYS 11
 DB ||||| ||
 1 EEVVPXGMSYS 11
 RESULT 25
 ABB80523
 ID ABB80523 standard; peptide; 11 AA.
 XX ABB80523;
 XX 08-OCT-2002 (first entry)
 XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #3.
 DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX virucide.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT WO200208251-A2.
 XX 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 XX 21-JUL-2000; 2000US-220101P.
 XX (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease
 XX
 XX Claim 17; Page 64; 69pp; English.
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have

CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.

XX

SQ Sequence 11 AA;

Query Match 83.3%; Score 45; DB 23; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.034;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11

|||||||

Db 1 EEVVPXGMHYS 11

Search completed: June 10, 2003, 13:39:09

Job time : 31.3571 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:31:45 ; Search time 9.64286 Seconds
(without alignments)
33.564 Million cell updates/sec

Title: US-09-909-164-13
Perfect score: 54
Sequence: 1 EHVVPXGMDYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	36	66.7	341	US-08-853-948B-4	Sequence 4, Appli
2	36	66.7	348	US-08-853-948B-5	Sequence 5, Appli
3	36	66.7	368	US-09-697-367-24	Sequence 24, Appli
4	36	66.7	1068	US-08-429-054A-11	Sequence 11, Appli
5	36	66.7	1068	US-08-718-777-7	Sequence 7, Appli
6	36	66.7	1068	US-09-051-341-7	Sequence 7, Appli
7	34	63.0	140	US-08-569-147-76	Sequence 76, Appli
8	34	63.0	140	US-08-569-147-82	Sequence 82, Appli
9	33	61.1	59	US-08-963-851-14	Sequence 14, Appli
10	33	61.1	378	US-08-070-165F-8	Sequence 8, Appli
11	33	61.1	378	US-08-885-418-8	Sequence 8, Appli
12	33	61.1	801	US-09-383-630-6	Sequence 6, Appli
13	32	59.3	65	5177197-51	Patent No. 5177197
14	32	59.3	102	US-08-580-988A-23	Sequence 23, Appli
15	32	59.3	152	US-08-460-694-4	Sequence 4, Appli
16	32	59.3	152	US-08-460-744-4	Sequence 4, Appli
17	32	59.3	152	US-07-667-711B-4	Sequence 4, Appli
18	32	59.3	173	US-08-193-977-7	Sequence 7, Appli
19	32	59.3	189	US-08-464-517-21	Sequence 21, Appli
20	32	59.3	189	US-08-246-361A-21	Sequence 21, Appli
21	32	59.3	189	US-08-463-772-21	Sequence 21, Appli
22	32	59.3	189	PCT-US93-05000-21	Sequence 21, Appli
23	32	59.3	231	US-08-926-842B-20	Sequence 20, Appli
24	32	59.3	236	US-08-464-517-22	Sequence 22, Appli
25	32	59.3	236	US-08-246-361A-22	Sequence 22, Appli
26	32	59.3	236	US-08-463-772-22	Sequence 22, Appli
27	32	59.3	236	PCT-US93-05000-22	Sequence 22, Appli

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Patent No. 5177197
Sequence 10, Appli
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Sequence 2, Appli
Sequence 5, Appli
Sequence 7, Appli
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Sequence 4, Appli
Sequence 5, Appli
Patent No. 5177197
Sequence 514, Ap
Sequence 57, Appli
Sequence 3003, Ap
Sequence 4, Appli
Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-853-948B-4
; Sequence 4, Application US/08853948B
; Patent No. 6210943
; GENERAL INFORMATION:
; APPLICANT: AKIHAMA, Toyota
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE FROM CITRUS AND DNA ENCODING
; TITLE OF INVENTION: THE SAME
; FILE REFERENCE: 0049-0235-0
; CURRENT APPLICATION NUMBER: US/08/853,948B
; CURRENT FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Citrus unshiu
; FEATURE:
; OTHER INFORMATION: Xaa at position 109 is one of Ala, Arg, Asn, Asp,
; Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe,

OTHER INFORMATION: Pro, Ser, Thr, Tyr, or Val
US-08-853-948B-4

Query Match 66.7%; Score 36; DB 4; Length 341;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
I:| | | | |
Db 228 VIPPGMDFS 236

RESULT 2

US-08-853-948B-5
Sequence 5, Application US/08853948B
Patent No. 6210943

GENERAL INFORMATION:
APPLICANT: AKIHAMA, Toyota

TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE FROM CITRUS AND DNA ENCODING
TITLE OF INVENTION: THE SAME

FILE REFERENCE: 0049-0235-0
CURRENT APPLICATION NUMBER: US/08/853,948B

CURRENT FILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 5

LENGTH: 348
TYPE: PRT

ORGANISM: Citrus unshiu
US-08-853-948B-5

Query Match

Best Local Similarity 66.7%; Score 36; DB 4; Length 348;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
I:| | | | |
Db 234 VIPPGMDFS 242

RESULT 3

US-09-697-367-24
Sequence 24, Application US/09697367

Patent No. 6323015
GENERAL INFORMATION:

APPLICANT: Orozco Jr., Emil M.
APPLICANT: Calmi, Perry G.

APPLICANT: Weng, Zude
APPLICANT: Tarczynski, Mitchell

TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE
FILE REFERENCE: BB1166 US NA

CURRENT APPLICATION NUMBER: US/09/697,367
CURRENT FILING DATE: 2000-10-26

PRIOR FILING DATE: 2000-10-26
PRIOR APPLICATION NUMBER: 60/084,529

PRIOR FILING DATE: 1998-MAY-07
PRIOR APPLICATION NUMBER: PCT/US99/09865

NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97

SEQ ID NO 24
LENGTH: 368

TYPE: PRT
ORGANISM: Zea mays

US-09-697-367-24

Query Match

Best Local Similarity 66.7%; Score 36; DB 4; Length 368;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
I:| | | | |
Db 217 VIPPGMDFS 225

RESULT 4

US-08-429-054A-11

Sequence 11, Application US/08429054A
Patent No. 5917126

GENERAL INFORMATION:
APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,

APPLICANT: JEAN; VOELKER, TONI; GERVAIS, MONICA
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHETASE (SPS),

TITLE OF INVENTION: A PREPARATION METHOD AND CDNA THEREFOR, AND USE OF THE
TITLE OF INVENTION: CDNA FOR MODIFYING SPS EXPRESSION IN PLANT CELLS

NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:

ADDRESSEE: BIERMAN AND MUSERLIAN
STREET: 600 THIRD AVENUE

CITY: NEW YORK
STATE: NEW YORK

COUNTRY: USA
ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/429,054A
FILING DATE: 26-APR-1995

CLASSIFICATION: 800
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 842,337
FILING DATE: 20-March-1992

APPLICATION NUMBER: PCT/FR 91/00593
FILING DATE: 18-July-1991

CLASSIFICATION: 800
PRIOR APPLICATION DATA:

APPLICATION NUMBER: French 90402094.9
FILING DATE: 20-July-1990

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:

NAME: Charles A. Musserlian
REGISTRATION NUMBER: 19,683

REFERENCE/DOCKET NUMBER: 146.1137
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 661-8000
TELEFAX: (212) 661-8002

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:

LENGTH: 1068
TYPE: Amino acid

STRANDEDNESS: Single
TOPOLOGY: Unknown

MOLECULE TYPE: Peptide
US-08-429-054A-11

Query Match 66.7%; Score 36; DB 2; Length 1068;

Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
I:| | | | |

Db 435 VIPPGMDFS 443

RESULT 5

US-08-718-777-7

Sequence 7, Application US/08718777
Patent No. 5981852

GENERAL INFORMATION:
APPLICANT: Van Assche, C.

APPLICANT: Lando, D.
APPLICANT: Bruneau, J. M.

APPLICANT: Voelker, T.
APPLICANT: Gervais, M.

;; TITLE OF INVENTION: MODIFICATION OF SUCROSE
;; TITLE OF INVENTION: PHOSPHATE
;; TITLE OF INVENTION: SYNTHASE IN PLANTS
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Law Offices of Barbara Rae-Venter
;; STREET: 260 Sheridan Avenue, Suite 440
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94306
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/718,777
;; FILING DATE: NOT YET ASSIGNED
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/175,471
;; FILING DATE: 27-DEC-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Barbara Rae-Venter
;; REGISTRATION NUMBER: 32,750
;; REFERENCE/DOCKET NUMBER: CGNE.072.02US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415)328-4400
;; TELEFAX: (415)328-4477
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1068 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-718-777-7

Query Match 66.7%; Score 36; DB 2; Length 1068;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPGMDYS 11
|:|:|:|:|
Db 435 VVPGMDFS 443

RESULT 6
US-09-051-341-7
; Sequence 7, Application US/09051341
; Patent No. 6124528
; GENERAL INFORMATION:
; APPLICANT: Shewmaker, C. K.
; TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rae-Venter Law Group, P.C.
; STREET: 260 Sheridan Avenue, Suite 440
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/051,341
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: PCT/US96/17351
;; FILING DATE: 25-OCT-1996
;; APPLICATION NUMBER: US 08/549,016
;; FILING DATE: 27-OCT-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/372,200
;; FILING DATE: 12-JAN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Barbara Rae-Venter, Ph.D.,
;; REGISTRATION NUMBER: 32,750
;; REFERENCE/DOCKET NUMBER: CGNE.110.02US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415)328-4400
;; TELEFAX: (415)328-4477
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1068 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-051-341-7

Query Match 66.7%; Score 36; DB 3; Length 1068;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPGMDYS 11
|:|:|:|:|
Db 435 VVPGMDFS 443

RESULT 7
US-08-569-147-76
; Sequence 76, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6180377ris, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 76:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-569-147-76

Query Match 63.0%; Score 34; DB 4; Length 140;
Best Local Similarity 75.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGMDY 10
| | | | |
Db 122 VVPTGFDY 129

RESULT 8

US-08-569-147-82

; Sequence 82, Application US/08569147

; Patent No. 6180377

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: HUMANISED ANTIBODIES

; NUMBER OF SEQUENCES: 95

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &

; ADDRESSEE: No. 6180377ris, LLP

; STREET: One Liberty Place - 46th Floor

; CITY: Philadelphia

; STATE: PA

; COUNTRY: U.S.A.

; ZIP: 19103

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/569,147

; FILING DATE: 25-March-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Trujillo, Doreen Yanko

; REGISTRATION NUMBER: 35,719

; REFERENCE/DOCKET NUMBER: CARP-0047

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (215) 568-3100

; TELEFAX: (215) 568-3439

; INFORMATION FOR SEQ ID NO: 82:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 140 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-569-147-82

Query Match 63.0%; Score 34; DB 4; Length 140;

Best Local Similarity 75.0%; Pred. No. 13;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGMDY 10

| | | | |

Db 122 VVPTGFDY 129

RESULT 9

US-08-963-851-14

; Sequence 14, Application US/08963851

; Patent No. 6300116

; GENERAL INFORMATION:

; APPLICANT: VAN DER OSTEN, CLAUD

; APPLICANT: HALKIER, TORDEN

; APPLICANT: ANDERSEN, CARSTEN

; APPLICANT: BAUDITZ, PETER

; APPLICANT: HANSEN, PETER KAMP

; TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS

; FILE REFERENCE: 4946,200-US

; CURRENT APPLICATION NUMBER: US/08/963,851

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 14

; LENGTH: 59

; TYPE: PRT

; ORGANISM: Enterococcus faecalis

US-08-963-851-14

Query Match 61.1%; Score 33; DB 4; Length 59;

Best Local Similarity 45.5%; Pred. No. 7.5;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11

| : : | : : | |

Db 38 EXHIPGGLYS 48

RESULT 10

US-08-070-165F-8

; Sequence 8, Application US/08070165F

; Patent No. 5750365

; GENERAL INFORMATION:

; APPLICANT: Chiu, Ing-Ming

; APPLICANT: Poulin, Matthew L

; TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ing-Ming Chiu

; STREET: S2052 Davis Medical Research Center, 480 West

; CITY: Columbus

; STATE: Ohio

; COUNTRY: USA

; ZIP: 43210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/070,165F

; FILING DATE:

; CLASSIFICATION: 435

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (614)-293-8093

; TELEFAX: (614)-293-5631

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 378 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-070-165F-8

Query Match 61.1%; Score 33; DB 1; Length 378;

Best Local Similarity 85.7%; Pred. No. 64;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PXGMDYS 11

| | | | |

Db 139 PPGMDYS 145

RESULT 11

US-08-885-418-8

; Sequence 8, Application US/08885418

; Patent No. 5925528

; GENERAL INFORMATION:

; APPLICANT: Chiu, Ing-Ming

; APPLICANT: Poulin, Matthew L

; TITLE OF INVENTION: Acidic Fibroblast Growth Factor (aFGF)

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ing-Ming Chiu

; STREET: S2052 Davis Medical Research Center, 480 West

; CITY: Columbus

; STATE: Ohio

; COUNTRY: USA

; ZIP: 43210

```
; CITY: Columbus
; STATE: Ohio
; COUNTRY: USA
; ZIP: 43210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/885,418
; FILING DATE:
; CLASSIFICATION: 435
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (614)-293-8093
; TELEFAX: (614)-293-5631
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-885-418-8

Query Match 61.1%; Score 33; DB 2; Length 378;
Best Local Similarity 85.7%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PXGMDYS 11
Db 139 PPGMDYS 145

RESULT 12
US-09-383-630-6
; Sequence 6, Application US/09383630A
; Patent No. 6265632
; GENERAL INFORMATION:
; APPLICANT: Avner Yayon et al.
; TITLE OF INVENTION: ANIMAL MODEL FOR FIBROBLAST GROWTH
; FACTOR RECEPTOR ASSOCIATED
; CHONDRODYSPLASIA
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 2001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted
; to an ASCII file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/383,630A
; FILING DATE: 26-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 1402/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-562553
; TELEFAX: 972-3-562554
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 801
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-383-630-6

Query Match 61.1%; Score 33; DB 4; Length 801;
Best Local Similarity 85.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PXGMDYS 11
Db 566 PPGMDYS 572

RESULT 13
5177197-51
; Patent No. 5177197
; APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;
; WERNSTEDT, CHRISTOPHER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAESSENS-WELSH,
; LENA; HELDIN, CARL-HENRIK
; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
; NUMBER OF SEQUENCES: 53
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/487,343
; FILING DATE: 27-FEB-1990
; SEQ ID NO: 51:
; LENGTH: 65
; 5177197-51

Query Match 59.3%; Score 32; DB 6; Length 65;
Best Local Similarity 45.5%; Pred. No. 13;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDYS 11
Db 52 KEICPGMGYT 62

RESULT 14
US-08-580-988A-23
; Sequence 23, Application US/08580988A
; Patent No. 5856161
; GENERAL INFORMATION:
; APPLICANT: Aggarwal et al.
; TITLE OF INVENTION: Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
; TITLE OF INVENTION: For Its Use
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,988A
; FILING DATE: January 3, 1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D., J.D.
```

REGISTRATION NUMBER: 35,423
REFERENCE/DOCKET NUMBER: D5721CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-777-2321
TELEFAX: 713-777-6908
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: no
HYPOTHETICAL: no
ANTI-SENSE: no
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
US-08-580-988A-23

Query Match 59.3%; Score 32; DB 2; Length 102;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
DB 24 EEVFPPLAMNY 33

RESULT 15
US-08-460-694-4
Sequence 4, Application US/08460694
Patent No. 5858655
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: Prad1 Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide

Query Match 59.3%; Score 32; DB 2; Length 152;
Best Local Similarity 60.0%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10

DB 20 EEVFPPLAMNY 29

RESULT 16
US-08-460-744-4
Sequence 4, Application US/08460744
Patent No. 6107541
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: Prad1 Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide

Query Match 59.3%; Score 32; DB 3; Length 152;
Best Local Similarity 60.0%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
DB 20 EEVFPPLAMNY 29

RESULT 17
US-07-667-711B-4
Sequence 4, Application US/07667711B
Patent No. 6110700
GENERAL INFORMATION:
APPLICANT: ARNOLD, ANDREW
TITLE OF INVENTION: Prad1 Cyclin and its cDNA
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/667,711B
;; FILING DATE: 11-MAR-1991
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MCPHAIL, DONALD R.
;; REGISTRATION NUMBER: 35,811
;; REFERENCE/DOCKET NUMBER: 0609.4070000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 371-2600
;; TELEFAX: (202) 371-2540
;; INFORMATION FOR SEQ ID NO: 4:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 152 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: not relevant
;; MOLECULE TYPE: peptide
US-07-667-711B-4

Query Match 59.3%; Score 32; DB 3; Length 152;
Best Local Similarity 60.0%; Pred. No. 35;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
||| | | |
DB 20 EEVFPLAMNY 29

RESULT 18
US-08-193-977-7
;; Sequence 7, Application US/08193977
;; Patent No. 5625031
;; GENERAL INFORMATION:
;; APPLICANT: WEBSTER, KEVIN R.
;; APPLICANT: COLEMAN, KEVIN G.
;; TITLE OF INVENTION: PEPTIDE INHIBITORS OF THE P33CDK2 AND
;; TITLE OF INVENTION: P34CDK2 CELL CYCLE REGULATORY KINASES AND HUMAN
;; TITLE OF INVENTION: PAPILLOMAVIRUS E7 ONCOPROTEIN
;; NUMBER OF SEQUENCES: 34
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: REED & ROBINS
;; STREET: 635 BRYANT STREET
;; CITY: PALO ALTO
;; STATE: CALIFORNIA
;; COUNTRY: UNITED STATES OF AMERICA
;; ZIP: 94301
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/193,977
;; FILING DATE: 08-FEB-1994
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: ROBINS, ROBERTA L.
;; REGISTRATION NUMBER: 33,208
;; REFERENCE/DOCKET NUMBER: 5998-0016
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 617-8999
;; TELEFAX: (415) 327-3231
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 173 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-193-977-7
Query Match 59.3%; Score 32; DB 1; Length 173;

Best Local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 EEVVPXGMDY 10
||| | | |
DB 55 EEVFPLAMNY 64

RESULT 19
US-08-464-517-21
;; Sequence 21, Application US/08464517
;; Patent No. 5869640
;; GENERAL INFORMATION:
;; APPLICANT: BEACH, DAVID H.
;; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
;; NUMBER OF SEQUENCES: 50
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD
;; STREET: 60 State Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII(text)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/464,517
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/963,308
;; FILING DATE: 16-OCT-1992
;; APPLICATION NUMBER: US 07/888,178
;; FILING DATE: 26-MAY-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/701,514
;; FILING DATE: 16-MAY-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Matthew P. Vincent
;; REGISTRATION NUMBER: 36,709
;; REFERENCE/DOCKET NUMBER: MII-004C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 227-7400
;; TELEFAX: (617) 227-5941
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 189 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-464-517-21

Query Match 59.3%; Score 32; DB 2; Length 189;
Best Local Similarity 60.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 EEVVPXGMDY 10
||| | | |
DB 74 EEVFPLAMNY 83

RESULT 20
US-08-246-361A-21
;; Sequence 21, Application US/08246361A
;; Patent No. 5998582
;; GENERAL INFORMATION:
;; APPLICANT: BEACH, DAVID H.
;; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
;; NUMBER OF SEQUENCES: 50

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD
;; STREET: 60 State Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02109
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII(text)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/246,361A
;; FILING DATE: 19-MAY-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/963,308
;; FILING DATE: 16-OCT-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/888,178
;; FILING DATE: 26-MAY-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/701,514
;; FILING DATE: 16-MAY-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Matthew P. Vincent
;; REGISTRATION NUMBER: 36,709
;; REFERENCE/DOCKET NUMBER: MII-004C
;; TELEPHONE: (617) 227-7400
;; TELEFAX: (617) 227-5941
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 189 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-246-361A-21

Query Match 59.3%; Score 32; DB 2; Length 189;
Best Local Similarity 60.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
Db 74 EEVFLPMNY 83

RESULT 21
US-08-463-772-21
; Sequence 21, Application US/08463772
; Patent No. 6086501
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,772
; FILING DATE:

;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/963,308
;; FILING DATE: 16-OCT-1992
;; APPLICATION NUMBER: US 07/888,178
;; FILING DATE: 26-MAY-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/701,514
;; FILING DATE: 16-MAY-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Matthew P. Vincent
;; REGISTRATION NUMBER: 36,709
;; REFERENCE/DOCKET NUMBER: MII-004C
;; TELEPHONE: (617) 227-7400
;; TELEFAX: (617) 227-5941
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 189 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-463-772-21

Query Match 59.3%; Score 32; DB 3; Length 189;
Best Local Similarity 60.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
Db 74 EEVFLPMNY 83

RESULT 22
PCT-US93-05000-21
; Sequence 21, Application PC/TUS9305000
; GENERAL INFORMATION:
; APPLICANT: MITOTIX
; TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05000
; FILING DATE: 19930525
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/888,178
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL91-02A
; TELEPHONE: 617-861-6240
; TELEFAX: 616-861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: protein

PCT-US93-05000-21

Query Match 59.3%; Score 32; DB 5; Length 189;
Best Local Similarity 60.0%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
||| | | | |
Db 74 EEVFLAMNY 83

RESULT 23

US-08-926-842B-20
; Sequence 20, Application US/08926842B
; Patent No. 6030807
; GENERAL INFORMATION:
; APPLICANT: Sa-No. 6030807ueira, Isabel
; APPLICANT: de Lencastre, Herminia
; TITLE OF INVENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/926,842B
; FILING DATE: 10-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-089 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521

INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
US-08-926-842B-20

Query Match 59.3%; Score 32; DB 3; Length 231;
Best Local Similarity 55.6%; Pred. No. 58;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
: | | | | |
Db 41 IKPSGVDYS 49

RESULT 24

US-08-464-517-22
; Sequence 22, Application US/08464517
; Patent No. 5869640
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO

NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,517
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew P. Vincent
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-004C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-464-517-22

Query Match 59.3%; Score 32; DB 2; Length 236;
Best Local Similarity 60.0%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMDY 10
||| | | | |
Db 20 EEVFLAMNY 29

RESULT 25

US-08-246-361A-22
; Sequence 22, Application US/08246361A
; Patent No. 5998582
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246,361A
; FILING DATE: 19-MAY-1994

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew P. Vincent
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-004C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-246-361A-22

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Query Match          59.3%; Score 32; DB 2; Length 236;
Best Local Similarity 60.0%; Pred. No. 59;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 EEVVPXGMDY 10
Db      20 EEVFFLAMNY 29

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Search completed: June 10, 2003, 13:51:34
Job time : 9.64286 secs

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Result No.	Score	Query 8		Length	DB	ID	Description
		Match					
1	36	66.7	1049	9	US-10-217-700-10	Sequence 10, Appl	
2	36	66.7	1068	9	US-10-217-700-8	Sequence 8, Appl	
3	36	66.7	1081	9	US-10-217-700-4	Sequence 4, Appl	
4	36	66.7	1083	9	US-10-217-700-11	Sequence 11, Appl	
5	36	66.7	1084	9	US-10-217-700-9	Sequence 9, Appl	
6	35	64.8	440	9	US-09-813-408-27	Sequence 27, Appl	
7	34	63.0	1062	10	US-09-815-242-511	Sequence 511, Appl	
8	34	63.0	3472	9	US-10-027-806-4	Sequence 4, Appl	
9	34	63.0	3472	9	US-10-034-623-4	Sequence 4, Appl	
10	34	63.0	3472	9	US-10-027-801-4	Sequence 4, Appl	
11	33	61.1	59	10	US-09-948-080-14	Sequence 14, Appl	
12	33	61.1	283	9	US-09-738-626-4881	Sequence 4881, Appl	
13	33	61.1	299	10	US-09-815-242-10697	Sequence 10697, Appl	
14	33	61.1	736	9	US-09-978-295A-526	Sequence 526, Appl	
15	33	61.1	736	9	US-09-978-697-526	Sequence 526, Appl	
16	33	61.1	736	9	US-09-978-192A-526	Sequence 526, Appl	
17	33	61.1	736	9	US-09-999-832A-526	Sequence 526, Appl	
18	33	61.1	736	9	US-09-978-189-526	Sequence 526, Appl	
19	33	61.1	736	9	US-10-174-590-420	Sequence 420, Appl	

; EARLIER APPLICATION NUMBER: 09/394,272
; EARLIER FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 1049
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-217-700-10

Query Match 66.7%; Score 36; DB 9; Length 1049;
Best Local Similarity 66.7%; Pred. No. 96;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
|:| |||:|
Db 436 VIPPGMDFS 444

RESULT 2
US-10-217-700-8
; Sequence 8, Application US/10217700
; Publication No. US20030070191A1
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; FILE REFERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/10/217,700
; EARLIER FILING DATE: 2002-08-12
; EARLIER APPLICATION NUMBER: 09/394,272
; EARLIER FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1068
; TYPE: PRT
; ORGANISM: Zea mays
US-10-217-700-8

Query Match 66.7%; Score 36; DB 9; Length 1068;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
|:| |||:|
Db 435 VIPPGMDFS 443

RESULT 3
US-10-217-700-4
; Sequence 4, Application US/10217700
; Publication No. US20030070191A1
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; FILE REFERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/10/217,700
; EARLIER FILING DATE: 2002-08-12
; EARLIER APPLICATION NUMBER: 09/394,272
; EARLIER FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1081
; TYPE: PRT
; ORGANISM: Craterostigma plantagineum
US-10-217-700-4

Query Match 66.7%; Score 36; DB 9; Length 1081;

Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
|:| |||:|
Db 445 VIPPGMDFS 453

RESULT 4
US-10-217-700-11
; Sequence 11, Application US/10217700
; Publication No. US20030070191A1
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; FILE REFERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/10/217,700
; EARLIER FILING DATE: 2002-08-12
; EARLIER APPLICATION NUMBER: 09/394,272
; EARLIER FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-217-700-11

Query Match 66.7%; Score 36; DB 9; Length 1083;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
|:| |||:|
Db 483 VIPPGMDFS 491

RESULT 5
US-10-217-700-9
; Sequence 9, Application US/10217700
; Publication No. US20030070191A1
; GENERAL INFORMATION:
; APPLICANT: Haigler, Candace H.
; APPLICANT: Holaday, A. Scott
; TITLE OF INVENTION: TRANSGENIC FIBER PRODUCING PLANTS WITH INCREASED
; FILE REFERENCE: 201304/1000
; CURRENT APPLICATION NUMBER: US/10/217,700
; EARLIER FILING DATE: 2002-08-12
; EARLIER APPLICATION NUMBER: 09/394,272
; EARLIER FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1084
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-217-700-9

Query Match 66.7%; Score 36; DB 9; Length 1084;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMDYS 11
|:| |||:|
Db 453 VIPPGMDFS 461

RESULT 6
US-09-813-408-27
; Sequence 27, Application US/09813408

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:24:45 ; Search time 31.3571 Seconds
(without alignments)
46.744 Million cell updates/sec

Title: US-09-909-164-43
Perfect score: 48
Sequence: 1 EHVPGXSYS 11

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Watch 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
1	45	93.8	11	23	ABB80544	Hepatitis C virus
2	45	93.8	11	23	ABB80545	Hepatitis C virus
3	45	93.8	11	23	ABB80549	Hepatitis C virus
4	45	93.8	11	23	ABB80552	Hepatitis C virus
5	45	93.8	11	23	ABB80553	Hepatitis C virus
6	44	91.7	11	23	ABB80521	Hepatitis C virus
7	44	91.7	11	23	ABB80522	Hepatitis C virus
8	44	91.7	11	23	ABB80525	Hepatitis C virus
9	44	91.7	11	23	ABB80526	Hepatitis C virus
10	44	91.7	11	23	ABB80530	Hepatitis C virus

11	44	91.7	11	23	ABB80535	Hepatitis C virus
12	44	91.7	11	23	ABB80536	Hepatitis C virus
13	44	91.7	11	23	ABB80539	Hepatitis C virus
14	44	91.7	11	23	ABB80540	Hepatitis C virus
15	44	91.7	11	23	ABB80559	Hepatitis C virus
16	44	91.7	11	23	ABB80563	Hepatitis C virus
17	44	91.7	11	23	ABB80564	Hepatitis C virus
18	44	91.7	11	23	ABB80565	Hepatitis C virus
19	44	91.7	11	23	ABB80566	Hepatitis C virus
20	44	91.7	11	23	ABB80567	Hepatitis C virus
21	44	91.7	11	23	ABB80568	Hepatitis C virus
22	41	85.4	11	23	ABB80547	Hepatitis C virus
23	41	85.4	11	23	ABB80548	Hepatitis C virus
24	41	85.4	11	23	ABB80551	Hepatitis C virus
25	41	85.4	11	23	ABB80556	Hepatitis C virus
26	41	85.4	11	23	ABB80557	Hepatitis C virus
27	40	83.3	11	23	ABB80524	Hepatitis C virus
28	40	83.3	11	23	ABB80528	Hepatitis C virus
29	40	83.3	11	23	ABB80529	Hepatitis C virus
30	40	83.3	11	23	ABB80533	Hepatitis C virus
31	40	83.3	11	23	ABB80534	Hepatitis C virus
32	40	83.3	11	23	ABB80538	Hepatitis C virus
33	40	83.3	11	23	ABB80542	Hepatitis C virus
34	40	83.3	11	23	ABB80543	Hepatitis C virus
35	40	83.3	11	23	ABB80546	Hepatitis C virus
36	40	83.3	11	23	ABB80550	Hepatitis C virus
37	40	83.3	11	23	ABB80554	Hepatitis C virus
38	40	83.3	11	23	ABB80555	Hepatitis C virus
39	40	83.3	11	23	ABB80561	Hepatitis C virus
40	40	83.3	11	23	ABB80562	Hepatitis C virus
41	39	81.2	11	23	ABB80523	Hepatitis C virus
42	39	81.2	11	23	ABB80527	Hepatitis C virus
43	39	81.2	11	23	ABB80531	Hepatitis C virus
44	39	81.2	11	23	ABB80532	Hepatitis C virus
45	39	81.2	11	23	ABB80537	Hepatitis C virus
46	39	81.2	11	23	ABB80541	Hepatitis C virus
47	39	81.2	11	23	ABB80558	Hepatitis C virus
48	39	81.2	11	23	ABB80560	Hepatitis C virus
49	38	79.2	1022	22	ABG03621	Novel human diago
50	38	79.2	1022	22	ABG05826	Novel human diago
51	38	79.2	1022	22	ABG08173	Novel human diago
52	37	77.1	244	21	AA12881	Murine JNK3 bindin
53	37	77.1	484	21	AA12882	Murine JNK3 bindin
54	36	75.0	1070	22	AAU14378	Human novel protei
55	36	75.0	3472	21	AA90913	Cenarchaeum symbio
56	34	70.8	20	20	AAU76810	Hepatitis C virus
57	34	70.8	398	20	AA59885	Human normal uteru
58	34	70.8	440	21	AA27201	Hela cell library
59	34	70.8	478	20	AA70281	Secreted protein c
60	34	70.8	478	22	AA39754	Human polypeptide
61	34	70.8	483	22	AA41540	Human polypeptide
62	33	68.8	280	22	AB68883	Drosophila melanog
63	33	68.8	299	22	ABG00168	Novel human diago
64	32	66.7	109	23	ABG06850	Human nPCR-Seq106
65	32	66.7	410	22	AA40649	Human polypeptide
66	32	66.7	413	21	AA41846	Human ORFX ORF1610
67	32	66.7	602	23	AB92316	Herbicidally activ
68	32	66.7	947	21	AA325105	Pinus radiata cell
69	32	66.7	1732	23	AB90754	Human Tumour Endot
70	32	66.7	4472	17	AA97245	Virulence gene clu
71	31	64.6	25	23	ABG62372	Eubacterial DNA po
72	31	64.6	80	22	AA952865	Human digestive sy
73	31	64.6	80	23	AA52683	Human nucleotide r
74	31	64.6	99	22	AA976703	Human colon cancer
75	31	64.6	159	18	AAW44125	Streptococcus pneu

ALIGNMENTS

RESULT 1
ABB80544
ID ABB80544 standard; peptide; 11 AA.


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FT Misc-difference 9
FT Modified-site 11 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
XX WO200208251-A2.
XX 31-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-US23169.
XX
XX 21-JUL-2000; 2000US-220101P.
XX (CORV-) CORVAS INT INC.
XX
XX Lim-wilby M, Levy OE, Brunck TK;
XX WPI; 2002-361643/39.
XX
XX Novel peptide compound having hepatitis C virus protease inhibitory
XX activity useful for treating disorders associated with hepatitis C
XX virus protease
XX
XX Claim 17; Page 65; 69pp; English.
XX
XX The sequence represents a peptide compound of the invention having
XX hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
XX invention are alpha-ketoamide peptide analogues. The peptides have
XX virucide activity, and are useful for treating and in the manufacture of
XX a medicament to treat disorders associated with HCV protease. A
XX pharmaceutical composition comprising the peptide as an active ingredient
XX is useful for treating disorders associated with hepatitis C virus.
XX
XX Sequence 11 AA;
XX
XX Query Match 93.8%; Score 45; DB 23; Length 11;
XX Best Local Similarity 90.9%; Pred. No. 0.0094;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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XX 1 EEVVPXGSSYS 11
XX
XX Db
XX
XX RESULT 4
XX ABB80552
XX ID ABB80552 standard; peptide; 11 AA.
XX
XX AC ABB80552;
XX
XX 08-OCT-2002 (first entry)
XX
XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #32.
XX
XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX virucide.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1 /note= "N-terminal acetyl"
XX Modified-site 6 /note= "N-terminal acetyl"
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XX Misc-difference 8 /note= "D-form residue"
XX Misc-difference 9 /note= "D-form residue"
XX Modified-site 11 /note= "C-terminal amide"
XX
XX WO200208251-A2.
XX
XX 31-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-US23169.
XX
XX 21-JUL-2000; 2000US-220101P.
XX (CORV-) CORVAS INT INC.
XX
XX PA

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XX 19-JUL-2001; 2001WO-US23169.
XX
XX 21-JUL-2000; 2000US-220101P.
XX (CORV-) CORVAS INT INC.
XX
XX Lim-wilby M, Levy OE, Brunck TK;
XX WPI; 2002-361643/39.
XX
XX Novel peptide compound having hepatitis C virus protease inhibitory
XX activity useful for treating disorders associated with hepatitis C
XX virus protease
XX
XX Claim 17; Page 65; 69pp; English.
XX
XX The sequence represents a peptide compound of the invention having
XX hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
XX invention are alpha-ketoamide peptide analogues. The peptides have
XX virucide activity, and are useful for treating and in the manufacture of
XX a medicament to treat disorders associated with HCV protease. A
XX pharmaceutical composition comprising the peptide as an active ingredient
XX is useful for treating disorders associated with hepatitis C virus.
XX
XX Sequence 11 AA;
XX
XX Query Match 93.8%; Score 45; DB 23; Length 11;
XX Best Local Similarity 90.9%; Pred. No. 0.0094;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 EEVVPXGXSYS 11
XX | | | | | | | |
XX 1 EEVVPXGSSYS 11
XX
XX Db
XX
XX RESULT 5
XX ABB80553
XX ID ABB80553 standard; peptide; 11 AA.
XX
XX AC ABB80553;
XX
XX 08-OCT-2002 (first entry)
XX
XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #33.
XX
XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX virucide.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Modified-site 1 /note= "N-terminal acetyl"
XX Modified-site 6 /note= "N-terminal acetyl"
XX
XX Misc-difference 8 /note= "D-form residue"
XX Misc-difference 9 /note= "D-form residue"
XX Modified-site 11 /note= "C-terminal amide"
XX
XX WO200208251-A2.
XX
XX 31-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-US23169.
XX
XX 21-JUL-2000; 2000US-220101P.
XX (CORV-) CORVAS INT INC.
XX
XX PA

```

XX Lim-wilby M, Levy OE, Brunck TK;
XX WPI; 2002-361643/39.
XX Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease -
XX
XX Claim 17; Page 65; 69pp; English.
XX
XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
XX Sequence 11 AA;
PS
PS
Query Match 93.8%; Score 45; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0094;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EEVVPXGXSYS 11
DB 1 EEVVPXGSSYS 11
RESULT 6
ABB80521
ID ABB80521 standard; peptide; 11 AA.
XX
XX ABB80521;
XX
XX 08-OCT-2002 (first entry)
DT
DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1.
XX
XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT residue 7"
FT Modified-site 11 /note= "C-terminal amide"
FT
FT WO200208251-A2.
XX
XX 31-JAN-2002.
PD
XX
XX 19-JUL-2001; 2001WO-US233169.
XX
XX 21-JUL-2000; 2000US-220101P.
PR
XX
XX (CORV-) CORVAS INT INC.
PA
XX
XX Lim-wilby M, Levy OE, Brunck TK;
PI
XX
XX WPI; 2002-361643/39.
XX
XX Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease -
XX
XX Claim 17; Page 64; 69pp; English.

XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
XX Sequence 11 AA;
PS
PS
Query Match 91.7%; Score 44; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EEVVPXGXSYS 11
DB 1 EEVVPXGMSYS 11
RESULT 7
ABB80522
ID ABB80522 standard; peptide; 11 AA.
XX
XX ABB80522;
XX
XX 08-OCT-2002 (first entry)
DT
DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
XX
XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT residue 7"
FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
FT
FT WO200208251-A2.
XX
XX 31-JAN-2002.
PD
XX
XX 19-JUL-2001; 2001WO-US233169.
XX
XX 21-JUL-2000; 2000US-220101P.
PR
XX
XX (CORV-) CORVAS INT INC.
PA
XX
XX Lim-wilby M, Levy OE, Brunck TK;
PI
XX
XX WPI; 2002-361643/39.
XX
XX Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease -
XX
XX Claim 17; Page 64; 69pp; English.
XX
XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.

XX SQ Sequence 11 AA;

Query Match 91.7%; Score 44; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11
||||| |||

DB 1 EEVVPXGXSYS 11

RESULT 8
ABB80525

ID ABB80525 standard; peptide; 11 AA.

XX AC ABB80525;

XX DT 08-OCT-2002 (first entry)

XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5.

XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.

XX OS Synthetic.

XX FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6

FT FT /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"

FT FT Misc-difference 8 /note= "D-form residue"

FT FT Modified-site 11 /note= "C-terminal amide"

XX WO200208251-A2.

XX PD 31-JAN-2002.

XX PF 19-JUL-2001; 2001WO-US23169.

XX PR 21-JUL-2000; 2000US-220101P.

XX PA (CORV-) CORVAS INT INC.

XX PI Lim-wilby M, Levy OE, Brunck TK;

XX DR WPI; 2002-361643/39.

XX PT Novel peptide compound having hepatitis C virus protease inhibitory
activity useful for treating disorders associated with hepatitis C
virus protease

XX PS Claim 17; Page 64; 69pp; English.

XX CC The sequence represents a peptide compound of the invention having
hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
invention are alpha-ketoamide peptide analogues. The peptides have
virucide activity, and are useful for treating and in the manufacture of
a medicament to treat disorders associated with HCV protease. A
pharmaceutical composition comprising the peptide as an active ingredient
is useful for treating disorders associated with hepatitis C virus.

XX SQ Sequence 11 AA;

Query Match 91.7%; Score 44; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11

DB 1 EEVVPXGXSYS 11
||||| |||

RESULT 9
ABB80526

ID ABB80526 standard; peptide; 11 AA.

XX AC ABB80526;

XX DT 08-OCT-2002 (first entry)

XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6.
XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.

XX OS Synthetic.

XX FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6

FT FT /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"

FT FT Misc-difference 8 /note= "D-form residue"

FT FT Modified-site 11 /note= "C-terminal amide"

XX WO200208251-A2.

XX PD 31-JAN-2002.

XX PF 19-JUL-2001; 2001WO-US23169.

XX PR 21-JUL-2000; 2000US-220101P.

XX PA (CORV-) CORVAS INT INC.

XX PI Lim-wilby M, Levy OE, Brunck TK;

XX DR WPI; 2002-361643/39.

XX PT Novel peptide compound having hepatitis C virus protease inhibitory
activity useful for treating disorders associated with hepatitis C
virus protease

XX PS Claim 17; Page 64; 69pp; English.

XX CC The sequence represents a peptide compound of the invention having
hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
invention are alpha-ketoamide peptide analogues. The peptides have
virucide activity, and are useful for treating and in the manufacture of
a medicament to treat disorders associated with HCV protease. A
pharmaceutical composition comprising the peptide as an active ingredient
is useful for treating disorders associated with hepatitis C virus.

XX SQ Sequence 11 AA;

Query Match 91.7%; Score 44; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11
||||| |||

DB 1 EEVVPXGXSYS 11

RESULT 10
ABB80530

ID ABB0530 standard; peptide; 11 AA.
AC ABB0530;
XX
DT 08-OCT-2002 (first entry)
DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #10.
XX
KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminal acetyl"
FT Modified-site 6
FT /note= "Norvalyl carbonyl forming keto-amide linkage with
FT residue 7"
FT Modified-site 11
FT /note= "C-terminal amide"
XX
PN WO200208251-A2.
XX
PD 31-JAN-2002.
XX
PF 19-JUL-2001; 2001WO-US23169.
XX
PR 21-JUL-2000; 2000US-220101P.
XX
PA (CORV-) CORVAS INT INC.
XX
PI Lim-wilby M, Levy OE, Brunck TK;
XX
DR WPI; 2002-361643/39.
XX
PT Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease -
XX
PS Claim 17; Page 64; 69pp; English.
XX
CC The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
SQ Sequence 11 AA;
XX
Query Match 91.7%; Score 44; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EEVVPXGXSYS 11
DB 1 EEVVPXGXSYS 11
XX
RESULT 11
ABB0535
ID ABB0535 standard; peptide; 11 AA.
XX
AC ABB0535;
XX
DT 08-OCT-2002 (first entry)
XX
DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #15.
XX
KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.

XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminal acetyl"
FT Modified-site 6
FT /note= "Norvalyl carbonyl forming keto-amide linkage with
FT residue 7"
FT Modified-site 11
FT /note= "C-terminal amide"
XX
PN WO200208251-A2.
XX
PD 31-JAN-2002.
XX
PF 19-JUL-2001; 2001WO-US23169.
XX
PR 21-JUL-2000; 2000US-220101P.
XX
PA (CORV-) CORVAS INT INC.
XX
PI Lim-wilby M, Levy OE, Brunck TK;
XX
DR WPI; 2002-361643/39.
XX
PT Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease -
XX
PS Claim 17; Page 64; 69pp; English.
XX
CC The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
SQ Sequence 11 AA;
XX
Query Match 91.7%; Score 44; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EEVVPXGXSYS 11
DB 1 EEVVPXGXSYS 11
XX
RESULT 12
ABB0536
ID ABB0536 standard; peptide; 11 AA.
XX
AC ABB0536;
XX
DT 08-OCT-2002 (first entry)
XX
DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #16.
XX
KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminal acetyl"
FT Modified-site 6
FT /note= "Norvalyl carbonyl forming keto-amide linkage with
FT residue 7"
FT Misc-difference 9

FT Modified-site /note= "D-form residue"
 FT 11
 FT /note= "C-terminal amide"
 XX

PN WO200208251-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease

XX Claim 17; Page 64; 69pp; English.

XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 91.7%; Score 44; DB 23; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.015;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11

DB 1 EEVVPXGQSYS 11

RESULT 13

ABB80539

ID ABB80539 standard; peptide; 11 AA.

XX ABB80539;

XX 08-OCT-2002 (first entry)

XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #19.

XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6

FT /note= "Norvalyl carbonyl forming keto-amide linkage with
 residue 7"

FT Misc-difference 8

FT /note= "D-form residue"

FT Modified-site 11

FT /note= "C-terminal amide"

XX WO200208251-A2.

XX 31-JAN-2002.

XX

XX

XX

PF 19-JUL-2001; 2001WO-US23169.

PR 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease

XX Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 91.7%; Score 44; DB 23; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.015;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11

DB 1 EEVVPXGQSYS 11

RESULT 14

ABB80540

ID ABB80540 standard; peptide; 11 AA.

XX ABB80540;

XX 08-OCT-2002 (first entry)

XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #20.

XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6

FT /note= "Norvalyl carbonyl forming keto-amide linkage with
 residue 7"

FT Misc-difference 8

FT /note= "D-form residue"

FT Misc-difference 9

FT /note= "D-form residue"

FT Modified-site 11

FT /note= "C-terminal amide"

XX WO200208251-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

FI activity useful for treating disorders associated with hepatitis C

The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides have an amino acid sequence corresponding to the amino acid sequence of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is also provided.

CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 91.7%; Score 44; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.015;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11

DB 1 EEVVPXGXSYS 11

RESULT 17

ABB80564
ID ABB80564 standard; peptide; 11 AA.

XX

AC ABB80564;

XX 08-OCT-2002 (first entry)

XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44.

XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal acetyl"

FT Modified-site 6

FT /note= "Leucyl carbonyl forming keto-amide linkage with
residue 7"

FT Modified-site 11

FT /note= "C-terminal amide"

XX WO200208251-A2.

XX 31-JAN-2002.

PF 19-JUL-2001; 2001WO-US23169.

PR 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease

XX Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 91.7%; Score 44; DB 23; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.015;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11

|||||

DB 1 EEVVPXGXSYS 11

RESULT 18

ABB80565

ID ABB80565 standard; peptide; 11 AA.

XX ABB80565;

XX 08-OCT-2002 (first entry)

XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #45.

XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-terminal acetyl"

FT Modified-site 6

FT /note= "Norleucyl carbonyl forming keto-amide linkage
with residue 7"

FT Modified-site 11

FT /note= "C-terminal amide"

XX WO200208251-A2.

XX 31-JAN-2002.

PF 19-JUL-2001; 2001WO-US23169.

PR 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease

XX Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 91.7%; Score 44; DB 23; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.015;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11

|||||

DB 1 EEVVPXGXSYS 11

RESULT 19

ABB80566

ID ABB80566 standard; peptide; 11 AA.

XX ABB80566;

XX 08-OCT-2002 (first entry)

XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46.
XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1
FT Modified-site 6 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "2-aminoisobutyl carbonyl residue forming a
FT keto-amide linkage with residue 7"
FT Modified-site 11
FT /note= "C-terminal amide"
XX WO200208251-A2.
XX 31-JAN-2002.
XX 19-JUL-2001; 2001WO-US23169.
XX 21-JUL-2000; 2000US-220101P.
XX (CORV-) CORVAS INT INC.
XX Lim-wilby M, Levy OE, Brunck TK;
XX WPI; 2002-361643/39.
XX Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease
XX
XX Claim 17; Page 65; 69pp; English.
XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
XX Sequence 11 AA;
XX
XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
XX Query Match 91.7%; Score 44; DB 23; Length 11;
XX Best Local Similarity 90.9%; Pred. No. 0.015;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EEVVPXGXSYS 11
DB ||||| |||
DB 1 EEVVPXGMSYS 11
RESULT 20
ABB80567
ID ABB80567 standard; peptide; 11 AA.
XX
XX ABB80567;
XX
XX 08-OCT-2002 (first entry)
DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #47.
XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1

FT Modified-site 6 /note= "N-terminal acetyl"
FT /note= "(S,S)allothreonyl carbonyl residue forming a
FT keto-amide linkage with residue 7"
FT Modified-site 11
FT /note= "C-terminal amide"
XX WO200208251-A2.
XX 31-JAN-2002.
XX 19-JUL-2001; 2001WO-US23169.
XX 21-JUL-2000; 2000US-220101P.
XX (CORV-) CORVAS INT INC.
XX Lim-wilby M, Levy OE, Brunck TK;
XX WPI; 2002-361643/39.
XX Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease
XX
XX Claim 17; Page 65; 69pp; English.
XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
XX Sequence 11 AA;
XX
XX Query Match 91.7%; Score 44; DB 23; Length 11;
XX Best Local Similarity 90.9%; Pred. No. 0.015;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EEVVPXGXSYS 11
DB ||||| |||
DB 1 EEVVPXGMSYS 11
RESULT 21
ABB80568
ID ABB80568 standard; peptide; 11 AA.
XX
XX ABB80568;
XX
XX 08-OCT-2002 (first entry)
DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #48.
XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1
FT Modified-site 6 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Alpha-propionyl-glycyl carbonyl residue forming
FT a keto-amide linkage with residue 7"
FT Modified-site 11
FT /note= "C-terminal amide"
XX WO200208251-A2.
XX 31-JAN-2002.

XX PF 19-JUL-2001; 2001WO-US23169.
XX PR 21-JUL-2000; 2000US-220101P.
XX PA (CORV-) CORVAS INT INC.
XX PI Lim-wilby M, Levy OE, Brunck TK;
XX XX WPI; 2002-361643/39.
XX DR
XX XX Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
XX virus protease -
XX
XX PS Claim 17; Page 65; 69pp; English.
XX
XX CC The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
SQ Sequence 11 AA;

Query Match 91.7%; Score 44; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.015; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1;

QY 1 EEVVPXGXSYS 11
|||||
DB 1 EEVVPXGMSYS 11

RESULT 22
ABB80547
ID ABB80547 standard; peptide; 11 AA.
AC ABB80547;
XX
XX DT 08-OCT-2002 (first entry)
XX
XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #27.
XX
XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX virucide.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT Modified-site 11 residue 7"
FT Modified-site 11 /note= "C-terminal amide"
XX
XX PN WO200208251-A2.
XX
XX PD 31-JAN-2002.
XX
XX PF 19-JUL-2001; 2001WO-US23169.
XX
XX PR 21-JUL-2000; 2000US-220101P.
XX
XX PA (CORV-) CORVAS INT INC.
XX
XX PI Lim-wilby M, Levy OE, Brunck TK;
XX WPI; 2002-361643/39.
XX
XX DR

XX PT Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease -
XX
XX PS Claim 17; Page 65; 69pp; English.
XX
XX CC The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
SQ Sequence 11 AA;

Query Match 85.4%; Score 41; DB 23; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.063;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11
|||||
DB 1 EEVVPXGTDYS 11

RESULT 23
ABB80548
ID ABB80548 standard; peptide; 11 AA.
XX
XX AC ABB80548;
XX
XX DT 08-OCT-2002 (first entry)
XX
XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #28.
XX
XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX virucide.
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT Modified-site 9 residue 7"
FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
FT
XX
XX PN WO200208251-A2.
XX
XX PD 31-JAN-2002.
XX
XX PF 19-JUL-2001; 2001WO-US23169.
XX
XX PR 21-JUL-2000; 2000US-220101P.
XX
XX PA (CORV-) CORVAS INT INC.
XX
XX PI Lim-wilby M, Levy OE, Brunck TK;
XX WPI; 2002-361643/39.
XX
XX PT Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease -
XX
XX PS Claim 17; Page 65; 69pp; English.
XX
XX CC The sequence represents a peptide compound of the invention having

CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 85.4%; Score 41; DB 23; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.063;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11

DB 1 EEVVPXGTDYS 11

RESULT 24

ABB80551

ID ABB80551 standard; peptide; 11 AA.

XX AC ABB80551;

XX DT 08-OCT-2002 (first entry)

XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #31.

XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;

XX KW virucide.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with

FT residue 7"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

XX WO200208251-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory

PT activity useful for treating disorders associated with hepatitis C

PT virus protease

XX Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having

CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the

CC invention are alpha-ketoamide peptide analogues. The peptides have

CC virucide activity, and are useful for treating and in the manufacture of

CC a medicament to treat disorders associated with HCV protease. A

CC pharmaceutical composition comprising the peptide as an active ingredient

CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 85.4%; Score 41; DB 23; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.063;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11

DB 1 EEVVPXGSDYS 11

RESULT 25

ABB80556

ID ABB80556 standard; peptide; 11 AA.

XX AC ABB80556;

XX DT 08-OCT-2002 (first entry)

XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #36.

XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;

XX KW virucide.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with

FT residue 7"

FT Misc-difference 8 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

XX WO200208251-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory

PT activity useful for treating disorders associated with hepatitis C

PT virus protease

XX Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having

CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the

CC invention are alpha-ketoamide peptide analogues. The peptides have

CC virucide activity, and are useful for treating and in the manufacture of

CC a medicament to treat disorders associated with HCV protease. A

CC pharmaceutical composition comprising the peptide as an active ingredient

CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 85.4%; Score 41; DB 23; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.063;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11

DB 1 EEVVPXGSDYS 11

Wed Jun 11 15:42:50 2003

us-09-909-164-43.rag

Page 13

Search completed: June 10, 2003, 13:39:10
Job time : 32.3571 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:31:45 ; Search time 9.64286 Seconds
(without alignments)
33.564 Million cell updates/sec

Title: US-09-909-164-43
Perfect score: 48
Sequence: 1 EEVXPXGXSYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued_Patents_AA.*
1: /cgn2.6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2.6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2.6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2.6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2.6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2.6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	66.7	45	2	US-08-637-759B-236
2	32	66.7	45	3	US-08-871-355A-236
3	32	66.7	45	4	US-09-201-945-236
4	32	66.7	947	4	US-09-228-986-73
5	31	64.6	159	2	US-08-844-086-4
6	31	64.6	159	3	US-09-018-211-4
7	31	64.6	513	5	PCT-US91-02714-26
8	31	64.6	622	2	US-08-459-146-2
9	31	64.6	622	2	US-08-459-065-2
10	31	64.6	688	1	US-07-688-352C-28
11	31	64.6	688	2	US-08-474-379C-28
12	31	64.6	688	3	US-09-146-249A-28
13	31	64.6	688	3	US-08-206-188B-28
14	31	64.6	833	2	US-08-844-086-2
15	31	64.6	833	3	US-09-018-211-2
16	30	62.5	121	4	US-09-152-060-85
17	30	62.5	121	4	US-09-152-060-85
18	30	62.5	122	2	US-08-879-995A-1
19	30	62.5	122	3	US-09-215-096-1
20	30	62.5	241	3	US-08-834-776A-2
21	30	62.5	480	1	US-07-803-636A-2
22	30	62.5	626	4	US-08-961-083-220
23	30	62.5	3072	4	US-09-413-814-93
24	30	62.5	3079	4	US-09-413-814-80
25	29	60.4	10	2	US-08-361-517-19
26	29	60.4	10	5	PCT-US93-07964-19
27	29	60.4	20	1	US-08-440-861-53

28	29	60.4	28	1	US-07-971-096-8	Sequence 8, Appl
29	29	60.4	28	1	US-08-175-096-8	Sequence 27, Appl
30	29	60.4	100	2	US-09-047-125-27	Sequence 27, Appl
31	29	60.4	100	3	US-07-736-335B-27	Sequence 27, Appl
32	29	60.4	145	4	US-08-413-974-4	Sequence 4, Appl
33	29	60.4	145	4	US-08-434-418-4	Sequence 4, Appl
34	29	60.4	145	4	US-08-433-288-4	Sequence 4, Appl
35	29	60.4	145	4	US-08-174-739A-4	Sequence 4, Appl
36	29	60.4	145	4	US-08-434-256-4	Sequence 4, Appl
37	29	60.4	263	1	US-07-971-096-4	Sequence 4, Appl
38	29	60.4	263	1	US-08-175-096-4	Sequence 4, Appl
39	29	60.4	263	4	US-08-413-974-6	Sequence 6, Appl
40	29	60.4	263	4	US-08-434-418-6	Sequence 6, Appl
41	29	60.4	263	4	US-08-433-288-6	Sequence 6, Appl
42	29	60.4	263	4	US-08-174-739A-6	Sequence 6, Appl
43	29	60.4	263	4	US-08-434-256-6	Sequence 6, Appl
44	29	60.4	382	3	US-08-582-740-70	Sequence 70, Appl
45	29	60.4	382	4	US-09-109-879-70	Sequence 70, Appl
46	29	60.4	406	3	US-08-582-740-68	Sequence 68, Appl
47	29	60.4	406	4	US-09-109-879-68	Sequence 68, Appl
48	29	60.4	529	4	US-09-240-639-4	Sequence 4, Appl
49	29	60.4	894	2	US-08-867-941-15	Sequence 15, Appl
50	29	60.4	1043	2	US-08-724-354D-4	Sequence 4, Appl
51	29	60.4	1043	3	US-09-270-984A-4	Sequence 4, Appl
52	29	60.4	1118	2	US-08-724-354D-2	Sequence 2, Appl
53	29	60.4	1118	3	US-09-270-984A-2	Sequence 2, Appl
54	29	60.4	2432	4	US-09-074-658-15	Sequence 15, Appl
55	28	58.3	59	4	US-08-963-851-14	Sequence 14, Appl
56	28	58.3	232	1	US-08-468-036-7	Sequence 7, Appl
57	28	58.3	232	2	US-08-376-843-7	Sequence 7, Appl
58	28	58.3	290	4	US-09-370-807-14	Sequence 14, Appl
59	28	58.3	290	4	US-09-921-259-14	Sequence 14, Appl
60	28	58.3	316	4	US-09-325-932A-62	Sequence 62, Appl
61	28	58.3	438	4	US-09-044-718-2	Sequence 2, Appl
62	28	58.3	430	4	US-09-044-718-15	Sequence 15, Appl
63	28	58.3	466	4	US-08-868-435-35	Sequence 35, Appl
64	28	58.3	466	4	US-08-744-231-35	Sequence 35, Appl
65	28	58.3	499	2	US-09-032-315-2	Sequence 2, Appl
66	28	58.3	499	2	US-08-993-318A-2	Sequence 2, Appl
67	28	58.3	499	4	US-09-399-886-2	Sequence 2, Appl
68	28	58.3	499	4	US-09-396-260-2	Sequence 2, Appl
69	28	58.3	499	4	US-09-576-281-2	Sequence 2, Appl
70	28	58.3	520	1	US-08-462-484-2	Sequence 2, Appl
71	28	58.3	520	1	US-08-441-147-2	Sequence 2, Appl
72	28	58.3	520	5	PCT-US95-07536-2	Sequence 2, Appl
73	28	58.3	565	4	US-09-370-807-8	Sequence 8, Appl
74	28	58.3	565	4	US-09-321-259-8	Sequence 8, Appl
75	28	58.3	873	3	US-08-990-140-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-637-759B-236
; Sequence 236, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,759B
FILING DATE: 03-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-637-759B-236

Query Match 66.7%; Score 32; DB 2; Length 45;
Best Local Similarity 60.0%; Pred. No. 6.5;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSX 10
DB 1 EEISPLGWSY 10

RESULT 2
US-08-871-355A-236
Sequence 236, Application US/08871355A
Patent No. 6015669
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,355A
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/02875
FILING DATE: 11-DEC-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101 CON
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:

LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-871-355A-236

Query Match 66.7%; Score 32; DB 3; Length 45;
Best Local Similarity 60.0%; Pred. No. 6.5;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSX 10
DB 1 EEISPLGWSY 10

RESULT 3
US-09-201-945-236
Sequence 236, Application US/09201945
Patent No. 6342215
GENERAL INFORMATION:
APPLICANT: David William Holden
TITLE OF INVENTION: Identification of Genes
NUMBER OF SEQUENCES: 501
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/201,945
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA: 08/637,759
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: RPMS 101
TELEPHONE: (404) 873-8794
TELEFAX: (404) 873-8795
INFORMATION FOR SEQ ID NO: 236:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-09-201-945-236

Query Match 66.7%; Score 32; DB 4; Length 45;
Best Local Similarity 60.0%; Pred. No. 6.5;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSX 10
DB 1 EEISPLGWSY 10

RESULT 4

US-09-228-986-73
; Sequence 73, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 947
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-228-986-73

Query Match 66.7%; Score 32; DB 4; Length 947;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXSY 11
|:| | | | |
Db 686 VMPGSGISY 694

RESULT 5
US-08-844-086-4
; Sequence 4, Application US/08844086
; Patent No. 5866390
; GENERAL INFORMATION:
; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: No. 5866390el Compounds
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,086
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9607993.4
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P31457-4
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 159 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-844-086-4

Query Match 64.6%; Score 31; DB 2; Length 159;

Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 BEVVPXGXS 9
|:| | | | |
Db 123 BEVLPDGT 131

RESULT 6
US-09-018-211-4
; Sequence 4, Application US/09018211
; Patent No. 6048716
; GENERAL INFORMATION:
; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: No. 6048716el Compounds
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/018,211
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/844,086
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: 9607993.4
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P31457-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 159 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-018-211-4

Query Match 64.6%; Score 31; DB 3; Length 159;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 BEVVPXGXS 9
|:| | | | |
Db 123 BEVLPDGT 131

RESULT 7
PCT-US91-02714-26
; Sequence 26, Application PC/TUS9102714
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02714
FILING DATE: 19910419
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 27805/30197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 513 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US91-02714-26

Query Match 54.6%; Score 31; DB 5; Length 513;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXSY 10
||| | | |
Db 201 VVPAGSY 208

RESULT 8
US-08-459-146-2
; Sequence 2, Application US/08459146
; Patent No. 5866405
; GENERAL INFORMATION:
; APPLICANT: Choi, Gil Ho
; APPLICANT: Nuss, Donald Lee
; TITLE OF INVENTION: Genetically Engineered Transmissible
; TITLE OF INVENTION: Hypovirulence
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,146
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/832,117

; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Roseman, Catherine R
; REGISTRATION NUMBER: 34,240
; REFERENCE/DOCKET NUMBER: 8589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-6208
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 622 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Endothia parasitica (Cryphonectria
; ORGANISM: parasitica)
; STRAIN: EP713
; US-08-459-146-2

Query Match 64.6%; Score 31; DB 2; Length 622;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
||||| |
Db 31 EEVVPAG 37

RESULT 9
US-08-459-065-2
; Sequence 2, Application US/08459065
; Patent No. 5882642
; GENERAL INFORMATION:
; APPLICANT: Choi, Gil Ho
; APPLICANT: Nuss, Donald Lee
; TITLE OF INVENTION: Genetically Engineered Transmissible
; TITLE OF INVENTION: Hypovirulence
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,065
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/832,117
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Roseman, Catherine R
; REGISTRATION NUMBER: 34,240
; REFERENCE/DOCKET NUMBER: 8589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-6208
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 622 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO

;; ORIGINAL SOURCE:
;; ORGANISM: Endothia parasitica (Cryphonectria
;; ORGANISM: parasitica)
;; STRAIN: Ep713
US-08-459-065-2

Query Match 64.6%; Score 31; DB 2; Length 622;
Best Local Similarity 85.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
Db 31 EEVVPAG 37

RESULT 10
US-07-688-352C-28
; Sequence 28, Application US/07688352C
; Patent No. 5527896
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/688,352C
FILING DATE: 19910419
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 27805/30197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-688-352C-28

Query Match 64.6%; Score 31; DB 1; Length 688;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXSX 10
Db 201 VVPAGGSY 208

RESULT 11
US-08-474-379C-28

; Sequence 28, Application US/08474379C
; Patent No. 5977305
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
; TITLE OF INVENTION: PROCESSES
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,379C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,188
FILING DATE: 01-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,352
FILING DATE: 19-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 27866/32771
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 688 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-474-379C-28

Query Match 64.6%; Score 31; DB 2; Length 688;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXSX 10
Db 201 VVPAGGSY 208

RESULT 12
US-09-146-249A-28
; Sequence 28, Application US/09146249A
; Patent No. 6069240
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America

;; ZIP: 60606-6402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/146,249A
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/511,715
;; FILING DATE: 20-APR-1990
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clough, David W.
;; REGISTRATION NUMBER: 36,107
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/474-6300
;; TELEFAX: 312-474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 28:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 688 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-146-249A-28

Query Match 64.6%; Score 31; DB 3; Length 688;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXSX 10
||| | |
Db 201 VVPAGGSY 208

RESULT 13
US-08-206-188B-28
; Sequence 28, Application US/08206188B
; Patent No. 6100025
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/206,188B
; FILING DATE: 01-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W.
; REGISTRATION NUMBER: 36107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856

;; INFORMATION FOR SEQ ID NO: 28:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 688 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-206-188B-28

Query Match 64.6%; Score 31; DB 3; Length 688;
Best Local Similarity 75.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXSX 10
||| | |
Db 201 VVPAGGSY 208

RESULT 14
US-08-844-086-2
; Sequence 2, Application US/08844086
; Patent No. 5866390
; GENERAL INFORMATION:
; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: NO. 5866390el Compounds
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/844,086
; FILING DATE: 18-APR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9607993.4
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P31457-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:

;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 833 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-844-086-2

Query Match 64.6%; Score 31; DB 2; Length 833;
Best Local Similarity 66.7%; Pred. NO. 2.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXS 9
||| | |
Db 169 EEVLPGTS 177

RESULT 15
US-09-018-211-2
; Sequence 2, Application US/09018211

; Patent No. 6048716
; GENERAL INFORMATION:
; APPLICANT: Lawlor, Elizabeth
; TITLE OF INVENTION: No. 6048716el Compounds
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/018,211
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/844,086
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: 9607993.4
; FILING DATE: 18-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmi, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P31457-4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 833 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-018-211-2

Query Match 64.6%; Score 31; DB 3; Length 833;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGS 9
| | | | | | |
Db 169 EEVLPDGT 177

RESULT 16
US-09-152-060-68
; Sequence 68, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (89)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-152-060-85

; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-152-060-68

Query Match 62.5%; Score 30; DB 4; Length 121;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
| | | | | |
Db 28 EEVVPXG 34

RESULT 17
US-09-152-060-85
; Sequence 85, Application US/09152060
; Patent No. 6448230
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (89)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; US-09-152-060-85

Query Match 62.5%; Score 30; DB 4; Length 121;

Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
Db 28 EEVPPG 34

RESULT 18
US-08-879-995A-1
; Sequence 1, Application US/08879995A
; Patent No. 5985606
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT03
; CLONE: 2109906
; US-08-879-995A-1

Query Match 62.5%; Score 30; DB 2; Length 122;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
Db 28 EEVPPG 34

RESULT 19
US-09-215-096-1
; Sequence 1, Application US/09215096
; Patent No. 6008194
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.

; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215,096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,995
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT03
; CLONE: 2109906
; US-09-215-096-1

Query Match 62.5%; Score 30; DB 3; Length 122;
Best Local Similarity 85.7%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
Db 28 EEVPPG 34

RESULT 20
US-08-834-776A-2
; Sequence 2, Application US/08834776A
; Patent No. 6060241
; GENERAL INFORMATION:
; APPLICANT: Corthesy-Theulaz, Irene
; TITLE OF INVENTION: Compositions and Methods Relating to
; TITLE OF INVENTION: Drug Discovery and Detection and Treatment of
; TITLE OF INVENTION: Gastrointestinal Diseases
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,776A

```

; FILING DATE: 03-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ashton, Nina M.
; REGISTRATION NUMBER: 37,273
; REFERENCE/DOCKET NUMBER: GAST-001/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-834-776A-2

Query Match 62.5%; Score 30; DB 3; Length 241;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 3
   ||:| |
Db 199 EEIVPAG 205

RESULT 21
US-07-803-636A-2
; Sequence 2, Application US/07803636A
; Patent No. 5422428
; GENERAL INFORMATION:
; APPLICANT: MCGUIRE, TRAVIS C., TERRY F. MCELWAIN, LANCE E. PERRYMAN,
; APPLICANT: WILLIAM C. DAVIS
; TITLE OF INVENTION: IMMUNIZATION AGAINST BABESIOSIS USING
; TITLE OF INVENTION: PURIFIED SURFACE ANTIGENS OF BABESIA BIGEMINA AND SIMILAR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID R. SALIWANCHIK
; STREET: 2421 NW 41ST STREET, SUITE A-1
; CITY: GAINESVILLE
; STATE: FLORIDA
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07/803.636A
; FILING DATE: 19911206
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: SALIWANCHIK, DAVID R
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: WA4-059.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-5800
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 480 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-803-636A-2

Query Match 62.5%; Score 30; DB 1; Length 480;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 EEVVPXGXS 9
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Db 407 EETVPSGDS 415

RESULT 22
US-08-961-083-220
; Sequence 220, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 220:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 626 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-961-083-220

Query Match 62.5%; Score 30; DB 4; Length 626;
Best Local Similarity 75.0%; Pred. No. 3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXS 10
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Db 70 VVPNGKSY 77

RESULT 23
US-09-413-814-93
; Sequence 93, Application US/09413814
; Patent No. 6225064
; GENERAL INFORMATION:
; APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
; APPLICANT: Bristol-Myers Squibb, Co.
; APPLICANT: Beyer, Stefan
; APPLICANT: Bloecker, Helmut
; APPLICANT: Brandt, Petra
; APPLICANT: Cino, Paul M
; APPLICANT: Dougherty, Brian A
; APPLICANT: Goldberg, Steven L
; APPLICANT: Hofle, Gerhard
; APPLICANT: Mueller, Joachim
; APPLICANT: Reichenbach, Hans

```

;; TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
;; FILE REFERENCE: PCT/US 99/23535
;; CURRENT APPLICATION NUMBER: US/09/413.814
;; CURRENT FILING DATE: 1999-10-07
;; EARLIER APPLICATION NUMBER: DE 198 46 493.2
;; EARLIER FILING DATE: 1998-10-09
;; NUMBER OF SEQ ID NOS: 107
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 93
;; LENGTH: 3072
;; TYPE: PRT
;; ORGANISM: Sorangium cellulosum
US-09-413-814-93

Query Match 62.5%; Score 30; DB 4; Length 3072;
Best Local Similarity 36.4%; Pred. No. 1.7e+03;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11
|:::| |:::
DB 2013 EQLPGGTAYN 2023

RESULT 24
US-09-413-814-80
; Sequence 80, Application US/09413814
; Patent No. 6225064
; GENERAL INFORMATION:
; APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
; APPLICANT: Bristol-Myers Squibb, Co.
; APPLICANT: Beyer, Stefan
; APPLICANT: Bloecker, Helmut
; APPLICANT: Brandt, Petra
; APPLICANT: Cino, Paul M
; APPLICANT: Dougherty, Brian A
; APPLICANT: Goldberg, Steven L
; APPLICANT: Hofle, Gerhard
; APPLICANT: Mueller, Joachim
; APPLICANT: Reichenbach, Hans
; TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
; FILE REFERENCE: PCT/US 99/23535
; CURRENT APPLICATION NUMBER: US/09/413.814
; CURRENT FILING DATE: 1999-10-07
; EARLIER APPLICATION NUMBER: DE 198 46 493.2
; EARLIER FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 80
; LENGTH: 3079
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-09-413-814-80

Query Match 62.5%; Score 30; DB 4; Length 3079;
Best Local Similarity 36.4%; Pred. No. 1.7e+03;
Matches 4; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11
|:::| |:::
DB 2019 EQLPGGTAYN 2029

RESULT 25
US-08-361-517-19
; Sequence 19, Application US/08361517
; Patent No. 5916876
; GENERAL INFORMATION:
; APPLICANT: George A. Heavner and Leon A. Epps
; TITLE OF INVENTION: Peptide Inhibitors of Leukocyte
; TITLE OF INVENTION: Adhesion
; NUMBER OF SEQUENCES: 42

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
;; ADDRESSEE: and No. 5916876ris
;; STREET: One Liberty Place - 46th Floor
;; CITY: Philadelphia
;; STATE: PA
;; COUNTRY: U.S.A.
;; ZIP: 19103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WordPerfect 5.1
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/361,517
;; FILING DATE: herewith
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/941,652
;; FILING DATE: September 8, 1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Dianne B. Elderkin
;; REGISTRATION NUMBER: 28,598
;; REFERENCE/DOCKET NUMBER: CCOR-0209
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 215-568-3100
;; TELEFAX: 215-568-3439
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acid residues
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: unknown
;; MOLECULE TYPE:
;; DESCRIPTION: Amide terminated
US-08-361-517-19
Query Match 60.4%; Score 29; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 5;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 EEVVPXGXSY 10
|:::| |:::
DB 1 KVLPGSSY 9
Search completed: June 10, 2003, 13:51:35
Job time : 10.6429 secs

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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:46:50 ; Search time 15 Seconds
(without alignments)
75.710 Million cell updates/sec

Title: US-09-909-164-43
Perfect score: 48
Sequence: 1 EEWVPXGXSYS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Published Applications, AA:*

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3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB pep.*
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5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	75.0	3472	9 US-10-027-806-4	Sequence 4, Appli
2	36	75.0	3472	9 US-10-034-623-4	Sequence 4, Appli
3	36	75.0	3472	9 US-10-027-801-4	Sequence 4, Appli
4	34	70.8	478	9 US-09-924-340-108	Sequence 108, App
5	34	70.8	478	9 US-09-992-600A-108	Sequence 108, App
6	34	70.8	478	9 US-09-746-783-184	Sequence 184, App
7	34	70.8	478	9 US-10-000-489-108	Sequence 108, App
8	34	70.8	478	9 US-10-000-986-108	Sequence 108, App
9	32	66.7	426	9 US-10-214-766-43	Sequence 43, Appli
10	32	66.7	947	9 US-10-101-464A-73	Sequence 73, Appli
11	31	64.6	597	10 US-09-815-242-13226	Sequence 13226, A
12	31	64.6	653	9 US-09-820-843A-26	Sequence 26, Appli
13	31	64.6	1083	9 US-09-835-976B-2	Sequence 2, Appli
14	31	64.6	1083	9 US-09-835-976B-14	Sequence 14, Appli
15	31	64.6	1099	9 US-09-835-976B-10	Sequence 10, Appli
16	31	64.6	1116	9 US-09-835-976B-12	Sequence 12, Appli
17	31	64.6	1135	9 US-09-835-976B-4	Sequence 4, Appli
18	31	64.6	1135	9 US-09-835-976B-6	Sequence 6, Appli
19	31	64.6	1150	9 US-09-835-976B-8	Sequence 8, Appli

RESULT 1

US-10-027-806-4
; Sequence 4, Application US/10027806
; Patent No. US20020160476A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; APPLICANT: Schleper, Christa
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAUM SYMBIOSUM
; FILE REFERENCE: DCOIP.002A
; CURRENT APPLICATION NUMBER: US/10/027.806
; CURRENT FILING DATE: 2001-12-21

ALIGNMENTS

31	64.6	1150	9	US-09-835-976B-16	Sequence 16, Appli
20	62.5	7	9	US-09-909-062-1	Sequence 1, Appli
21	62.5	7	9	US-09-909-062-9	Sequence 9, Appli
22	62.5	7	9	US-09-909-062-130	Sequence 130, App
23	62.5	121	9	US-09-852-797-68	Sequence 68, Appli
24	62.5	121	9	US-09-852-797-85	Sequence 85, Appli
25	62.5	121	10	US-09-853-161-68	Sequence 68, Appli
26	62.5	121	10	US-09-853-161-85	Sequence 85, Appli
27	62.5	121	10	US-09-852-659A-68	Sequence 68, Appli
28	62.5	121	10	US-09-852-659A-85	Sequence 85, Appli
29	62.5	135	9	US-09-992-598-359	Sequence 359, App
30	62.5	135	9	US-09-989-293A-359	Sequence 359, App
31	62.5	135	9	US-09-989-735-359	Sequence 359, App
32	62.5	135	9	US-09-989-735-359	Sequence 359, App
33	62.5	135	9	US-09-989-730-359	Sequence 359, App
34	62.5	135	9	US-09-990-436-359	Sequence 359, App
35	62.5	135	9	US-09-990-436-359	Sequence 359, App
36	62.5	135	9	US-09-991-181-359	Sequence 359, App
37	62.5	135	9	US-09-993-687-359	Sequence 359, App
38	62.5	135	9	US-09-989-734-359	Sequence 359, App
39	62.5	135	9	US-09-997-653-359	Sequence 359, App
40	62.5	135	9	US-10-174-590-444	Sequence 444, App
41	62.5	135	9	US-10-176-758-444	Sequence 444, App
42	62.5	135	9	US-10-175-737-444	Sequence 444, App
43	62.5	135	9	US-09-993-667-359	Sequence 359, App
44	62.5	135	9	US-10-173-706-444	Sequence 444, App
45	62.5	135	9	US-10-175-738-444	Sequence 444, App
46	62.5	135	9	US-10-175-752-444	Sequence 444, App
47	62.5	135	9	US-10-176-482-444	Sequence 444, App
48	62.5	135	9	US-10-176-757-444	Sequence 444, App
49	62.5	135	9	US-10-176-913-444	Sequence 444, App
50	62.5	135	9	US-10-180-552-444	Sequence 444, App
51	62.5	135	9	US-10-180-557-444	Sequence 444, App
52	62.5	135	9	US-09-990-438-359	Sequence 359, App
53	62.5	135	9	US-09-990-562-359	Sequence 359, App
54	62.5	135	9	US-09-997-428-359	Sequence 359, App
55	62.5	135	9	US-09-997-666-359	Sequence 359, App
56	62.5	135	9	US-10-173-700-444	Sequence 444, App
57	62.5	135	9	US-10-174-572-444	Sequence 444, App
58	62.5	135	9	US-10-174-579-444	Sequence 444, App
59	62.5	135	9	US-10-174-582-444	Sequence 444, App
60	62.5	135	9	US-10-174-588-444	Sequence 444, App
61	62.5	135	9	US-10-175-739-444	Sequence 444, App
62	62.5	135	9	US-10-175-740-444	Sequence 444, App
63	62.5	135	9	US-10-175-743-444	Sequence 444, App
64	62.5	135	9	US-10-176-488-444	Sequence 444, App
65	62.5	135	9	US-10-176-492-444	Sequence 444, App
66	62.5	135	9	US-10-176-747-444	Sequence 444, App
67	62.5	135	9	US-10-176-750-444	Sequence 444, App
68	62.5	135	9	US-10-176-985-444	Sequence 444, App
69	62.5	135	9	US-10-176-987-444	Sequence 444, App
70	62.5	135	9	US-10-176-991-444	Sequence 444, App
71	62.5	135	9	US-10-176-992-444	Sequence 444, App
72	62.5	135	9	US-10-176-993-444	Sequence 444, App
73	62.5	135	9	US-10-184-658-444	Sequence 108, App
74	62.5	135	9	US-10-227-884-108	Sequence 359, App
75	62.5	135	9	US-09-990-711-359	

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3472
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-806-4

Query Match 75.0%; Score 36; DB 9; Length 3472;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11
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DB 2294 EDVIPRGISFS 2304

RESULT 2
US-10-034-623-4
; Sequence 4, Application US/10034623
; Publication No. US20020198365A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCOIP.002A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US/10/034,623
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/408,020
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3472
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-034-623-4

Query Match 75.0%; Score 36; DB 9; Length 3472;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11
|:|:| | | |
DB 2294 EDVIPRGISFS 2304

RESULT 3
US-10-027-801-4
; Sequence 4, Application US/10027801
; Publication No. US20030054364A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; APPLICANT: Schleper, Christa
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCOIP.002A
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US/10/027,801
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3472
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-801-4

Query Match 75.0%; Score 36; DB 9; Length 3472;
Best Local Similarity 54.5%; Pred. No. 1.6e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11
|:|:| | | |
DB 2294 EDVIPRGISFS 2304

RESULT 4
US-09-924-340-108
; Sequence 108, Application US/09924340
; Publication No. US20030027248A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US2.REG
; CURRENT APPLICATION NUMBER: US/09/924,340
; CURRENT FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 108
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-924-340-108

Query Match 70.8%; Score 34; DB 9; Length 478;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EEVVPXGXSYS 11
|:|:| | | |
DB 239 EVAPAGASYN 248

RESULT 5
US-09-992-600A-108
; Sequence 108, Application US/0992600A
; Publication No. US20030027161A1
; GENERAL INFORMATION:
; APPLICANT: Bejanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US4.DIV
; CURRENT APPLICATION NUMBER: US/09/992,600A
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: JPatent
; SEQ ID NO 108
; LENGTH: 478

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-600A-108

Query Match 70.8%; Score 34; DB 9; Length 478;
Best Local Similarity 60.0%; Pred. No. 51;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVPGXSYS 11
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Db 239 EVAPAGASYN 248

RESULT 6

US-09-746-783-184

; Sequence 184, Application US/09746783

; Publication No. US20030044935A1

; GENERAL INFORMATION:

APPLICANT: Jacobs, Kenneth

McGoy, John M.

LaVallie, Edward R.

Racie, Lisa A.

Treacy, Maurice

Spaulding, Vikki

Agostino, Michael J.

Howes, Steven H.

Fechtel, Kim

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; Sequence 108, Application US/10000489
; Publication No. US20030092011A1
; GENERAL INFORMATION:

APPLICANT: Benjanin, Stephane

APPLICANT: Tanaka, Hiroaki

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; Sequence 108, Application US/10000489
; Publication No. US20030092011A1
; GENERAL INFORMATION:

APPLICANT: Benjanin, Stephane

APPLICANT: Tanaka, Hiroaki

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; Sequence 108, Application US/10000489
; Publication No. US20030092011A1
; GENERAL INFORMATION:

APPLICANT: Benjanin, Stephane

APPLICANT: Tanaka, Hiroaki

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QY 2 EVVPXGXSYS 11
|||
Db 239 EVAPAGASYN 248

RESULT 9

US-10-214-766-43
; Sequence 43, Application US/10214766
; Publication No. US20030084473A1
; GENERAL INFORMATION:
; APPLICANT: Gocal, Greg
; TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS
; FILE REFERENCE: CA1138
; CURRENT APPLICATION NUMBER: US/10/214,766
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,734
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-214-766-43

Query Match 66.7%; Score 32; DB 9; Length 426;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EVVPXGXSYS 10
|||
Db 223 EVIPAGQSY 232

RESULT 10

US-10-101-464A-73
; Sequence 73, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101.464A
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 947
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-73

Query Match 66.7%; Score 32; DB 9; Length 947;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXSYS 11
|||
Db 686 VMPGSGISYS 694

RESULT 11

Query Match 64.6%; Score 31; DB 9; Length 653;

US-09-815-242-13226
; Sequence 13226, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13226
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-815-242-13226

Query Match 64.6%; Score 31; DB 10; Length 597;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVVPXGXS 9
|||
Db 169 EEVLPGDGS 177

RESULT 12

US-09-820-843A-26
; Sequence 26, Application US/09820843A
; Publication No. US20030039963A1
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE P
; FILE REFERENCE: Q63915
; CURRENT APPLICATION NUMBER: US/09/820,843A
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Vibrio cholerae
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Iron(III) ABC transporter, permease protein
; NAME/KEY: misc_feature
; OTHER INFORMATION: g1|9654609
US-09-820-843A-26

Query Match

Best Local Similarity 85.7%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
| | | | |
Db 300 EEVVPXG 306

RESULT 13

US-09-835-976B-2
; Sequence 2, Application US/09835976B
; Publication No. US20030027983A1
; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
; CURRENT APPLICATION NUMBER: US/09/835,976B
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (53)
; OTHER INFORMATION: Xaa-Leu or Ile
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (86)
; OTHER INFORMATION: Xaa-Leu or Ile
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1028)
; OTHER INFORMATION: Xaa-Leu or Ile
US-09-835-976B-2

Query Match 64.6%; Score 31; DB 9; Length 1083;
Best Local Similarity 75.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXSX 10
| | | | |
Db 179 VVPAGGSY 186

RESULT 14

US-09-835-976B-14
; Sequence 14, Application US/09835976B
; Publication No. US20030027983A1
; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
; CURRENT APPLICATION NUMBER: US/09/835,976B
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 1083
; TYPE: PRT
; ORGANISM: mouse

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (71)
; OTHER INFORMATION: Xaa-Leu or Ile
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (155)
; OTHER INFORMATION: Xaa-Leu or Ile
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (467)
; OTHER INFORMATION: Xaa-Leu or Ile
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (586)
; OTHER INFORMATION: Xaa-Leu or Ile
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (639)
; OTHER INFORMATION: Xaa-Leu or Ile
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1023)
; OTHER INFORMATION: Xaa-Leu or Ile
US-09-835-976B-14

Query Match 64.6%; Score 31; DB 9; Length 1083;
Best Local Similarity 75.0%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXSX 10
| | | | |
Db 179 VVPAGGSY 186

RESULT 15

US-09-835-976B-10
; Sequence 10, Application US/09835976B
; Publication No. US20030027983A1
; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
; CURRENT APPLICATION NUMBER: US/09/835,976B
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1099
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (66)
; OTHER INFORMATION: Xaa-Leu or Ile
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (537)
; OTHER INFORMATION: Xaa-Leu or Ile
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (974)
; OTHER INFORMATION: n-c or a, Xaa-Leu or Ile
US-09-835-976B-10

Query Match 64.6%; Score 31; DB 9; Length 1099;
Best Local Similarity 75.0%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXSX 10
11111111
Db 195 VVPAGGSY 202

RESULT 16

US-09-835-976B-12
; Sequence 12, Application US/09835976B
; Publication No. US20030027983A1
; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
; CURRENT APPLICATION NUMBER: US/09/835,976B
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1116
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (120)
; OTHER INFORMATION: Xaa=Leu or Ile
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (358)
; OTHER INFORMATION: Xaa=Leu or Ile
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (916)
; OTHER INFORMATION: Xaa=Leu or Ile
US-09-835-976B-12

Query Match 64.6%; Score 31; DB 9; Length 1116;
Best Local Similarity 75.0%; Pred. No. 5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXSX 10
11111111
Db 158 VVPAGGSY 165

RESULT 17

US-09-835-976B-4
; Sequence 4, Application US/09835976B
; Publication No. US20030027983A1
; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
; CURRENT APPLICATION NUMBER: US/09/835,976B
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1135
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (35)
; OTHER INFORMATION: Xaa=Leu or Ile
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (472)
; OTHER INFORMATION: Xaa=Leu or Ile
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1075)
; OTHER INFORMATION: Xaa=Leu or Ile
US-09-835-976B-4

Query Match 64.6%; Score 31; DB 9; Length 1135;
Best Local Similarity 75.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXSX 10
11111111
Db 231 VVPAGGSY 238

RESULT 18

US-09-835-976B-6
; Sequence 6, Application US/09835976B
; Publication No. US20030027983A1
; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo
; APPLICANT: Alfred L. George, Jr.
; TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
; TITLE OF INVENTION: POLYPEPTIDES AND
; TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
; FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
; CURRENT APPLICATION NUMBER: US/09/835,976B
; CURRENT FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1135
; TYPE: PRT
; ORGANISM: mouse
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (102)
; OTHER INFORMATION: Xaa=Leu or Ile
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (631)
; OTHER INFORMATION: Xaa=Leu or Ile
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1113)
; OTHER INFORMATION: Xaa=Leu or Ile
US-09-835-976B-6

Query Match 64.6%; Score 31; DB 9; Length 1135;
Best Local Similarity 75.0%; Pred. No. 5.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXSX 10
11111111
Db 231 VVPAGGSY 238

RESULT 19

US-09-835-976B-8
; Sequence 8, Application US/09835976B
; Publication No. US20030027983A1
; GENERAL INFORMATION:
; APPLICANT: Mount, David B.
; APPLICANT: Delpire, Eric
; APPLICANT: Gamba, Gerardo

APPLICANT: Alfred L. George, Jr.
TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
TITLE OF INVENTION: POLYPEPTIDES AND
TITLE OF INVENTION: THERAPEUTIC AND SCREENING METHODS USING SAME
FILE REFERENCE: Attorney Docket No. US20030027983A1 1242-26-2
CURRENT FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 1150
TYPE: PRT
ORGANISM: mouse
FEATURE:
NAME/KEY: misc_feature
LOCATION: (35)
OTHER INFORMATION: Xaa-Leu or Ile
FEATURE:
NAME/KEY: misc_feature
LOCATION: (308)
OTHER INFORMATION: Xaa-Leu or Ile
FEATURE:
NAME/KEY: misc_feature
LOCATION: (848)
OTHER INFORMATION: Xaa-Leu or Ile
US-09-835-976B-8

Query Match 64.6%; Score 31; DB 9; Length 1150;
Best Local Similarity 75.0%; Pred. No. 5.2e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXSY 10
||| |||
Db 246 VVPAGGSY 253

RESULT 20
US-09-835-976B-16
Sequence 16, Application US/09835976B
Publication No. US20030027983A1
GENERAL INFORMATION:
APPLICANT: Mount, David B.
APPLICANT: Delpire, Eric
APPLICANT: Gamba, Gerardo
APPLICANT: Alfred L. George, Jr.
TITLE OF INVENTION: PURIFIED AND ISOLATED POTASSIUM-CHLORIDE COTRANSPORTER NUCLEIC AC
TITLE OF INVENTION: POLYPEPTIDES AND
FILE REFERENCE: THERAPEUTIC AND SCREENING METHODS USING SAME
CURRENT APPLICATION NUMBER: US/09/835,976B
CURRENT FILING DATE: 2001-04-16
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 1150
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (35)
OTHER INFORMATION: Xaa-Leu or Ile
FEATURE:
NAME/KEY: misc_feature
LOCATION: (346)
OTHER INFORMATION: Xaa-Leu or Ile
FEATURE:
NAME/KEY: misc_feature
LOCATION: (789)
OTHER INFORMATION: Xaa-Leu or Ile
US-09-835-976B-16

Query Match 64.6%; Score 31; DB 9; Length 1150;
Best Local Similarity 75.0%; Pred. No. 5.2e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 3 VVPXGXSY 10
||| |||
Db 246 VVPAGGSY 253
RESULT 21
US-09-909-062-1
Sequence 1, Application US/09909062
Publication No. US20030036501A1
GENERAL INFORMATION:
APPLICANT: Saksena, Anil K
APPLICANT: Girijavaliabhan, Viyyor M
APPLICANT: Lovey, Raymond G
APPLICANT: Jao, Edwin
APPLICANT: Bennett, Frank
APPLICANT: McCormick, Jinping L
APPLICANT: Pike, Russell E
APPLICANT: Bogen, Stephane L
APPLICANT: Liu, Yi-Tsung
APPLICANT: Arasappan, Ashok
APPLICANT: Pinto, Patrick A
APPLICANT: Njoroge, F George
APPLICANT: Ganguly, Ashit
TITLE OF INVENTION: NOVEL PEPTIDES AS NS3-SERINE PROTEASE INHIBITORS OF HEPATITIS
FILE REFERENCE: IN01157K-US
CURRENT APPLICATION NUMBER: US/09/909,062
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/220,109
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-C(=O)
US-09-909-062-1

Query Match 62.5%; Score 30; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
|||||||
Db 1 EEVVPXG 7

RESULT 22
US-09-909-062-9
Sequence 9, Application US/09909062
Publication No. US20030036501A1
GENERAL INFORMATION:
APPLICANT: Saksena, Anil K
APPLICANT: Girijavaliabhan, Viyyor M
APPLICANT: Lovey, Raymond G
APPLICANT: Jao, Edwin
APPLICANT: Bennett, Frank
APPLICANT: McCormick, Jinping L
APPLICANT: Pike, Russell E
APPLICANT: Bogen, Stephane L
APPLICANT: Liu, Yi-Tsung
APPLICANT: Arasappan, Ashok

```
; APPLICANT: Pinto, Patrick A
; APPLICANT: Njoroge, F George
; APPLICANT: Ganguly, Ashit
; TITLE OF INVENTION: NOVEL PEPTIDES AS NS3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
; FILE REFERENCE: IN01157K-US
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/220,109
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: norvaline-C(-O)
US-09-909-062-9

Query Match      62.5%; Score 30; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEVVPXG 7
Db      1 EEVVPXG 7

RESULT 23
US-09-909-062-130
; Sequence 130, Application US/09909062
; Publication No. US20030036501A1
; GENERAL INFORMATION:
; APPLICANT: Saksena, Anil K
; APPLICANT: Girijavaliabhan, Viyyor M
; APPLICANT: Lovey, Raymond G
; APPLICANT: Jao, Edwin
; APPLICANT: Bennett, Frank
; APPLICANT: McCormick, Jinping L
; APPLICANT: Pike, Russell E
; APPLICANT: Bogen, Stephanie L
; APPLICANT: Liu, Yi-Tsung
; APPLICANT: Arasappan, Ashok
; APPLICANT: Pinto, Patrick A
; APPLICANT: Njoroge, F George
; APPLICANT: Ganguly, Ashit
; TITLE OF INVENTION: NOVEL PEPTIDES AS NS3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
; FILE REFERENCE: IN01157K-US
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/220,109
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLATION
; FEATURE:

; APPLICANT: Njoroge, F George
; APPLICANT: Ganguly, Ashit
; TITLE OF INVENTION: AMIDATION
; NAME/KEY: MISC_FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: norvaline-(C-O)
US-09-909-062-130

Query Match      62.5%; Score 30; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEVVPXG 7
Db      1 EEVVPXG 7

RESULT 24
US-09-852-797-68
; Sequence 68, Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-68

Query Match      62.5%; Score 30; DB 9; Length 121;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 EEVVPXG 7
Db      28 EEVPPG 34

RESULT 25
US-09-852-797-85
; Sequence 85, Application US/09852797
; Patent No. US20020172994A1
; FEATURE:
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; APPLICANT: Njoroge, F George
; APPLICANT: Ganguly, Ashit
; TITLE OF INVENTION: AMIDATION
; NAME/KEY: MISC_FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: norvaline-(C-O)
US-09-909-062-130

Query Match      62.5%; Score 30; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 EEVVPXG 7
Db      1 EEVVPXG 7

RESULT 24
US-09-852-797-68
; Sequence 68, Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: PZ003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-68

Query Match      62.5%; Score 30; DB 9; Length 121;
Best Local Similarity 85.7%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 EEVVPXG 7
Db      28 EEVPPG 34

RESULT 25
US-09-852-797-85
; Sequence 85, Application US/09852797
; Patent No. US20020172994A1
; FEATURE:
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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003p2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
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; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (89)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-852-797-85

Query Match      62.5%; Score 30; DB 9; Length 121;
Best Local Similarity 85.7%; Pred. NO. 80;
Matches      6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 EEVVPXG 7
Db      28 EEVPPGG 34

Search completed: June 10, 2003, 14:35:45
Job time : 16.0714 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:31:15 ; Search time 11.2143 Seconds
(without alignments)
94.297 Million cell updates/sec

Title: US-09-909-164-43
Perfect score: 48
Sequence: 1 EEVVPXGXSYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_73:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	75.0	3472	2 T31308	hypothetical 367k
2	35	72.9	225	2 S57810	hypothetical prote
3	34	70.8	102	2 A42452	VI protein - tobac
4	34	70.8	165	2 D69493	hypothetical prote
5	34	70.8	259	2 T34536	hypothetical prote
6	34	70.8	1028	2 AF3286	ATP-dependent DNA
7	33	68.8	124	1 VKLJSE	trans-regulatory s
8	33	68.8	427	2 F64084	tolB protein - Hae
9	32	66.7	227	2 E75619	hypothetical prote
10	32	66.7	425	2 T24111	hypothetical prote
11	32	66.7	426	2 D82163	3-phosphoshikimate
12	32	66.7	670	2 S22293	zinc finger protei
13	32	66.7	890	2 A30481	bacteriocin BCN5 -
14	32	66.7	2717	2 A34203	DNA-binding protei
15	31	64.6	123	2 E69342	conserved hypotet
16	31	64.6	284	2 S75817	hypothetical prote
17	31	64.6	319	2 S03833	hypothetical prote
18	31	64.6	361	2 S15299	dtppglucose 4,6-de
19	31	64.6	361	2 AF0767	hypothetical prote
20	31	64.6	437	2 AC2945	periplasmic sorbit
21	31	64.6	450	2 C98337	ATP-dependent DNA
22	31	64.6	541	2 AH2679	probable ABC subst
23	31	64.6	544	2 C82900	type II secretion
24	31	64.6	561	2 C84239	DNA ligase (AB0425
25	31	64.6	573	2 F97461	hypothetical prote
26	31	64.6	612	2 T05331	hypothetical prote
27	31	64.6	622	2 S15009	probable beta-gala
28	31	64.6	646	2 C95978	iron(III) ABC tran
29	31	64.6	653	2 D82352	

30	31	64.6	701	2 S61239	hypothetical prote
31	31	64.6	829	2 H86726	leucine-tRNA ligas
32	31	64.6	833	2 H95029	leucyl-tRNA synthe
33	31	64.6	833	2 C97901	leucine-tRNA ligas
34	31	64.6	840	2 T39116	probable sulfate p
35	31	64.6	877	2 T40413	sulfate permease -
36	31	64.6	926	2 AG1860	hypothetical prote
37	31	64.6	1014	2 T17275	hypothetical prote
38	31	64.6	1081	1 A42399	isoleucine-tRNA li
39	31	64.6	1085	2 T18369	K-Cl cotransport p
40	31	64.6	1085	2 T31429	K-Cl cotransport p
41	31	64.6	1086	2 T14114	K-Cl cotransport p
42	31	64.6	1088	2 D82246	probable chitinase
43	31	64.6	1116	2 T31432	K-Cl cotransport p
44	31	64.6	1152	2 D87046	conserved hypotet
45	31	64.6	1152	2 T04456	hypothetical prote
46	30	62.5	84	2 E97333	hypothetical prote
47	30	62.5	118	2 F84263	transcription repr
48	30	62.5	163	2 F97332	hypothetical prote
49	30	62.5	175	2 P0616	transport protein
50	30	62.5	192	2 D83632	hypothetical prote
51	30	62.5	224	2 G70709	probable purQ prot
52	30	62.5	224	2 F87186	phosphoribosylform
53	30	62.5	224	2 D84345	phosphoribosylform
54	30	62.5	227	2 C71211	probable phosphori
55	30	62.5	232	2 C71908	3-oxoadipate coA-t
56	30	62.5	232	2 C64606	melanoma antigen M
57	30	62.5	234	2 I38667	beta-ketoacyl-ACP
58	30	62.5	298	2 T47670	hypothetical prote
59	30	62.5	299	2 C97102	melanoma antigen M
60	30	62.5	315	2 I38668	hypothetical prote
61	30	62.5	327	2 D71378	hypothetical prote
62	30	62.5	363	2 G95237	conserved hypotet
63	30	62.5	363	2 H98101	conserved hypotet
64	30	62.5	363	2 D69551	conserved hypotet
65	30	62.5	404	2 S57178	2-nitropropane dio
66	30	62.5	430	2 B40646	folyl-polyglutamat
67	30	62.5	435	2 T46443	hypothetical prote
68	30	62.5	449	2 A99286	conserved hypotet
69	30	62.5	454	2 F83760	hypothetical prote
70	30	62.5	480	1 A45614	merozoite surface
71	30	62.5	480	2 D45661	merozoite surface
72	30	62.5	498	2 B90604	conserved hypotet
73	30	62.5	526	2 T13687	hypothetical prote
74	30	62.5	540	2 E95260	ABC transporter, A
75	30	62.5	540	2 H98125	hypothetical prote

ALIGNMENTS

RESULT 1

T31308 hypothetical 367k protein - Cenarchaeum symbiosum

C:Species: Cenarchaeum symbiosum

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000

C:Accession: T31308

R:Schleper, C.; DeLong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V.

J. Bacteriol. 180, 5003-5009, 1998

A:Title: Genomic analysis reveals chromosomal variation in natural populations of 1

A:Reference number: Z20994; MUID:98422450; PMID:9748430

A:Accession: T31308

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-3472 <SCH>

A:Cross-references: EMBL:AF083072; NID:g3599393; PID:g3599394; PIDN:AAC62699.1

C:Superfamily: Cenarchaeum symbiosum hypothetical 367k protein

Query Match 75.0%; Score 36; DB 2; Length 3472;

Best Local Similarity 54.5%; Pred. No. 79; Indels 0; Gaps 0;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11

Db 2294 EDVIPRGLSFS 2304
||||| |

RESULT 2

S57810

hypothetical protein precursor (clone TPP11) - tomato

C:Species: Lycopersicon esculentum (tomato)

C>Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000

C:Accession: S57810

R:Milligan, S.B.; Gasser, C.S.

Plant Mol. Biol. 28, 691-711, 1995

A:Title: Nature and regulation of pistil-expressed genes in tomato.

A:Reference number: S57808; MUID:93375233; PMID:7647301

A:Accession: S57810

A>Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-225 <MIL>

A:Cross-references: EMBL:U20592; NID:g924625; PIDN:AAA80497.1; PID:g924626

C:Superfamily: plant Kunitz-type proteinase inhibitor

Query Match

Best Local Similarity 72.9%; Score 35; DB 2; Length 225;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11

:||||| |

Db 32 DEVVPGNKTYA 42

RESULT 3

A42452

V1 protein - tobacco yellow dwarf virus (strain Australia)

C:Species: tobacco yellow dwarf virus

C>Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999

C:Accession: A42452

R:Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.

Virology 187, 633-642, 1992

A:Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yellow

A:Reference number: A42452; MUID:92188538; PMID:1546458

A:Molecule type: DNA

A:Residues: 1-102 <MOR>

A:Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284

Query Match

Best Local Similarity 70.8%; Score 34; DB 2; Length 102;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EEVVPXGXSYS 11

:||||| |

Db 7 QVVPSSGINYS 16

RESULT 4

D69493

hypothetical protein AFI949 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000

C:Accession: D69493

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: D69493

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-165 <KLE>

A:Cross-references: GB:AE000968; GB:AE000782; NID:g2689291; PIDN:AAB89307.1; PID:g264859

C:Superfamily: Archaeoglobus fulgidus hypothetical protein AFI949

Query Match 70.8%; Score 34; DB 2; Length 165;

Best Local Similarity 60.0%; Pred. No. 8.2;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSY 10

||| |

Db 60 EESIPDGASY 69

RESULT 5

T34536

hypothetical protein DKFZp434C031.1 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T34536

R:Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, October 1999

A:Reference number: Z21540

A:Accession: T34536

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-259 <POU>

A:Cross-references: EMBL:AL122063

A:Experimental source: adult testis; clone DKFZp434C031

C:Genetics:

A>Note: DKFZp434C031.1

Query Match

Best Local Similarity 70.8%; Score 34; DB 2; Length 259;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EWVPXGXSYS 11

||| |

Db 22 EVAPAGASYN 31

RESULT 6

AF3286

ATP-dependent DNA helicase BMEI0275 [imported] - Brucella melitensis (strain 16M)

C:Species: Brucella melitensis

C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

C:Accession: AF3286

R:DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mijer, C.; Los, T.; Ivan

; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; L

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella mel

A:Reference number: AD3252; PMID:11756688

A:Accession: AF3286

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1028 <KUR>

A:Cross-references: GB:AE008917; PIDN:AAL51457.1; PID:g17982167; GSPDB:GN00190

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BMEI0275

A:Map position: 1

Query Match

Best Local Similarity 70.8%; Score 34; DB 2; Length 1028;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11

||| |

Db 76 EKIVPPGARYS 86

RESULT 7

VKLJ51

trans-regulatory splicing protein - simian immunodeficiency virus SIVcpz

N:Alternate names: anti-repression trans-activator; art protein; rev protein; trs

C:Species: simian immunodeficiency virus SIVcpz

A:Note: host Pan troglodytes (chimpanzee)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
 C:Accession: S09988
 R:Huet, T.; Chevner, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
 Nature 345, 356-359, 1990
 A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
 A:Reference number: S09983; MUID:90259077; PMID:2188136
 A:Accession: S09988
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-124 <HUE>
 A:Cross-references: EMBL:X52154; NID:g58866; PIDN:CAA36405.1; PID:g763085
 C:Genetics:
 A:Gene: rev; trs; art
 A:Introns: 27/1
 C:Superfamily: AIDS trans-regulatory splicing protein
 C:Keywords: AIDS; immunodeficiency; splicing protein; transcription regulation

Query Match 68.8%; Score 33; DB 1; Length 124;
 Best Local Similarity 60.0%; Pred. No. 10;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVPXGXSYS 11
 ||| |
 Db 107 ETVPAGNGYS 116

RESULT 8
 F64064
 tolB protein - Haemophilus influenzae (strain Rd KW20)
 C:Species: Haemophilus influenzae
 C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
 C:Accession: F64064; JC5213
 R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J.
 Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrman, J.L.; Geoghegan, N.S.M.
 Science 269, 496-512, 1995
 A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.
 A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
 A:Reference number: A64000; MUID:95350630; PMID:7542800
 A:Accession: F64064
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-427 <TTGR>
 A:Cross-references: GB:U32722; GB:U42023; NID:g1573348; PIDN:AAC22040.1; PID:g15733352;
 A:Experimental source: strain Rd KW20
 R:Sen, K.; Sikkema, D.J.; Murphy, T.F.
 Gene 178, 75-81, 1996
 A:Title: Isolation and characterization of the Haemophilus influenzae tolQ, tolR, tolA
 A:Reference number: JC5212; MUID:97080550; PMID:8921895
 A:Accession: JC5213
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-5, 'H', 7-13, 'I', 15-16, 'ITH', 20, 'V', 22-78, 'H', 80-128, 'A', 130-159, 'G', 161-236
 A:Cross-references: GB:U32470; NID:g1685076; PIDN:AAC44597.1; PID:g1685080
 A:Experimental source: strain 1479
 C:Genetics:
 A:Gene: tolB
 C:Function:
 A:Description: involved in transport of colicins and phages across the cell envelope; ph

Query Match 68.8%; Score 33; DB 2; Length 427;
 Best Local Similarity 60.0%; Pred. No. 38;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVPXGXSYS 11
 ||| |
 Db 103 QVVPSCNGYS 112

RESULT 9
 E75619
 hypothetical protein DRB0013 - Deinococcus radiodurans (strain R1)

C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
 C:Accession: E75619
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.
 M.; Shen, H.O.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.M.
 S.; Smith, M.O.; Venter, J.C.; Fraser, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: E75619
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-227 <WHI>
 A:Cross-references: GB:AE001826; NID:g6460827; PIDN:AAF12657.1; PID:g6460953; TIGR:
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DRB0013
 A:Map position: megaplasmid
 A:Genome: plasmid
 A:Note: plasmid MP1
 C:Superfamily: Deinococcus radiodurans megaplasmid hypothetical protein DRB0013

Query Match 66.7%; Score 32; DB 2; Length 227;
 Best Local Similarity 54.5%; Pred. No. 31;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11
 ||| |
 Db 43 ESVLPIGHSFS 53

RESULT 10
 T24111
 hypothetical protein R10D12.10 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
 C:Accession: T24111
 R:Percy, C.
 submitted to the EMBL Data Library, October 1996
 A:Reference number: Z19842
 A:Accession: T24111
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-425 <WIL>
 A:Cross-references: EMBL:Z81109; PIDN:CAB03241.1; GSPDB:GN00023; CESP:R10D12.10
 A:Experimental source: clone R10D12
 C:Genetics:
 A:Gene: CESP:R10D12.10
 A:Map position: 5
 A:Introns: 23/3; 56/3; 113/3; 257/2

Query Match 66.7%; Score 32; DB 2; Length 425;
 Best Local Similarity 50.0%; Pred. No. 62;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 10
 ||| |
 Db 335 EQIVPGGLQY 344

RESULT 11
 D82163
 3-phosphoshikimate 1-carboxyvinyltransferase VC1732 [imported] - Vibrio cholerae (C:Species: Vibrio cholerae
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: D82163
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, C.
 Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sell
 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: D82163

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <HEI>
A:Cross-references: GB:AE004251; GB:AE003852; NID:g9656248; PIDN:AAF94882.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1732
A:Map position: 1
C:Superfamily: 3-phosphoshikimate 1-carboxyvinyltransferase; 3-phosphoshikimate 1-carboxy
Query Match 66.7%; Score 32; DB 2; Length 426;
Best Local Similarity 60.0%; Pred. No. 62;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 EEVVPXGXSY 10
| | | | |
Db 223 EFVIPAGQSY 232

RESULT 12
S22293
zinc finger protein AT-BP2 - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 20-Sep-1999
C:Accession: S22293; I78656
R:Mitchellmore, C.; Traboni, C.; Cortese, R.
Nucleic Acids Res. 19, 141-147, 1991
A:Title: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-
A:Reference number: I58280; MUID:91187610; PMID:1901405
A:Accession: S22293
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-670 <MIT>
A:Cross-references: EMBL:X54250; NID:g57519; PIDN:CAA38151.1; PID:g57520
A:Note: the authors did not translate the codon for residue 1
C:Superfamily: HIV-EP2 enhancer-binding protein
C:Keywords: DNA binding; transcription regulation; zinc finger
Query Match 66.7%; Score 32; DB 2; Length 670;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 VVPXGXSY 11
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Db 376 VVPAGLTYS 384

RESULT 13
A30481
bacteriocin BCN5 - Clostridium perfringens plasmid pIP404
C:Species: Clostridium perfringens
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Nov-1999
C:Accession: A30481; S03779
R:Garnier, T.; Cole, S.T.
J. Bacteriol. 168, 1189-1196, 1986
A:Title: Characterization of a bacteriocinogenic plasmid from Clostridium perfringens and
A:Reference number: JTO354; MUID:87057020; PMID:2877971
A:Accession: A30481
A:Molecule type: DNA
A:Residues: 1-890 <GAR>
A:Cross-references: GB:M32882; GB:J03309; NID:g150738; PIDN:AAA98249.1; PID:g150739
C:Genetics:
A:Gene: bcn
A:Genome: plasmid
C:Superfamily: Clostridium perfringens plasmid pIP404 bacteriocin BCN5
C:Keywords: bacteriocin
Query Match 66.7%; Score 32; DB 2; Length 890;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 EVVPXGXSY 10
| | | | |

Db 170 EVVPGGFTY 178

RESULT 14
A34203
DNA-binding protein PRDII-BF1 - human
N:Alternate names: major histocompatibility complex enhancer-binding protein 1
C:Species: Homo sapiens (man)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 20-Sep-1999
C:Accession: A34203; A34779
R:Fan, C.M.; Maniatis, T.
Genes Dev. 4, 29-42, 1990
A:Title: A DNA-binding protein containing two widely separated zinc finger motifs
A:Reference number: A34779; MUID:90169514; PMID:2108471
A:Accession: A34203
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-2717 <FAN>
A:Cross-references: EMBL:X51435; NID:g38017; PIDN:CAA35798.1; PID:g38018
R:Baldwin Jr., A.S.; LeClair, K.P.; Singh, H.; Sharp, P.A.
Mol. Cell. Biol. 10, 1406-1414, 1990
A:Title: A large protein containing zinc finger domains binds to related sequence
A:Reference number: A34779; MUID:90205817; PMID:2108316
A:Accession: A34779
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 801-1072, 'N', 1074-1168, 'K', 1170-1225, 'V', 1227-1434, 'N', 1436-1607, 'I', 1609-1670, 'I', 1672-1717, 'I', 1719-1770, 'I', 1772-1817, 'I', 1819-1867, 'I', 1869-1917, 'I', 1919-1967, 'I', 1969-2017, 'I', 2019-2067, 'I', 2069-2117, 'I', 2119-2167, 'I', 2169-2217, 'I', 2219-2267, 'I', 2269-2317, 'I', 2319-2367, 'I', 2369-2417, 'I', 2419-2467, 'I', 2469-2517, 'I', 2519-2567, 'I', 2569-2617, 'I', 2619-2667, 'I', 2669-2717, 'I', 2719-2767, 'I', 2769-2817, 'I', 2819-2867, 'I', 2869-2917, 'I', 2919-2967, 'I', 2969-3017, 'I', 3019-3067, 'I', 3069-3117, 'I', 3119-3167, 'I', 3169-3217, 'I', 3219-3267, 'I', 3269-3317, 'I', 3319-3367, 'I', 3369-3417, 'I', 3419-3467, 'I', 3469-3517, 'I', 3519-3567, 'I', 3569-3617, 'I', 3619-3667, 'I', 3669-3717, 'I', 3719-3767, 'I', 3769-3817, 'I', 3819-3867, 'I', 3869-3917, 'I', 3919-3967, 'I', 3969-4017, 'I', 4019-4067, 'I', 4069-4117, 'I', 4119-4167, 'I', 4169-4217, 'I', 4219-4267, 'I', 4269-4317, 'I', 4319-4367, 'I', 4369-4417, 'I', 4419-4467, 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C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S75817
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S75817
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-284 <RAN>
A:Cross-references: EMBL:D90913; GB:AB001339; NID:gl653348; PIDN:BAAL8276.1; PID:d101900
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 64.6%; Score 31; DB 2; Length 284;
Best Local Similarity 55.6%; Pred. No. 66;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXSY 11
|:|:|:|:
DB 208 VIPAGVSYT 216

RESULT 17
S03833
hypothetical protein 1 - chestnut blight fungus
C:Species: *Cryphonectria parasitica*, *Endothia parasitica* (Chestnut blight fungus)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Sep-1997
C:Accession: S03833
R:Rae, B.P.; Hillman, B.I.; Tartaglia, J.; Nuss, D.L.
EMBO J. 8, 657-663, 1989
A:Title: Characterization of double-stranded RNA genetic elements associated with biological activity of *Cryphonectria parasitica*
A:Reference number: S03833; MUID:89251594; PMID:2721496
A:Accession: S03833
A:Molecule type: DNA
A:Residues: 1-319 <RAN>
A:Cross-references: EMBL:X14524; NID:g2624; PID:g2625
A:Note: the authors translated the codon CAG for residue 156 as Gly

Query Match 64.6%; Score 31; DB 2; Length 319;
Best Local Similarity 85.7%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
|:|:|:|:
DB 31 EEVVPAG 37

RESULT 18
S15299
dUDPglucose 4,6-dehydratase (EC 4.2.1.46) - *Salmonella typhimurium*
C:Species: *Salmonella typhimurium*
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 24-Oct-1997
C:Accession: S15299
R:Jiang, X.M.; Neal, B.; Santiago, F.; Lee, S.J.; Romana, L.K.; Reeves, P.R.
Mol. Microbiol. 5, 695-713, 1991
A:Title: Structure and sequence of the rfb (O antigen) gene cluster of *Salmonella serovar* *typhimurium*
A:Reference number: S15299; MUID:91260454; PMID:1710759
A:Accession: S15299
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-361 <MOL>
C:Genetics: rfb
A:Gene: rfb
C:Superfamily: *Escherichia coli* UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
C:Keywords: carbon-oxygen lyase; hydro-lyase
F:3-341/Domain: UDPglucose 4-epimerase homology <UDP>

Query Match 64.6%; Score 31; DB 2; Length 361;
Best Local Similarity 50.0%; Pred. No. 85;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSY 10
|:|:|:|:
DB 278 DEIVPKATSY 287

RESULT 19
AF0767
dUDP-glucose 4,6-dehydratase [imported] - *Salmonella enterica* subsp. *enterica* serovar *typhi*
C:Species: *Salmonella enterica* subsp. *enterica* serovar *typhi*
A:Note: this species has also been called *Salmonella typhi*
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C:Accession: AF0767
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Fairhead, S.; Mouton, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parkhill, J.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Fairhead, S.; Mouton, S.; O'Gaora, P.
A:Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serovar *typhi*
A:Reference number: AB0502; PMID:11677608
A:Accession: AF0767
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-361 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD02460.1; PID:gl6503327; GSPDB:GN00176
C:Genetics: *Escherichia coli* UDPglucose 4-epimerase; UDPglucose 4-epimerase homology
C:Superfamily: *Escherichia coli* UDPglucose 4-epimerase; UDPglucose 4-epimerase homology

Query Match 64.6%; Score 31; DB 2; Length 361;
Best Local Similarity 50.0%; Pred. No. 85;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSY 10
|:|:|:|:
DB 278 DEIVPKATSY 287

RESULT 20
AG2945
hypothetical protein Atu3165 [imported] - *Agrobacterium tumefaciens* (strain C58, D)
C:Species: *Agrobacterium tumefaciens*
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AG2945
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; Mader, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Boon, E.W.
A:Title: The Genome of the Natural Genetic Engineer *Agrobacterium tumefaciens* C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AG2945
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-437 <KUR>
A:Cross-references: GB:AE008689; PIDN:AAL43981.1; PID:gi17741537; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics: *Agrobacterium tumefaciens* C58
A:Gene: Atu3165
A:Map position: linear chromosome

Query Match 64.6%; Score 31; DB 2; Length 437;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EEVVPXGXSY 11
|:|:|:|:
DB 289 EVTPNGSSWS 298

RESULT 21

C98337
 periplasmic sorbitol-binding protein, smcE (AF018073) [imported] - Agrobacterium tumefaciens
 C:Species: Agrobacterium tumefaciens
 C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
 C:Accession: C98337
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens 294, 2323-2328, 2001
 A:Reference number: A97359; PMID:11743194
 A:Accession: C98337
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-450 <KUR>
 A:Cross-references: GB:AE007870; PIDN:AAK90221.1; PID:g15160234; GSPDB:GN00170
 C:Genetics:
 A:Gene: AGR_L3289
 A:Map position: linear chromosome

Query Match 64.6%; Score 31; DB 2; Length 450;
 Best Local Similarity 60.0%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 EVVPXGXSYS 11
 |||||
 Db 302 EVTPNGSSWS 311

RESULT 22
 AH2679
 ATP-dependent DNA ligase Atu0840 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
 C:Accession: AH2679
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClellan, S.; Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.; E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; PMID:11743193
 A:Accession: AH2679
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-541 <KUR>
 A:Cross-references: GB:AE008688; PIDN:AAK41854.1; PID:g17739214; GSPDB:GN00186
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu0840
 A:Map position: circular chromosome

Query Match 64.6%; Score 31; DB 2; Length 541;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGXSYS 10
 |||||
 Db 442 EQLVPVGKAY 451

RESULT 23
 C82900
 probable ABC substrate-binding protein, iron U0359 [imported] - Ureaplasma urealyticum
 C:Species: Ureaplasma urealyticum
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
 C:Accession: C82900
 R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000
 A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a minor variant
 A:Reference number: AB2870
 A:Accession: C82900
 A:Status: preliminary

A:Molecule type: DNA
 A:Residues: 1-544 <GLA>
 A:Cross-references: GB:AE002133; GB:AF222894; NID:g6899339; PIDN:AAF30768.1; GSPDB:GN00169
 A:Experimental source: serovar 13; biovar 1
 C:Genetics:
 A:Gene: ABCsbp-5; U0359
 A:Genetic code: SGC3

Query Match 64.6%; Score 31; DB 2; Length 544;
 Best Local Similarity 70.0%; Pred. No. 1.3e+02;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EEVVPXGXSYS 10
 |||||
 Db 135 EEVVPHYLSY 144

RESULT 24
 C84239
 type II secretion system protein [imported] - Halobacterium sp. NRC-1
 C:Species: Halobacterium sp. NRC-1
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
 C:Accession: C84239
 R:Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lathia, K.H.; Alam, M.; Freitas, T.; Jung, K.H.; Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.N.
 A:Title: Genome sequence of Halobacterium species NRC-1.
 A:Reference number: AB4160; MUID:20504483; PMID:11016950
 A:Accession: C84239
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-561 <STO>
 A:Cross-references: GB:AE004437; NID:g10580393; PIDN:AAG19279.1; GSPDB:GN00138
 C:Genetics:
 A:Gene: gspE2
 C:Superfamily: conserved hypothetical protein MJ0900

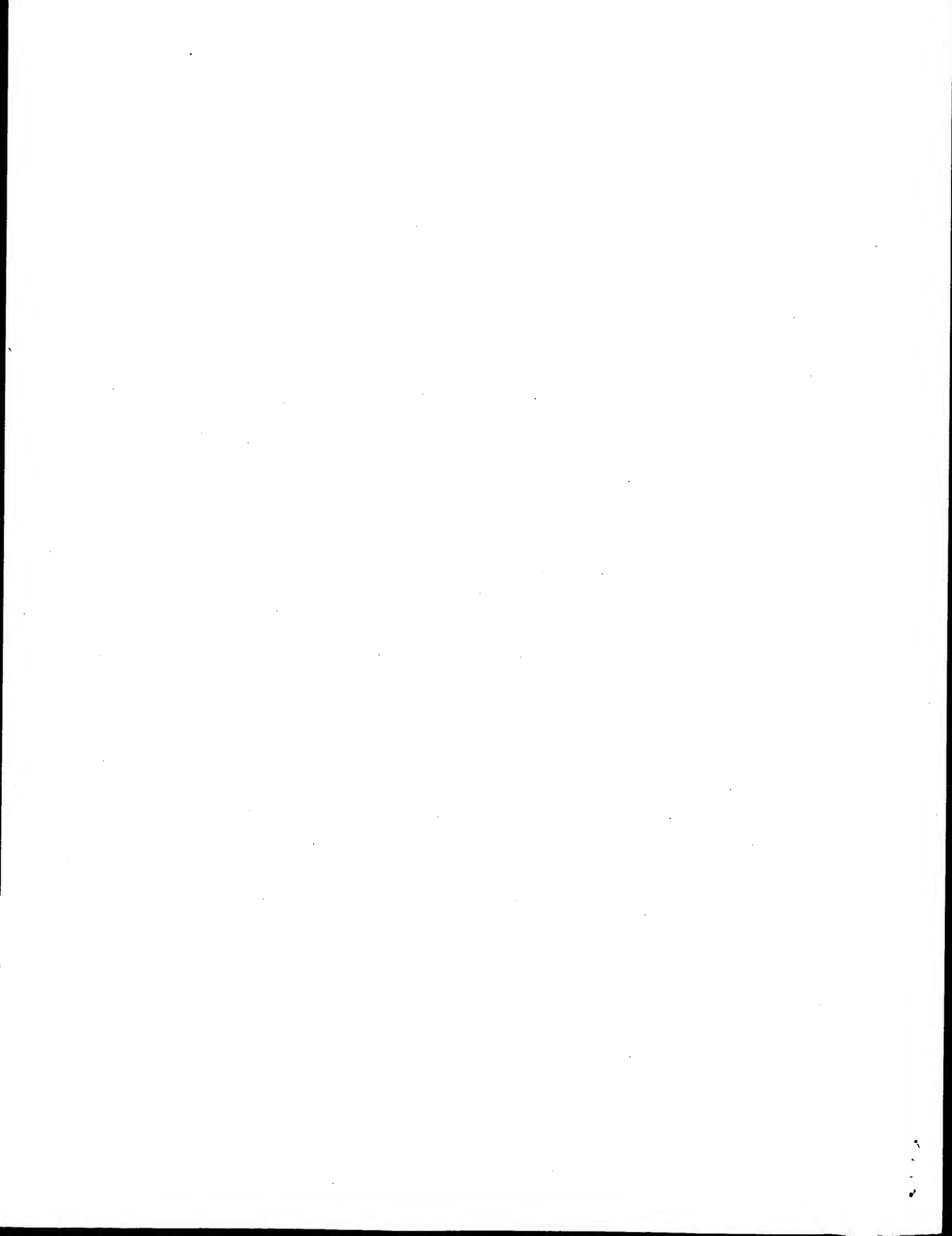
Query Match 64.6%; Score 31; DB 2; Length 561;
 Best Local Similarity 45.5%; Pred. No. 1.4e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EEVVPXGXSYS 11
 |||||
 Db 251 EEVTPRGSAFT 261

RESULT 25
 F97461
 DNA ligase (AB042527) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
 C:Species: Agrobacterium tumefaciens
 C>Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
 C:Accession: F97461
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens 294, 2323-2328, 2001
 A:Reference number: A97359; PMID:11743194
 A:Accession: F97461
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-573 <KUR>
 A:Cross-references: GB:AE007869; PIDN:AAK86647.1; PID:g15155825; GSPDB:GN00169
 C:Genetics:
 A:Gene: AGR_C_1536
 A:Map position: circular chromosome

Query Match 64.6%; Score 31; DB 2; Length 573;
 Best Local Similarity 50.0%; Pred. No. 1.4e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGXSYS 10

Db 474 EQLVPVGKAY 483

Search completed: June 10, 2003, 13:49:16
Job time : 12.2143 secs



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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:25:04 ; Search time 4.5 seconds
(without alignments)
101.387 Million cell updates/sec

Title: US-09-909-164-43
Perfect score: 48
Sequence: 1 EEVVPXGXSYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	36	75.0	1499	1 A10C_HUMAN	O60312 homo sapien
2	35	72.9	1058	1 CARB_FUSNN	Q8r986 fusobacteri
3	34	70.8	102	1 Y11K_TYDVA	P31619 tobacco yel
4	34	70.8	478	1 GSR2_HUMAN	O9pzm5 homo sapien
5	33	68.8	124	1 REV_SIVCZ	P17280 chimpanzee
6	33	68.8	427	1 TOLB_HAEIN	P44677 haemophilus
7	32	66.7	426	1 AROA_VIBCH	Q9krb0 vibrio chol
8	32	66.7	890	1 BCN5_CLOPE	P08696 clostridium
9	32	66.7	2717	1 ZEP1_HUMAN	P15822 homo sapien
10	31	64.6	319	1 YHAI_CRYPA	P10941 cryphonectr
11	31	64.6	361	1 REBB_SALTY	P26391 salmonella
12	31	64.6	507	1 THDI_BURCE	P53607 burkholderi
13	31	64.6	829	1 SYL_LACLA	Q9chb6 lactococcus
14	31	64.6	877	1 SULH_SCHPO	O74377 schizosacch
15	31	64.6	1081	1 SYL_TETTH	P36422 tetrahymena
16	30	62.5	121	1 TKNK_HUMAN	Q9uhf0 homo sapien
17	30	62.5	223	1 PURQ_PYRHO	O59619 pyrococcus
18	30	62.5	224	1 PURQ_HALNI	Q9hnu2 halobacteri
19	30	62.5	224	1 PURQ_MYCLE	O05756 mycobacteri
20	30	62.5	224	1 PURQ_MYCTU	P71841 mycobacteri
21	30	62.5	225	1 PURQ_CORAM	Q9rhx0 corynebacte
22	30	62.5	232	1 SCOA_HELPJ	Q921e3 helicobacte
23	30	62.5	232	1 SCOA_HELPY	P56006 helicobacte
24	30	62.5	234	1 MAG8_HUMAN	P43361 homo sapien
25	30	62.5	315	1 MAG9_HUMAN	P43362 homo sapien
26	30	62.5	404	1 YJ9N_YEAST	P47177 saccharomyc
27	30	62.5	430	1 FOLC_BACSU	Q05865 bacillus su
28	30	62.5	471	1 TMLH_NEUCR	Q96ub1 neurospora
29	30	62.5	509	1 CHLB_MESVI	Q9mur9 mesostigma
30	30	62.5	726	1 PRTP_HSV60	P28931 human herpe
31	30	62.5	993	1 VIA_TAV	P20786 rattus norv
32	30	62.5	1088	1 PGDS_RAT	P20786 rattus norv
33	30	62.5	1401	1 RPOC_VIBCH	Q9kv29 vibrio chol

34	30	62.5	1498	1 Y1A9_CLOAB	Q04351 clostridium
35	30	62.5	3099	1 POLG_PEMVM	O56075 p genome po
36	29	60.4	126	1 YK50_ARCFU	O38229 archaeoglob
37	29	60.4	154	1 PSB4_PIG	Q29384 sus scrofa
38	29	60.4	218	1 PURQ_METHH	O26270 methanobact
39	29	60.4	223	1 PURQ_RHIME	Q92p11 rhizobium m
40	29	60.4	230	1 PURQ_METJA	Q59042 methanococc
41	29	60.4	242	1 PSB4_XENLA	P28024 xenopus lae
42	29	60.4	263	1 MPLA_LOLPR	P14946 lolium pere
43	29	60.4	264	1 PSB4_MOUSE	P28070 homo sapien
44	29	60.4	264	1 PSB4_MOUSE	P99026 mus musculu
45	29	60.4	271	1 POBR_ACICA	Q34992 acinetobact
46	29	60.4	298	1 MIAA_AGR5	P38436 agrobacteri
47	29	60.4	354	1 VGLI_VZVD	P09258 varicella-z
48	29	60.4	400	1 ARRB_CALVI	P51487 calliphora
49	29	60.4	400	1 NUCM_PROWI	Q37619 prototheca
50	29	60.4	421	1 ACDM_HUMAN	P11310 homo sapien
51	29	60.4	421	1 ACDM_PIG	P41367 sus scrofa
52	29	60.4	429	1 GSAB_BACSU	P71084 bacillus su
53	29	60.4	432	1 PURA_YEAST	P80210 saccharomyc
54	29	60.4	455	1 HXK2_SCHPO	P50521 schizosacch
55	29	60.4	529	1 ENP3_HUMAN	O75355 homo sapien
56	29	60.4	670	1 OATP_RAT	P46720 rattus norv
57	29	60.4	691	1 OAT6_MOUSE	Q9y616 homo sapien
58	29	60.4	827	1 PLSB_MOUSE	Q61586 mus musculu
59	29	60.4	828	1 PLSB_RAT	P97564 rattus norv
60	29	60.4	831	1 SYFB_MYCTU	P94985 mycobacteri
61	29	60.4	1097	1 RNT1_FUGRU	Q98tr3 fuqu rubrip
62	29	60.4	1113	1 RNT1_MOUSE	Q98pu0 mus musculu
63	29	60.4	1129	1 RNT1_HUMAN	Q92900 homo sapien
64	29	60.4	1377	1 RHSA_ECOLI	P16916 escherichia
65	29	60.4	1397	1 RHSC_ECOLI	P16918 escherichia
66	29	60.4	1411	1 RHSE_ECOLI	P15917 escherichia
67	29	60.4	3828	1 TRX_DROVI	Q24742 drosophila
68	28	58.3	119	1 YHHM_ECOLI	P37615 escherichia
69	28	58.3	207	1 ENO_CAMPE	O30885 campylobact
70	28	58.3	223	1 PURQ_PYRAB	Q9uxw5 pyrococcus
71	28	58.3	224	1 PURQ_ANASP	Q8yu79 anabaena sp
72	28	58.3	255	1 PRDC_HELPJ	Q92mn9 helicobacte
73	28	58.3	255	1 PRDC_HELPY	O09912 helicobacte
74	28	58.3	279	1 ATND_RAT	Q63377 rattus norv
75	28	58.3	286	1 3HAO_RAT	P46953 rattus norv

ALIGNMENTS

RESULT 1
A10C_HUMAN STANDARD; PRT; 1499 AA.
ID A10C_HUMAN Q96914; PRT; 1499 AA.
AC O60312; Q96914;
DT 30-MAY-2000 (Rel. 39, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Potential phospholipid-transferring ATPase VC (EC 3.6.3.1) (ATPVC)
DE (Aminophospholipid translocase VC).
GN ATP10C OR ATPVC OR KIAA0566.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2125279; PubMed=11326269;
RA Oshimura M.;
RA P47177 saccharomyc
RT "A novel maternally expressed gene, ATP10C, encodes a putative
RL aminophospholipid translocase associated with Angelman syndrome.";
RN [2]
RP Nat. Genet. 28:19-20(2001).
RX SEQUENCE FROM N.A.
RX MEDLINE=21313119; PubMed=11353404;
RA Herzling L.B.K., Kim S.-J., Cook E.H. Jr., Ledbetter D.H.;

"The human aminophospholipid-transporting ATPase gene ATP10C maps adjacent to UBE3A and exhibits similar imprinted expression.";
An. J. Hum. Genet. 68:1501-1505(2001).

[3]

SEQUENCE OF 337-1499 FROM N.A.

TISSUE=Brain;

MEDLINE=98290545; PubMed=9628581;

Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,

Nomura N., Ohara O.;

"Prediction of the coding sequences of unidentified human genes. IX.

The complete sequences of 100 new cDNA clones from brain which can

code for large proteins in vitro.";

DNA Res. 5:31-39(1998).

-1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.

-1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

-1- TISSUE SPECIFICITY: Wide expression, with highest levels in

kidney, followed by lung, brain, prostate, testis, ovary, and

small intestine.

-1- DISEASE: Defects in ATP10C may be a cause of Angelman syndrome

(AS), also known as 'happy puppet syndrome'.

-1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2

ATPASES). SUBFAMILY IV.

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EMBL; AB051358; BAB47392.1; .

EMBL; AY029504; AAK33100.1; JOINED.

EMBL; AY029487; AAK33100.1; JOINED.

EMBL; AY029488; AAK33100.1; JOINED.

EMBL; AY029489; AAK33100.1; JOINED.

EMBL; AY029490; AAK33100.1; JOINED.

EMBL; AY029491; AAK33100.1; JOINED.

EMBL; AY029492; AAK33100.1; JOINED.

EMBL; AY029493; AAK33100.1; JOINED.

EMBL; AY029494; AAK33100.1; JOINED.

EMBL; AY029495; AAK33100.1; JOINED.

EMBL; AY029496; AAK33100.1; JOINED.

EMBL; AY029497; AAK33100.1; JOINED.

EMBL; AY029498; AAK33100.1; JOINED.

EMBL; AY029499; AAK33100.1; JOINED.

EMBL; AY029500; AAK33100.1; JOINED.

EMBL; AY029501; AAK33100.1; JOINED.

EMBL; AY029502; AAK33100.1; JOINED.

EMBL; AY029503; AAK33100.1; JOINED.

EMBL; AB011138; BAA25492.1; .

Genew; HGNC:13547; ATP10C.

MIM; 605855; .

MIM; 105830; .

InterPro: IPR001757; ATPase_E1-E2.

InterPro: IPR001454; Hlgase/hydriase.

Pfam: PF00702; Hydrolase; 1.

PRINTS; PR00119; CATATPASE.

PROSITE; PS00154; ATPASE_E1_E2; 1.

Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;

Multigene family.

DOMAIN 1 86

TRANSMEM 87 106

DOMAIN 107 110

TRANSMEM 111 128

DOMAIN 129 309

TRANSMEM 310 332

DOMAIN 337 362

TRANSMEM 363 384

DOMAIN 385 1087

TRANSMEM 1088 1108

DOMAIN 1109 1119

TRANSMEM 1120 1140

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EMBL; AE010554; AAL94625.1; ALT_INIT.

InterPro: IPR005483; CPhase_L.

InterPro: IPR005479; CPhase_L_D2.

InterPro: IPR005480; CPhase_L_D3.

FT DOMAIN 1141 1170
FT TRANSMEM 1171 1192
FT DOMAIN 1193 1199
FT TRANSMEM 1200 1222
FT DOMAIN 1223 1228
FT TRANSMEM 1229 1249
FT DOMAIN 1250 1267
FT TRANSMEM 1268 1292
FT DOMAIN 1293 1499
FT MOD_RES 427 427
FT METAL 1031 1031
FT METAL 1035 1035
FT METAL 467 470
FT CONFLICT 388 388
SQ SEQUENCE 1499 AA; 167687 MW; D4996A4D0635A68D CRC64;
Query Match 75.0%; Score 36; DB 1; Length 1499;
Best Local Similarity 72.7%; Pred. NO. 12;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEWVPXGXSYS 11

Db 469 EEWVPGGSVS 479

RESULT 2

CARB_FUSNN

ID CARB_FUSNN STANDARD; PRT; 1058 AA.

AC QRG86;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-

GN CARB OR FN0422.

OS Fusobacterium nucleatum (subsp. nucleatum).

OC Bacteria; Fusobacteria; Fusobacterium.

OX NCBI_TaxID=76856;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21886394; PubMed=11899109;

RA Kaputthal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,

RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,

RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,

RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,

RA Fonstein M., Kyripides N., Overbeek R.;

RT "Genome sequence and analysis of the oral bacterium Fusobacterium

RL J. Bacteriol. 184:2005-2018(2002).

CC -1- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +

CC phosphate + L-glutamate + carbamoyl phosphate.

CC -1- COFACTOR: Binds three manganese ions (By similarity).

CC -1- PATHWAY: Arginine biosynthesis.

CC -1- PATHWAY: Pyrimidine biosynthesis; first step.

CC -1- SUBUNIT: Composed of two chains; the small (or glutamine) chain

CC promotes the hydrolysis of glutamine to ammonia, which is used by

CC the large (or ammonia) chain to synthesize carbamoyl phosphate (By

CC similarity).

CC -1- SIMILARITY: BELONGS TO THE CARB FAMILY.

DR InterPro: IPR005481; CPase_L.N.
 DR InterPro: IPR004362; MGS_Like.
 DR Pfam: PF00289; CPase_L_Chain; 2.
 DR Pfam: PF02786; CPase_L_D2; 2.
 DR Pfam: PF02787; CPase_L_D3; 1.
 DR Pfam: PF02142; MGS; 1.
 DR PRINTS: PR00098; CPASE.
 DR PROSITE: PS00866; CPASE.1; 2.
 DR PROSITE: PS00867; CPASE.2; 2.
 KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
 KW ATP-binding; Manganese; Complete proteome.
 FT DOMAIN 1 401 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
 FT DOMAIN 402 546 OLIGOMERIZATION DOMAIN.
 FT DOMAIN 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
 FT DOMAIN 930 1058 ALLOSTERIC DOMAIN.
 FT REPEAT 1 546
 FT REPEAT 547 1058
 FT NP_BIND 153 210 ATP (POTENTIAL).
 FT NP_BIND 302 352 ATP (POTENTIAL).
 FT METAL 284 284 MANGANESE 1 (BY SIMILARITY).
 FT METAL 298 298 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 300 300 MANGANESE 2 (BY SIMILARITY).
 FT METAL 820 820 MANGANESE 3 (BY SIMILARITY).
 FT METAL 832 832 MANGANESE 3 (BY SIMILARITY).
 SQ SEQUENCE 1058 AA; 117451 MW; ED7037AF77C1E39F CRC64;
 Query Match 72.98; Score 35; DB 1; Length 1058;
 Best Local Similarity 60.08; Pred. No. 14;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 EVVPXGXSYS 11
 Db 190 EIVPGLNYS 199
 RESULT 3
 YLIK_TYDVA STANDARD; PRT; 102 AA.
 AC P31619;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE Hypothetical 11.2 kDa protein.
 GN VI.
 OS Tobacco yellow dwarf virus (strain Australia) (TYDV).
 OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
 OX NCBI_TaxID=31599;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92188538; PubMed=1546458;
 RA Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
 RT "The nucleotide sequence of the infectious cloned DNA component of
 tobacco yellow dwarf virus reveals features of geminiviruses
 infecting monocotyledonous plants.";
 RL Virology 187:633-642(1992).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; M81103; AAA47947.1; -
 DR PIR; A42452; A42452.
 DR InterPro: IPR002621; Gemini_mov.
 DR Pfam: PF01708; Gemini_mov; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 102 AA; 11178 MW; A40CEFE0AF5B67 CRC64;
 Query Match 70.8%; Score 34; DB 1; Length 102;
 Best Local Similarity 60.0%; Pred. No. 2.1;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 EVVPXGXSYS 11
 Db 7 QVVPGSINYS 16
 RESULT 4
 GSR2_HUMAN STANDARD; PRT; 478 AA.
 ID GSR2_HUMAN Q9NZM5; Q9NPPI; Q9NPRI2; Q9BTC6; Q9HAX6;
 AC Q9NZM5; Q9NPPI; Q9NPRI2; Q9BTC6; Q9HAX6;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Glioma tumor suppressor candidate region gene 2 protein (p60).
 GN GLTSCR2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. AND TISSUE SPECIFICITY.
 RX MEDLINE=20175430; PubMed=10708517;
 RA Smith J.S., Tachibana I., Pohl U., Lee H.K., Thanarajasingam U.,
 RA Portier B.P., Geki K., Billings S., Ramasamy S., Mohrenweiser H.W.,
 RA Scheithauer B.W., Louis D.N., Jenkins R.B.;
 RT "A transcript map of the chromosome 19q-Arm glioma tumor suppressor
 region.";
 RL Genomics 64:44-50(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Muscle;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 9-478 FROM N.A., AND SUBCELLULAR LOCATION.
 RX MEDLINE=99214318; PubMed=10196275;
 RA Bruni R., Fineschi B., Ogle W.O., Roizman B.;
 RT "A novel cellular protein, p60, interacting with both herpes simplex
 virus 1 regulatory proteins ICP22 and ICP0 is modified in a
 cell-type-specific manner and is recruited to the nucleus after
 infection.";
 RL J. Virol. 73:3810-3817(1999).
 RN [4]
 RP SEQUENCE OF 12-478 FROM N.A.
 RA Andreu N., Estivill X., Escarceller M., Sumoy L.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 218-477 FROM N.A.
 RC TISSUE=Testis;
 RA Poustka A., Klein M., Mewes H.-W., Gassenhuber J., Wiemann S.;
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 CC -|- SUBUNIT: Interacts with HSV-1 early proteins ICP22 and ICP0.
 CC -|- SUBCELLULAR LOCATION: Nuclear.
 CC -|- TISSUE SPECIFICITY: Expressed at high levels in heart and
 CC pancreas, moderate levels in placenta, liver, skeletal muscle, and
 CC kidney, and low levels in brain and lung.
 CC -|- SIMILARITY: BELONGS TO THE GLTSCR2 FAMILY.
 CC -----
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 CC -----
 DR EMBL; AF182076; AAF62873.1; -
 DR EMBL; BC004229; AAH04229.1; -
 DR EMBL; BC006311; AAH06311.1; -
 DR EMBL; BC010095; AAH10095.1; -
 DR EMBL; AF296124; AAG30413.1; -
 DR EMBL; AL359335; CAB94786.1; -

DR EMBL; AL359336; CAB94787.1; -;
DR EMBL; AL22063; CAB9242.1; -;
DR SWISS-2DPAGE; Q9NZM5; HUMAN.
DR Genew; HGNC:4333; GLTSCR2.
DR MIM; 605691; -;
KW Nuclear protein; Polymorphism.
FT VARIANT 389 389 R -> Q.
FT /FTID=VAR_011486.
FT GGS -> HEG (IN REF. 2; AAH04229).
FT G -> R (IN REF. 3).
FT RRKEQLWEKLAKQGLPREVRAAQLNPSTRAPKPGPOD
FT TVERP -> SCRSSYGRSWPSRASSPGGAQGPSVPAQPCN
FT KGNPAPGHRIAA (IN REF. 3).
FT SDNPLDRPLVGODEFFLE -> LNNPDKPVVWPGCLFPG
FT (IN REF. 3).
FT A -> S (IN REF. 2; AAH04229).
FT D -> H (IN REF. 3).
FT PEGNLLDRFKSFQRNMIEPRERAKFKRYKVLVEKRAF
FT REIQ -> VLVVSCRGAPCPVMTPLPVPVPRGYGRHHGCP
FT WAGPVGPMRPG (IN REF. 5).
FT EGNLLDRFKSFQRNMIEPRERAKFKRYKVLVEKRAF
FT EIQQL -> RGQHSFETGSAFRGGI (IN REF. 3).
FT SEQUENCE 478 AA; 54417 MW; 7F18923E348CB52B CRC64;
Query Match 70.8%; Score 34; DB 1; Length 478;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 EVVPXGXSYS 11
Db 239 EVAPAGASYN 248
II I I I I;
RESULT 5
ID REV_SIVCZ STANDARD; PRT; 124 AA.
AC PI7280;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE REV protein (Anti-repression transactivator protein) (ART/TRS).
GN REV.
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP MEDLINE=90259077; PubMed=2188136;
RX Huet T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
RA "Genetic organization of a chimpanzee lentivirus related to HIV-1.";
RL Nature 345:356-359(1990).
CC -1- FUNCTION: REV APPEARS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE
CC NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.
CC -1- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.
CC -1- PTM: PHOSPHOPROTEIN WHOSE STATE OF PHOSPHORYLATION IS MEDIATED
CC BY A SPECIFIC SERINE KINASE ACTIVITY PRESENT IN THE NUCLEUS.
CC -----
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CC -----
DR EMBL; X52154; CAA36405.1; -;
DR PIR; S09988; VKLJSI.
DR HIV; X52154; REVSCPZ.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
KW Transcription regulation; AIDS; Phosphorylation; Nuclear protein.
SQ SEQUENCE 124 AA; 13701 MW; F5877D1BDF65A7B2 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 124;
Best Local Similarity 60.0%; Pred. No. 4.2;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVPXGXSYS 11
Db 107 ETVPAGGNY 116
II I I I I;
RESULT 6

TOLB_HAEIN STANDARD; PRT; 427 AA.
ID TOLB_HAEIN
AC P44677; P94811;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE TOLB protein precursor.
GN TOLB OR HI0382.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OX Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-T., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
RD.";
RL Science 269:496-512(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1479;
RX MEDLINE=97080550; PubMed=8921895;
RA Sen K., Sikkema D.J., Murphy T.F.;
RA "Isolation and characterization of the Haemophilus influenzae tolQ,
RA tolR, tolA and tolB genes.";
RL Gene 178:75-81(1996).
CC -1- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Periplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE TOLB FAMILY.
CC -----
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CC -----
DR EMBL; U32722; AAC22040.1; -;
DR EMBL; U32470; AAC44597.1; -;
DR HSP; P19935; ICRZ.
DR TIGR; HI0382; -;
KW Transport; Protein transport; Periplasmic; Signal; Complete proteome.
RN SIGNAL 1 23
FT CHAIN 24 427 TOLB PROTEIN
FT VARIANT 6 6 R -> H (IN STRAIN 1479).
FT VARIANT 14 14 V -> I (IN STRAIN 1479).
FT VARIANT 17 19 VGS -> ITH (IN STRAIN 1479).
FT VARIANT 21 21 A -> V (IN STRAIN 1479).
FT VARIANT 79 79 R -> H (IN STRAIN 1479).
FT VARIANT 129 129 T -> A (IN STRAIN 1479).
FT VARIANT 160 160 A -> G (IN STRAIN 1479).

FT VARIANT 237 237 A -> T (IN STRAIN 1479).
 FT VARIANT 322 322 S -> N (IN STRAIN 1479).
 FT VARIANT 326 326 A -> V (IN STRAIN 1479).
 FT VARIANT 328 328 A -> S (IN STRAIN 1479).
 SQ SEQUENCE 427 AA; 44967 MW; 0882201AEE9254B9 CRC64;

Query Match 68.8%; Score 33; DB 1; Length 427;
 Best Local Similarity 60.0%; Pred. No. 15;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVPXGXSYS 11
 DB 103 QVVPNGSGYS 112

RESULT 7

AROA_VIBCH STANDARD; PRT; 426 AA.
 ID AROA_VIBCH
 AC O9KR80;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-phosphorylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPS).
 DE enolpyruvylshikimate-3-phosphate synthase (EPSP synthase) (EPSPS).
 GN AROA OR VC1732.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EI Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
 RA "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae";
 RT Nature 406:477-483(2000).
 RL
 CC -|- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate = phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
 CC -|- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway; sixth step.
 CC -|- SUBUNIT: Monomer (By similarity).
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -|- SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY.
 CC
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 CC
 DR EMBL; AE004251; AAF94882.1; -;
 DR TIGR; VC1732; -;
 DR InterPro; IPR001986; EPSP_synthase.
 DR Pfam; PF00275; EPSP_synthase; 1.
 DR ProDom; PD001867; EPSP_synthase; 1.
 DR PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
 DR PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
 KW Aromatic amino acid biosynthesis; Transferrase; Complete proteome.
 SQ SEQUENCE 426 AA; 46101 MW; 38852D6483BFE1C3 CRC64;

Query Match 66.7%; Score 32; DB 1; Length 426;
 Best Local Similarity 60.0%; Pred. No. 24;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 10

Db 223 EEVIPAGQSY 232
 | | | | | | | | | |

RESULT 8
 BCN5_CLOPE
 ID BCN5_CLOPE STANDARD; PRT; 890 AA.
 AC P08696;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Bacteriocin BCN5.
 GN BCN.
 OS Clostridium perfringens.
 OG Plasmid pIP404.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1502;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CPN50;
 RX MEDLINE=88336297; PubMed=2901768;
 RA Garnier T., Cole S.T.;
 RT "Complete nucleotide sequence and genetic organization of the bacteriocinogenic plasmid, pIP404, from Clostridium perfringens.";
 RL Plasmid 19:134-150(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CPN50;
 RX MEDLINE=87057020; PubMed=2877971;
 RA Garnier T., Cole S.T.;
 RT "Characterization of a bacteriocinogenic plasmid from Clostridium perfringens and molecular genetic analysis of the bacteriocin-encoding gene";
 RL J. Bacteriol. 168:1189-1196(1986).
 RN [3]
 RP SEQUENCE OF 1-14 FROM N.A.
 RC STRAIN=CPN50;
 RX MEDLINE=89039249; PubMed=2460717;
 RA Garnier T., Cole S.T.;
 RT "Studies of UV-inducible promoters from Clostridium perfringens in vivo and in vitro";
 RL Mol. Microbiol. 2:607-614(1988).
 CC -|- FUNCTION: MAY FUNCTION AS AN IONOPHORE.
 CC -|- INDUCTION: BY UV IRRADIATION.

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 CC
 DR EMBL; M14481; AAA98248.1; -;
 DR EMBL; M32882; AAA98249.1; -;
 DR PIR; A30481; A30481.
 DR InterPro; IPR003646; SH3_bac.
 DR SMART; SM00287; SH3b; 3.
 DR Antitoxic; Bacteriocin; Plasmid.
 FT DOMAIN 815 869 HYDROPHOBIC.
 SQ SEQUENCE 890 AA; 96699 MW; F4E5E8971C31C6C6 CRC64;

Query Match 66.7%; Score 32; DB 1; Length 890;
 Best Local Similarity 66.7%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGXSYS 10

Db 170 EVVPGGFTY 178
 | | | | | | | | | |

RESULT 9

KW Hypothetical protein; Hydrolase; Thiol protease.
SQ SEQUENCE 319 AA; 35443 MW; A1F5F75F9ACE7A CRC64;

Query Match 64.6%; Score 31; DB 1; Length 319;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
| | | | |
Db 31 EEVVPAG 37

RESULT 11

ID RFBB_SALTY STANDARD; PRT; 361 AA.
AC P26391;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE dTDP-glucose 4,6-dehydratase (EC 4.2.1.46).
GN RFBB OR STM2097
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=91260454; PubMed=1710759;
RA Jiang X.-M., Neal B., Santiago F., Lee S.J., Romana L.K., Reeves P.R.;
RT "Structure and sequence of the rfb (O antigen) gene cluster of
RT Salmonella serovar typhimurium (strain LT2).";
RL Mol. Microbiol. 5:695-713(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
RL Nature 413:852-856(2001).
RP CATALYTIC ACTIVITY: dTDP-glucose -> dTDP-4-dehydro-6-deoxy-D-
glucose + H(2)O.
CC -1- COFACTOR: NAD.
CC -1- PATHWAY: dTDP-L-RHAMNOSE BIOSYNTHESIS WITHIN THE O ANTIGEN
BIOSYNTHESIS PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE SUGAR EPIMERASE FAMILY. DTDP-GLUCOSE
DEHYDRATASE SUBFAMILY.

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CC -----

EMBL; X56793; CAA40115.1; -.
DR EMBL; AE008792; AAL21001.1; -.
DR PIR; S15299; S15299.
DR HSP; P27830; 18X.
DR StyGene; SG10345; rfbB.
DR InterPro; IPR001509; Epimerase.Dh.
DR Pfam; PF01370; Epimerase; 1.
DR TIGRFAMs; TIGR01181; dTDP-gluc.dehyt. 1.
KW Lipopolysaccharide biosynthesis; Lyase; NAD; Complete proteome.
FT NP_BIND 7 13 NAD (POTENTIAL).
SQ SEQUENCE 361 AA; 40718 MW; 3A574B4D917EBC57 CRC64;

Query Match 64.6%; Score 31; DB 1; Length 361;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXS 10
: | : | | |
Db 278 DEIVPKATSY 287

RESULT 12

THDL_BURCE STANDARD; PRT; 507 AA.
AC P53607;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Threonine dehydratase biosynthetic (EC 4.2.1.16) (Threonine
DE deaminase).
GN ILVA.
OS Burkholderia cepacia (Pseudomonas cepacia).
OC Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
OC Burkholderia.
OX NCBI_TaxID=292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17616;
RA Bartell J.B., Lessie T.G.;
RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from
CC threonine in a two-step reaction. The first step is a dehydration
CC of threonine, followed by rehydration and liberation of ammonia.
CC -1- CATALYTIC ACTIVITY: L-threonine + H(2)O -> 2-oxobutanoate + NH(3) +
H(2)O.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE.
CC -1- PATHWAY: Isoleucine biosynthesis; first step.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
CC -----
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CC -----

EMBL; U40630; AAA83215.1; -.
DR HSP; P04968; ITDJ.
DR InterPro; IPR001926; B6_enzyme_beta.
DR InterPro; IPR000634; S/T_dehydrtase.
DR InterPro; IPR001721; ThrDh_C.
DR Pfam; PF00291; PALP; 1.
DR Pfam; PF00585; Thr_dehydrat_C; 2.
DR TIGRFAMs; TIGR01124; liva_2cterm; 1.
DR PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
KW Isoleucine biosynthesis; Lyase; Pyridoxal phosphate.
FT BINDING 52 PYRIDOXAL PHOSPHATE.
SQ SEQUENCE 507 AA; 55326 MW; E9A5D110B0597664 CRC64;

Query Match 64.6%; Score 31; DB 1; Length 507;
Best Local Similarity 60.0%; Pred. No. 48;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVVPXGXSYS 11
| | : | | | |
Db 120 EVIQAGESYS 129

RESULT 13

SYL_LACLA STANDARD; PRT; 829 AA.
ID SYL_LACLA
AC Q9CHB6;
DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS).
 GN LEUS OR LL0816.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL1403;
 RX MEDLINE=21235186; PubMed=11337471;
 RA Bolotin A., Wincker P., Mauer S., Jaillon O., Malarne K.,
 RA Weisenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 RT lactis ssp. lactis IL1403."
 RL Genome Res. 11:731-753(2001).
 CC -1- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(Leu) = AMP +
 CC diphosphate + L-leucyl-tRNA(Leu).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; AEO06315; AAK04914.1; -;
 DR InterPro: IPR002302; Leu-TRNA-syntla.
 DR InterPro: IPR002300; tRNA-synt_1a.
 DR InterPro: IPR001412; tRNA-synt_1.
 DR Pfam; PF00133; tRNA-synt_1; 1.
 DR PRINTS; PR00985; TRNASYNTHLEU.
 DR TIGRFAMS; TIGR00396; leuS.bact; 1.
 DR PROSITE; PS00178; AA-TRNA-LIGASE_I; 1.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 40 51 "HIGH" REGION.
 FT SITE 609 613 "KMSKS" REGION.
 FT BINDING 612 612 ATP (BY SIMILARITY).
 SQ SEQUENCE 829 AA; 93791 MW; F0F0A43014FC6389 CRC64;
 Query Match 64.6%; Score 31; DB 1; Length 829;
 Best Local Similarity 66.7%; Pred. No. 80;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGXS 9
 Db |||||
 168 EEVLDPGTS 176
 RESULT 14
 ID SULH_SCHPO STANDARD; PRT; 877 AA.
 AC 074377;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Probable sulfate permease C3H7.02.
 GN SPBC3H7.02.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Weijens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs N., Fritzc C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas R.R., Rochet M., Gallard C., Tallada V.A., Garzon A., Rhode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Usery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe."
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS.
 CC -1- SIMILARITY: CONTAINS 1 STAS DOMAIN.
 CC -----
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 CC -----
 DR EMBL; AL031261; CAA20298.1; -;
 DR InterPro: IPR002645; STAS.
 DR InterPro: IPR001902; Sulfate_transp.
 DR Pfam; PF00916; Sulfate_transp; 1.
 DR Pfam; PF01740; STAS; 1.
 DR TIGRFAMS; TIGR00815; sulp; 1.
 DR PROSITE; PS01130; SLC26A; 1.
 DR PROSITE; PS0801; STAS; 1.
 KW Transport; Transmembrane.
 FT TRANSMEM 133 153 POTENTIAL.
 FT TRANSMEM 161 181 POTENTIAL.
 FT TRANSMEM 186 206 POTENTIAL.
 FT TRANSMEM 221 241 POTENTIAL.
 FT TRANSMEM 243 263 POTENTIAL.
 FT TRANSMEM 292 312 POTENTIAL.
 FT TRANSMEM 329 349 POTENTIAL.
 FT TRANSMEM 384 404 POTENTIAL.
 FT TRANSMEM 424 444 POTENTIAL.
 FT TRANSMEM 461 481 POTENTIAL.
 FT TRANSMEM 484 504 POTENTIAL.
 FT TRANSMEM 518 538 POTENTIAL.
 FT TRANSMEM 543 563 POTENTIAL.
 FT DOMAIN 594 747 STAS.
 SQ SEQUENCE 877 AA; 96373 MW; 56995A8493371E43 CRC64;
 Query Match 64.6%; Score 31; DB 1; Length 877;
 Best Local Similarity 66.7%; Pred. No. 84;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 VVPXGXSYS 11
 Db |||||
 148 VVPGGMSYA 156
 RESULT 15

SYL_TETH
ID SYL_TETH STANDARD; PRT; 1081 AA.
AC P36422;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Isoleucyl-tRNA synthetase (EC 6.1.1.5) (Isoleucine--tRNA ligase)
DE (ilers).
GN ILSA OR CUPC.
OS Tetrahymena thermophila.
OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymena; Tetrahymena.
OX NCBI_TaxID=5911;
RN [1]
RP MEDLINE=92165815; PubMed=1371507;
RX Csank C., Martindale D.W.;
RT "Isoleucyl-tRNA synthetase from the ciliated protozoan Tetrahymena
thermophila. DNA sequence, gene regulation, and leucine zipper
motifs."
RL J. Biol. Chem. 267:4592-4599(1992).
CC -!- CATALYTIC ACTIVITY: ATP + L-isoleucine + tRNA(Ile) -> AMP +
diphosphate + L-isoleucyl-tRNA(Ile).
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC
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CC
CC EMBL; M30942; AAA30122.1; -
CC PIR; A42399; A42399.
CC HSPP; P56690; LILE.
CC InterPro; IPR002300; tRNA-synt_1a.
CC InterPro; IPR001412; tRNA-synt_1.
CC InterPro; IPR002301; tRNA-synt_1le.
CC Pfam; PF00133; tRNA-synt_1; 1.
CC PRINTS; PR00984; TRNASYNTHILE.
CC TIGRFAMs; TIGR00392; ileS; 1.
CC PROSITE; PS00178; AA.TRNA.LIGASE.I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SITE 53 63 "HIGH" REGION.
FT SITE 607 611 "KMSKS" REGION.
FT BINDING 610 610 ATP (BY SIMILARITY).
FT BINDING 1081 AA; 124850 MW; D4D72616AFB8C795 CRC64;
SQ SEQUENCE 1081 AA; 124850 MW; 124850 MW; 124850 MW; 124850 MW; 124850 MW;
Query Match 64.6%; Score 31; DB 1; Length 1081;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 EWPVPGXSY 10
Db :||| ||
796 KVPKGSY 804
RESULT 16
TKNK_HUMAN
ID TKNK_HUMAN STANDARD; PRT; 121 AA.
AC Q9UHF0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurokinin B precursor (NKB) (Neuromedin K) {ZNEUROK1}.
GN TAC3.
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Sheppard P., Jelinek L., Whitmore T., Blumberg H., Lehner J.,
O'Hara P.;
RN Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20322570; PubMed=1086201;
RA Page N.M., Woods R.J., Gardiner S.M., Lomthasong K., Gladwell R.T.,
Butlin D.J., Manyonda I.T., Lowry P.J.;
RT "Excessive placental neurokinin B secretion during the third trimester
causes pre-eclampsia."
RL Nature 405:797-800(2000).
CC -!- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
MUSCLES (BY similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DEVELOPMENTAL STAGE: In pregnancy, the expression of NKB is
confined to the outer syncytiotrophoblast of the placenta,
significant concentrations of NKB can be detected in plasma as
early as week 9, and plasma concentrations of NKB are grossly
elevated in pregnancy-induced hypertension and pre-eclampsia.
CC -!- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC
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CC
CC EMBL; AF186112; AAF01430.1; -
CC EMBL; AF216586; AAF76980.1; -
CC Genew; HGNC:11521; TAC3.
CC MIM; 162330; -
CC InterPro; IPR003635; Neurokinin.
CC InterPro; IPR002040; Tachykinin.
CC ProDom; PD020370; Neurokinin; 1.
CC PROSITE; PS00267; TACHYKININ; 1.
KW Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
KW Amidation; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT PROPEP 17 78 BY SIMILARITY.
FT PEPTIDE 81 90 NEUROKININ B.
FT PROPEP 94 121 BY SIMILARITY.
FT MOD_RES 90 90 AMIDATION (G-91 PROVIDE AMIDE GROUP) (BY
SIMILARITY).
SQ SEQUENCE 121 AA; 13438 MW; 14C9AFE2EE9EDEC64;
Query Match 62.5%; Score 30; DB 1; Length 121;
Best Local Similarity 85.7%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EEVVPXG 7
Db :||| |
28 EEVVPXG 34
RESULT 17
PURQ_PVRHO
ID PURQ_PVRHO STANDARD; PRT; 223 AA.
AC O59619;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphoribosylformylglycinamide synthase I (EC 6.3.5.3) (FCAM
synthase I)
GN PURQ OR PH1955.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;

RN
 RP SEQUENCE FROM N.A.
 RC STRAIN-OT3;
 RX MEDLINE-98344137; PubMed=9679194;
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).
 CC -1- CATALYTIC ACTIVITY: ATP + N(2)-formyl-N(1)-(5-phospho-D-
 ribosyl)glycinamide + L-glutamine + H(2)O = ADP + phosphate + 2-
 (formamido)-N(1)-(5-phospho-D-ribosyl)acetamidine + L-glutamate.
 CC -1- PATHWAY: De novo purine biosynthesis; fourth step.
 CC -1- SUBUNIT: HETERODIMER OF TWO SUBUNITS, PURQ AND PURL.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
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 CC
 DR EMBL: AP000007; BAA31082.1; ALT_INIT.
 DR InterPro: IPR000991; GATase_1.
 DR ProSite: PS002818; ThiJ.
 DR Pfam: PF01965; ThiJ; 1.
 DR ProSite: PS00442; GATASE_TYPE_I; 1.
 KW Purine biosynthesis; Ligase; Glutamine amidotransferase;
 KW Complete proteome.
 FT ACT_SITE 85 85 GATASE (BY SIMILARITY).
 SQ SEQUENCE 223 AA; 24933 MW; 9F685E2E39A92817 CRC64;
 Query Match 62.5%; Score 30; DB 1; Length 223;
 Best Local Similarity 55.6%; Pred. No. 34;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 3 VVPXGXSYS 11
 DB ||| |||
 45 VVPXGXSYS 53
 RESULT 18
 ID PURQ_HALN1 STANDARD; PRT; 224 AA.
 AC Q9HNU2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phosphoribosylformylglycinamide synthase I (EC 6.3.5.3) (FGM
 synthase I).
 DE PURQ OR VNG1945G.
 GN Halobacterium sp. (strain NRC-1).
 OS Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
 RA Leitkauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudis J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.;
 RT "Massive gene decay in the leprosy bacillus.";
 RL Nature 409:1007-1011(2001).
 CC -1- CATALYTIC ACTIVITY: ATP + N(2)-formyl-N(1)-(5-phospho-D-
 ribosyl)glycinamide + L-glutamine + H(2)O = ADP + phosphate + 2-
 (formamido)-N(1)-(5-phospho-D-ribosyl)acetamidine + L-glutamate.
 CC -1- PATHWAY: De novo purine biosynthesis; fourth step.
 CC -1- SUBUNIT: HETERODIMER OF TWO SUBUNITS, PURQ AND PURL.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
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RT
 RL "Genome sequence of Halobacterium species NRC-1.";
 Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 CC -1- CATALYTIC ACTIVITY: ATP + N(2)-formyl-N(1)-(5-phospho-D-
 ribosyl)glycinamide + L-glutamine + H(2)O = ADP + phosphate + 2-
 (formamido)-N(1)-(5-phospho-D-ribosyl)acetamidine + L-glutamate.
 CC -1- PATHWAY: De novo purine biosynthesis; fourth step.
 CC -1- SUBUNIT: HETERODIMER OF TWO SUBUNITS, PURQ AND PURL.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
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 CC
 DR EMBL: AE005091; AAG20128.1; -.
 DR InterPro: IPR000991; GATase_1.
 DR ProSite: PS00442; GATASE_TYPE_I; FALSE NEG.
 KW Purine biosynthesis; Ligase; Glutamine amidotransferase;
 KW Complete proteome.
 FT ACT_SITE 85 85 GATASE (BY SIMILARITY).
 SQ SEQUENCE 224 AA; 22979 MW; E13165BD3136330A CRC64;
 Query Match 62.5%; Score 30; DB 1; Length 224;
 Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 VVPXGXSYS 10
 DB ||| |||
 45 VVPXGXSYS 52
 RESULT 19
 ID PURQ_MYCLE STANDARD; PRT; 224 AA.
 AC O05756;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phosphoribosylformylglycinamide synthase I (EC 6.3.5.3) (FGM
 synthase I).
 DE PURQ OR ML2219.
 GN Mycobacterium leprae.
 OS Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1769;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-TN;
 RX MEDLINE-21128732; PubMed=11234002;
 RA Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R.,
 RA Wheelwright P.R., Honore N., Garnier T., Churcher C., Harris D.,
 RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,
 RA Holroyd S., Hornsby T., Jagers K., Lacroix C., Maclean J., Moule S.,
 RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
 RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
 RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
 RA Barrell B.G.;
 RT "Massive gene decay in the leprosy bacillus.";
 RL Nature 409:1007-1011(2001).
 CC -1- CATALYTIC ACTIVITY: ATP + N(2)-formyl-N(1)-(5-phospho-D-
 ribosyl)glycinamide + L-glutamine + H(2)O = ADP + phosphate + 2-
 (formamido)-N(1)-(5-phospho-D-ribosyl)acetamidine + L-glutamate.
 CC -1- PATHWAY: De novo purine biosynthesis; fourth step.
 CC -1- SUBUNIT: HETERODIMER OF TWO SUBUNITS, PURQ AND PURL.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
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DR EMBL; Z95151; CAB08429.1; -;
 DR EMBL; AL583924; CAC31174.1; -;
 DR Leprosoma; ML2219; -;
 DR InterPro; IPR000991; GATase_1.
 DR InterPro; IPR002818; ThiJ.
 DR Pfam; PF01965; ThiJ; 1.
 DR PROSITE; PS00442; GATASE_TYPE_I; 1.
 KW Purine biosynthesis; Ligase; Glutamine amidotransferase;
 KW Complete proteome.
 FT ACT_SITE 87 87 GATASE (BY SIMILARITY).
 SQ SEQUENCE 224 AA; 23818 MW; 717DED17A856E4A6 CRC64;

Query Match 62.5%; Score 30; DB 1; Length 224;
 Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXSX 10
 ||| | |
 Db 47 VVPGGFSY 54

RESULT 20
 PURQ_MYCTU STANDARD; PRT; 224 AA.
 AC P71841;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phosphoribosylformylglycinamide synthase I (EC 6.3.5.3) (FGAM
 DE synthase I).
 GN PURQ OR RV0788 OR MT0813 OR MTCY369.32.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1773;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-H37Rv;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekai F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RL Nature 393:537-544(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CDC 1551 / Oshkosh;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + N(2)-formyl-N(1)-(5-phospho-D-
 CC ribosyl)glycinamide + L-glutamine + H(2)O = ADP + phosphate + 2-
 CC (formamido)-N(1)-(5-phospho-D-ribosyl)acetamidine + L-glutamate.
 CC -1- PATHWAY: De novo purine biosynthesis; fourth step.
 CC -1- SUBUNIT: HETERODIMER OF TWO SUBUNITS, PURQ AND PURL.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
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DR EMBL; Z80226; CAB02378.1; -;
 DR EMBL; AE006971; AAK45055.1; -;
 DR TIGR; MT0813; -;
 DR TubercuList; RV0788; -;
 DR InterPro; IPR000991; GATase_1.
 DR InterPro; IPR002818; ThiJ.
 DR Pfam; PF01965; ThiJ; 1.
 DR PROSITE; PS00442; GATASE_TYPE_I; 1.
 KW Purine biosynthesis; Ligase; Glutamine amidotransferase;
 KW Complete proteome.
 FT ACT_SITE 87 87 GATASE (BY SIMILARITY).
 SQ SEQUENCE 224 AA; 23633 MW; 46B37215D1171D4E CRC64;

Query Match 62.5%; Score 30; DB 1; Length 224;
 Best Local Similarity 75.0%; Pred. No. 34;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXSX 10
 ||| | |
 Db 47 VVPGGFSY 54

RESULT 21
 PURQ_CORAM STANDARD; PRT; 225 AA.
 AC Q9RHX0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phosphoribosylformylglycinamide synthase I (EC 6.3.5.3) (FGAM
 DE synthase I).
 GN PURQ.
 OS Corynebacterium ammoniagenes (Brevibacterium ammoniagenes).
 OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Corynebacteriaceae;
 OC Corynebacterium.
 OX NCBI_TaxID=1697;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 6872;
 RA Yonetani Y., Teshiba S.;
 RT "Sequence analysis of Corynebacterium ammoniagenes purL.";
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + N(2)-formyl-N(1)-(5-phospho-D-
 CC ribosyl)glycinamide + L-glutamine + H(2)O = ADP + phosphate + 2-
 CC (formamido)-N(1)-(5-phospho-D-ribosyl)acetamidine + L-glutamate.
 CC -1- PATHWAY: De novo purine biosynthesis; fourth step.
 CC -1- SUBUNIT: HETERODIMER OF TWO SUBUNITS, PURQ AND PURL.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
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DR EMBL; AB003162; BAA89450.1; -;
 DR InterPro; IPR000991; GATase_1.
 DR PROSITE; PS00442; GATASE_TYPE_I; 1.

KW Purine biosynthesis; Ligase; Glutamine amidotransferase.
 FT ACT_SITE 87
 SQ SEQUENCE 225 AA; 23803 MW; 11CC6B5E5A5A256 CRC64;
 Query Match 62.5%; Score 30; DB 1; Length 225;
 Best Local Similarity 75.0%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 VVPXGXS 10
 DB 47 VVPXGXS 54
 RESULT 22
 SCOA_HELPJ STANDARD; PRT; 232 AA.
 ID SCOA_HELPJ
 AC 92LE3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5)
 DE (Succinyl-CoA:3-oxoacid-CoA-transferase) (OXCT A).
 GN SCOA OR JHP0637.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=65963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9923682;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.J.;
 RT "Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen Helicobacter pylori.";
 RL Nature 397:176-180(1999).
 CC -1- CATALYTIC ACTIVITY: Succinyl-CoA + a 3-oxo acid - succinate + a 3-
 CC OXO-acyl-CoA.
 CC -1- SUBUNIT: HETERODIMER OF A SUBUNIT A AND A SUBUNIT B.
 CC -1- SIMILARITY: BELONGS TO THE 3-OXOACID COA-TRANSFERASE SUBUNIT A
 CC FAMILY.
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 CC -----
 DR EMBL: AE001495; AAD06212.1; -
 DR InterPro: IPR004165; CoA.trans.
 DR InterPro: IPR004163; CoA.transf_1.
 DR Pfam: PF01144; CoA.trans. 1.
 DR PROSITE: PS01273; CoA.TRANSF.1; 1.
 KW Transferase; Complete proteome.
 FT DOMAIN 24 30 COA-BINDING (POTENTIAL).
 SQ SEQUENCE 232 AA; 25325 MW; 1657D27435A0E4AE CRC64;
 Query Match 62.5%; Score 30; DB 1; Length 232;
 Best Local Similarity 71.4%; Pred. No. 36;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXG 7
 DB 190 EEIVPAG 196
 RESULT 23
 SCOA_HELPJ STANDARD; PRT; 232 AA.
 ID SCOA_HELPJ
 AC 92LE3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5)
 DE (Succinyl-CoA:3-oxoacid-CoA-transferase) (OXCT A).
 GN SCOA OR JHP0637.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=65963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9923682;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.J.;
 RT "Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen Helicobacter pylori.";
 RL Nature 397:176-180(1999).
 CC -1- CATALYTIC ACTIVITY: Succinyl-CoA + a 3-oxo acid - succinate + a 3-
 CC OXO-acyl-CoA.
 CC -1- SUBUNIT: HETERODIMER OF A SUBUNIT A AND A SUBUNIT B.
 CC -1- SIMILARITY: BELONGS TO THE 3-OXOACID COA-TRANSFERASE SUBUNIT A
 CC FAMILY.
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 CC -----
 DR EMBL: AE001495; AAD06212.1; -
 DR InterPro: IPR004165; CoA.trans.
 DR InterPro: IPR004163; CoA.transf_1.
 DR Pfam: PF01144; CoA.trans. 1.
 DR PROSITE: PS01273; CoA.TRANSF.1; 1.
 KW Transferase; Complete proteome.
 FT DOMAIN 24 30 COA-BINDING (POTENTIAL).
 SQ SEQUENCE 232 AA; 25325 MW; 1657D27435A0E4AE CRC64;
 Query Match 62.5%; Score 30; DB 1; Length 232;
 Best Local Similarity 71.4%; Pred. No. 36;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXG 7
 DB 190 EEIVPAG 196
 RESULT 23
 SCOA_HELPJ STANDARD; PRT; 232 AA.
 ID SCOA_HELPJ
 AC 92LE3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5)
 DE (Succinyl-CoA:3-oxoacid-CoA-transferase) (OXCT A).
 GN SCOA OR JHP0637.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=65963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9923682;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
 RA Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 RA Trust T.J.;
 RT "Genomic sequence comparison of two unrelated isolates of the human
 RT gastric pathogen Helicobacter pylori.";
 RL Nature 397:176-180(1999).
 CC -1- CATALYTIC ACTIVITY: Succinyl-CoA + a 3-oxo acid - succinate + a 3-
 CC OXO-acyl-CoA.
 CC -1- SUBUNIT: HETERODIMER OF A SUBUNIT A AND A SUBUNIT B.
 CC -1- SIMILARITY: BELONGS TO THE 3-OXOACID COA-TRANSFERASE SUBUNIT A
 CC FAMILY.
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 CC -----
 DR EMBL: AE000582; AAD07743.1; -
 DR TIGR: HP0691; -
 DR InterPro: IPR004165; CoA.trans.
 DR InterPro: IPR004163; CoA.transf_1.
 DR Pfam: PF01144; CoA.trans. 1.
 DR PROSITE: PS01273; CoA.TRANSF.1; 1.
 KW Transferase; Complete proteome.
 FT DOMAIN 24 30 COA-BINDING (POTENTIAL).
 SQ SEQUENCE 232 AA; 25362 MW; 83CFEE57C0192F3D CRC64;
 Query Match 62.5%; Score 30; DB 1; Length 232;
 Best Local Similarity 71.4%; Pred. No. 36;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXG 7
 DB 190 EEIVPAG 196

AC P56006;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Succinyl-CoA:3-ketoacid-coenzyme A transferase subunit A (EC 2.8.3.5)
 DE (Succinyl-CoA:3-oxoacid-CoA-transferase) (OXCT A).
 GN SCOA OR HP0691.
 OS Helicobacter pylori (Campylobacter pylori).
 OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=26695 / ATCC 700392;
 RX MEDLINE=97394467; PubMed=9252185;
 RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
 RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
 RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
 RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
 RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
 RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
 RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
 RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
 RA Venter J.C.;
 RT "The complete genome sequence of the gastric pathogen Helicobacter
 RT pylori.";
 RL Nature 388:539-547(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX STRAIN=69A;
 RX MEDLINE=97467359; PubMed=9325289;
 RA Cortesey-Theulaz I.E., Bergonzelli G.E., Henry H., Bachmann D.,
 RA Schorderet D.F., Blum A.L., Ornston L.N.;
 RT "Cloning and characterization of Helicobacter pylori succinyl
 RT CoA:acetate CoA-transferase, a novel prokaryotic member of the
 RT CoA-transferase family.";
 RL J. Biol. Chem. 272:25659-25667(1997).
 CC -1- CATALYTIC ACTIVITY: Succinyl-CoA + a 3-oxo acid - succinate + a 3-
 CC OXO-acyl-CoA.
 CC -1- SUBUNIT: HETERODIMER OF A SUBUNIT A AND A SUBUNIT B.
 CC -1- SIMILARITY: BELONGS TO THE 3-OXOACID COA-TRANSFERASE SUBUNIT A
 CC FAMILY.
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 CC -----
 DR EMBL: AE000582; AAD07743.1; -
 DR TIGR: HP0691; -
 DR InterPro: IPR004165; CoA.trans.
 DR InterPro: IPR004163; CoA.transf_1.
 DR Pfam: PF01144; CoA.trans. 1.
 DR PROSITE: PS01273; CoA.TRANSF.1; 1.
 KW Transferase; Complete proteome.
 FT DOMAIN 24 30 COA-BINDING (POTENTIAL).
 SQ SEQUENCE 232 AA; 25362 MW; 83CFEE57C0192F3D CRC64;
 Query Match 62.5%; Score 30; DB 1; Length 232;
 Best Local Similarity 71.4%; Pred. No. 36;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXG 7
 DB 190 EEIVPAG 196

```

RESULT 24
MAG8_HUMAN
ID MAG8_HUMAN STANDARD; PRT; 234 AA.
AC P43361;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Melanoma-associated antigen 8 (MAGE-8 antigen).
GN MAGE8 OR MAGE8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95012457; PubMed=7927540;
RA de Plaen E., Arden K., Traversari C., Gaforio J.J., Szikora J.-P.,
RA de Smet C., Brasseur F., van der Bruggen P., Lethe B., Lurquin C.,
RA Brasseur R., Chomez P., de Backer O., Cavenee W., Boon T.;
RT "Structure, chromosomal localization, and expression of 12 genes of
RT the MAGE family.";
RL Immunogenetics 40:360-369(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX Timms K.M., Bondeson M.L., Ansari-Lari M.A., Lagerstedt K.,
RA Nelson D.L., Pettersson U., Gibbs R.A.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: NOT KNOWN. THOUGH MAY PLAY A ROLE IN EMBRYONAL
CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CC PROGRESSION.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES AND PLACENTA.
CC -!- SIMILARITY: CONTAINS 1 MAGE DOMAIN.
CC -----
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CC -----
DR EMBL; U10693; AAA68876.1; -
DR Genew; HGNC:6806; MAGE8.
DR MIM; 300341; -
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
DR Antigen; Multigene family; Tumor antigen.
KW DOMAIN 112 234
FT DOMAIN 40 43 POLY-SER.
FT SEQUENCE 234 AA; 25197 MW; 058A92EE6003A982 CRC64;
SQ SEQUENCE 234 AA; 25197 MW; 058A92EE6003A982 CRC64;

Query Match 62.5%; Score 30; DB 1; Length 234;
Best Local Similarity 60.0%; Pred. NO. 36;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSX 10
Db :||| | | | |

RESULT 25
MAG9_HUMAN
ID MAG9_HUMAN STANDARD; PRT; 315 AA.
AC P43362; Q92910;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Melanoma-associated antigen 9 (MAGE-9 antigen).
GN MAGE9 OR MAGE9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Timms K.M., Bondeson M.L., Ansari-Lari M.A., Lagerstedt K.,
RA Nelson D.L., Pettersson U., Gibbs R.A.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: NOT KNOWN. THOUGH MAY PLAY A ROLE IN EMBRYONAL
CC DEVELOPMENT AND TUMOR TRANSFORMATION OR ASPECTS OF TUMOR
CC PROGRESSION.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TUMORS OF SEVERAL TYPES,
CC SUCH AS MELANOMA, HEAD AND NECK SQUAMOUS CELL CARCINOMA, LUNG
CC CARCINOMA AND BREAST CARCINOMA, BUT NOT IN NORMAL TISSUES EXCEPT
CC FOR TESTES AND PLACENTA.
CC -!- SIMILARITY: CONTAINS 1 MAGE DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U10694; AAA68877.1; -
DR Genew; HGNC:6807; MAGEA9.
DR MIM; 300342; -
DR InterPro; IPR002190; MAGE.
DR Pfam; PF01454; MAGE; 1.
DR PROSITE; PS50838; MAGE; 1.
DR Antigen; Multigene family; Tumor antigen.
KW DOMAIN 108 307
FT DOMAIN 34 37 POLY-GLU.
FT DOMAIN 87 90 POLY-GLU.
FT SEQUENCE 315 AA; 35088 MW; 7FD2ED10D680D928 CRC64;
SQ SEQUENCE 315 AA; 35088 MW; 7FD2ED10D680D928 CRC64;

Query Match 62.5%; Score 30; DB 1; Length 315;
Best Local Similarity 60.0%; Pred. NO. 49;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSX 10
Db :||| | | | |

```

Search completed: June 10, 2003, 13:40:23
Job time : 6.5 secs

GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:30:25 ; Search time 25.7857 Seconds
(without alignments)
87.898 Million cell updates/sec

Title: US-09-909-164-43
Perfect score: 48
Sequence: 1 EEVVPXGXSYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

SPTREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.rvirus:*
16: sp.bacteriaph:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	77.1	471	11 Q8R126	Q8R126 mus musculus
2	37	77.1	484	11 Q8VD18	Q8VD18 mus musculus
3	36	75.0	1499	4 Q96914	Q96914 homo sapien
4	36	75.0	3472	1 Q74056	Q74056 cenarchaeum
5	35	72.9	225	10 Q40129	Q40129 lycopersico
6	35	72.9	1063	16 Q8RG86	Q8RG86 fusobacteri
7	34	70.8	143	17 Q8TX62	Q8TX62 methanopyru
8	34	70.8	165	17 Q28330	Q28330 archaeoglob
9	34	70.8	174	10 Q9M3T4	Q9M3T4 betula verr
10	34	70.8	479	4 Q96CS0	Q96CS0 homo sapien
11	34	70.8	541	16 Q98BP5	Q98BP5 rhizobium 1
12	34	70.8	678	12 Q9E1X6	Q9E1X6 cercopithec
13	34	70.8	1028	16 Q8YJ11	Q8YJ11 brucella me
14	34	70.8	1442	17 Q96YH5	Q96YH5 sulfolobus
15	33	68.8	78	6 Q9XST4	Q9XST4 canis famil
16	33	68.8	200	16 Q8XHX3	Q8XHX3 clostridium

RESULT 1

Q8R126
ID Q8R126 PRELIMINARY; PRT; 471 AA.
AC Q8R126
DT 01-JUN-2002 (TREMREL. 21, Created)
DT 01-JUN-2002 (TREMREL. 21, Last sequence update)
DT 01-JUN-2002 (TREMREL. 21, Last annotation update)
DE Hypothetical 54.5 kDa protein (Fragment).
OS Mus musculus (Mouse).

ALIGNMENTS

17	33	68.8	217	4	000404	000404 homo sapien
18	33	68.8	280	5	Q9VMN9	Q9VMN9 drosophila
19	33	68.8	299	4	Q9UEE9	Q9UEE9 homo sapien
20	33	68.8	815	10	Q9SF93	Q9SF93 arabidopsis
21	33	68.8	933	5	Q8SS39	Q8SS39 encephalito
22	32	66.7	96	3	Q9Y855	Q9Y855 kluyveromyc
23	32	66.7	219	17	Q971S2	Q971S2 sulfolobus
24	32	66.7	227	16	Q9RZU8	Q9RZU8 deinococcus
25	32	66.7	290	4	Q96MU1	Q96MU1 homo sapien
26	32	66.7	387	16	Q98FX1	Q98FX1 rhizobium 1
27	32	66.7	387	16	Q92MD6	Q92MD6 rhizobium m
28	32	66.7	425	5	Q9XVK4	Q9XVK4 caenorhabdi
29	32	66.7	556	4	Q43733	Q43733 homo sapien
30	32	66.7	583	5	Q9BHA5	Q9BHA5 plasmodium
31	32	66.7	583	5	Q9BH83	Q9BH83 plasmodium
32	32	66.7	602	10	Q9LUE0	Q9LUE0 arabidopsis
33	32	66.7	630	2	Q87110	Q87110 comamonas a
34	32	66.7	670	11	Q01487	Q01487 rattus norv
35	32	66.7	722	12	Q9QTC7	Q9QTC7 marek's dis
36	32	66.7	1735	4	Q9HBL0	Q9HBL0 homo sapien
37	32	66.7	1802	12	Q9J5C2	Q9J5C2 fowlpox vir
38	32	66.7	1902	4	Q14122	Q14122 homo sapien
39	31	64.6	121	2	Q33483	Q33483 pseudomonas
40	31	64.6	123	16	Q8ZLE6	Q8ZLE6 salmonella
41	31	64.6	123	17	Q29517	Q29517 archaeoglob
42	31	64.6	193	2	Q8VUA8	Q8VUA8 lactococcus
43	31	64.6	204	11	Q920M7	Q920M7 mus musculu
44	31	64.6	209	16	Q8RE56	Q8RE56 fusobacteri
45	31	64.6	225	11	Q9ET57	Q9ET57 mus musculu
46	31	64.6	266	4	Q96181	Q96181 homo sapien
47	31	64.6	284	16	P74187	P74187 synechocyst
48	31	64.6	301	2	Q9EM57	Q9EM57 salmonella
49	31	64.6	301	2	Q9EM52	Q9EM52 salmonella
50	31	64.6	301	2	Q9ETJ3	Q9ETJ3 salmonella
51	31	64.6	301	2	Q9F7G6	Q9F7G6 salmonella
52	31	64.6	301	2	Q9F7G5	Q9F7G5 salmonella
53	31	64.6	301	2	Q9F7G4	Q9F7G4 salmonella
54	31	64.6	301	2	Q9F7G3	Q9F7G3 salmonella
55	31	64.6	301	2	Q9F7G2	Q9F7G2 salmonella
56	31	64.6	301	2	Q9F7G1	Q9F7G1 salmonella
57	31	64.6	301	2	Q9F7G0	Q9F7G0 salmonella
58	31	64.6	301	2	Q9F7F9	Q9F7F9 salmonella
59	31	64.6	301	2	Q9F7F8	Q9F7F8 salmonella
60	31	64.6	301	2	Q9F7F7	Q9F7F7 salmonella
61	31	64.6	301	2	Q9F7F6	Q9F7F6 salmonella
62	31	64.6	301	2	Q9F7F5	Q9F7F5 salmonella
63	31	64.6	301	2	Q9F7F4	Q9F7F4 salmonella
64	31	64.6	301	2	Q9F7F3	Q9F7F3 salmonella
65	31	64.6	301	2	Q9F7F2	Q9F7F2 salmonella
66	31	64.6	358	9	Q9ZX56	Q9ZX56 mycobacteri
67	31	64.6	361	2	Q9EU31	Q9EU31 salmonella
68	31	64.6	361	2	Q9F7K1	Q9F7K1 salmonella
69	31	64.6	361	2	Q9F7J0	Q9F7J0 salmonella
70	31	64.6	361	2	Q9F7I1	Q9F7I1 salmonella
71	31	64.6	361	2	Q9F7H7	Q9F7H7 salmonella
72	31	64.6	361	2	Q9F7H0	Q9F7H0 salmonella
73	31	64.6	361	16	Q8Z5H9	Q8Z5H9 salmonella
74	31	64.6	450	16	Q8UB52	Q8UB52 agrobacteri
75	31	64.6	544	16	Q9PQD2	Q9PQD2 ureaplasma

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025810; AAH25810.1; -
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 471 AA; 54506 MW; E0DA685C374A9760 CRC64;

Query Match 77.1%; Score 37; DB 11; Length 471;
Best Local Similarity 60.0%; Pred. No. 9.3;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGXSYS 11
||:|:|:|:
Db 226 EVIPAGASYN 235

RESULT 2

Q8VD18 PRELIMINARY; PRT; 484 AA.
AC Q8VD18;
DT 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Similar to glioma tumor suppressor candidate region gene 2.
GN AW536441.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SALIVARY GLAND;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017637; AAH17637.1; -
DR MGD; MGI:2138595; AW536441.
SQ SEQUENCE 484 AA; 55835 MW; BBB45F3B4BE02A36 CRC64;

Query Match 77.1%; Score 37; DB 11; Length 484;
Best Local Similarity 60.0%; Pred. No. 9.5;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGXSYS 11
||:|:|:|:
Db 239 EVIPAGASYN 248

RESULT 3

Q969I4 PRELIMINARY; PRT; 1499 AA.
AC Q969I4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Putative aminophospholipid translocase (Aminophospholipid-transporting ATPase).
GN ATP10C.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21225279; PubMed=11326269;

RX Meguro M.; Kashiwagi A.; Mitsuoka K.; Nakao M.; Kondo I.; Saitoh S.;
RA Oshimura M.;
RT "A novel maternally expressed gene, ATP10C, encodes a putative

RT aminophospholipid translocase associated with Angelman syndrome.";
RL Nat. Genet. 28:19-20(2001).
RN [2]
RP SEQUENCE FROM N.A.

RX MEDLINE=21313119; PubMed=11353404;
RA Herzig L.B.K.; Kim S.J.; Cook E.H. Jr.; Ledbetter D.H.;

RT "The human aminophospholipid-transporting ATPase gene ATP10C maps adjacent to UBE3A and exhibits similar imprinted expression.";
RL Am. J. Hum. Genet. 68:1501-1505(2001).
DR EMBL; AB051358; BAB47392.1; -
DR EMBL; AY029504; AAK33100.1; -

DR EMBL; AY029487; AAK33100.1; JOINED.
DR EMBL; AY029488; AAK33100.1; JOINED.
DR EMBL; AY029489; AAK33100.1; JOINED.

DR EMBL; AY029490; AAK33100.1; JOINED.
DR EMBL; AY029491; AAK33100.1; JOINED.
DR EMBL; AY029492; AAK33100.1; JOINED.

DR EMBL; AY029493; AAK33100.1; JOINED.
DR EMBL; AY029494; AAK33100.1; JOINED.
DR EMBL; AY029495; AAK33100.1; JOINED.

DR EMBL; AY029496; AAK33100.1; JOINED.
DR EMBL; AY029497; AAK33100.1; JOINED.
DR EMBL; AY029498; AAK33100.1; JOINED.

DR EMBL; AY029499; AAK33100.1; JOINED.
DR EMBL; AY029500; AAK33100.1; JOINED.
DR EMBL; AY029501; AAK33100.1; JOINED.

DR EMBL; AY029502; AAK33100.1; JOINED.
DR EMBL; AY029503; AAK33100.1; JOINED.
DR InterPro; IPR001757; ATPase_E1-E2.

DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR001454; Hignase/hydriase.
DR Pfam; PF00702; Hydrolase; 1.

DR PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN_1.
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
SQ SEQUENCE 1499 AA; 167687 MW; D4996A4D0635A68D CRC64;

Query Match 75.0%; Score 36; DB 4; Length 1499;
Best Local Similarity 72.7%; Pred. No. 54;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11
|||||:|:
Db 469 EEVPRGGSVS 479

RESULT 4

O74056 PRELIMINARY; PRT; 3472 AA.
AC O74056;
DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 367.1 kDa protein.

OS Cenarchaeum symbiosum.
OC Archaea; Crenarchaeota; Cenarchaeum.

OX NCBI_TaxID=46770;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=B;
RA MEDLINE=98422450; PubMed=9748430;
RX Schleper C.; Delong E.F.; Preston C.M.; Feldman R.A.; Wu K.Y.;

RA Swanson R.V.;
RT "Genomic analysis reveals chromosomal variation in natural populations of the uncultured psychrophilic archaeon Cenarchaeum symbiosum.";
RL J. Bacteriol. 180:5003-5009(1998).

CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AF083072; AAC62699.1; -

DR InterPro; IPR000515; BPD_transp.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 4.

DR SMART; SM00320; WD40; 2.
DR PROSITE; PS00402; BPD_TRANSF_INN_MEMBER; UNKNOWN_1.
KW Hypothetical protein; Repeat; WD repeat.


```
SQ SEQUENCE 3472 AA; 367058 MW; 37F80707030F9355 CRC64;
Query Match 75.0%; Score 36; DB 1; Length 3472;
Best Local Similarity 54.5%; Pred. No. 1.4e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11
   :||| | | |
Db 2294 EDVIPRGSFS 2304

RESULT 5
Q40129 PRELIMINARY; PRT; 225 AA.
AC Q40129;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 25.2 kDa protein precursor.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF36; TISSUE=PISTIL;
RX MEDLINE=95375233; PubMed=7647301;
RA Milligan S.B., Gasser C.S.;
RT "Nature and regulation of pistil-expressed genes in tomato.";
RL Plant Mol. Biol. 28:691-711(1995).
DR EMBL: U20592; AAA80497.1;
DR InterPro: IPR002160; Kunitz_legume.
DR Pfam: PF00197; Kunitz_legume; 1.
DR ProDom: PD000891; Kunitz_legume; 1.
DR SMART: SM00452; ST1; 1.
DR PROSITE: PS00283; SOYBEAN_KUNITZ; UNKNOWN_1.
KW Hypothetical protein; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 225 UNKNOWN.
FT SEQUENCE 225 AA; 25188 MW; 1074C261D20CFDAD CRC64;

Query Match 72.9%; Score 35; DB 10; Length 225;
Best Local Similarity 54.5%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11
   :||| | | |
Db 32 DEVVPNGKTYA 42

RESULT 6
Q8RG86 PRELIMINARY; PRT; 1063 AA.
AC Q8RG86;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Carbamoyl-phosphate synthase large chain (EC 6.3.5.5).
GN FN0422.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RA Kapral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasiera O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Feinstein M., Kyrpides N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
```

```
RT nucleatum strain ATCC 25586.";
RL J. Bacteriol. 184:2005-2018(2002).
DR EMBL: AE010554; AAL94625.1;
KW Ligase; Complete proteome.
SQ SEQUENCE 1063 AA; 118008 MW; 39700E10B7CCB411 CRC64;

Query Match 72.9%; Score 35; DB 16; Length 1063;
Best Local Similarity 60.0%; Pred. No. 63;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGXSYS 11
   :||| | | |
Db 195 EIVPGLNYS 204

RESULT 7
Q8TX62 PRELIMINARY; PRT; 143 AA.
AC Q8TX62;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Uncharacterized conserved protein.
GN MK0814.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natale D.A., Rogozin I.B., Tatsov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozhavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR EMBL: AE010372; AAM02027.1;
KW Complete proteome.
SQ SEQUENCE 143 AA; 15734 MW; 4C8B28A1FBEDDOB CRC64;

Query Match 70.8%; Score 34; DB 17; Length 143;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 10
   :||| | | |
Db 75 EELVPQAGY 84

RESULT 8
Q28330 PRELIMINARY; PRT; 165 AA.
AC Q28330;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein AFI949.
GN AFI949.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Winn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
```

RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Cotton M.D., Spriggs T., Artach P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 reducing archaeon *Archaeoglobus fulgidus*.";
 RL Nature 390:364-370(1997).
 DR EMBL; AE000968; AAB89307.1; -;
 DR TIGR; AF1949; -;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 165 AA; 17588 MW; BBI7054810ADB8F8 CRC64;
 Query Match 70.8%; Score 34; DB 17; Length 165;
 Best Local Similarity 60.0%; Pred. No. 14;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EEVVPXGXSYS 10
 Db ||| | | | | |
 60 EESIPDGASY 69
 RESULT 9
 Q9M3T4 PRELIMINARY; PRT; 174 AA.
 AC Q9M3T4;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Acidic endochitinase (EC 3.2.1.14) (Fragment).
 GN PR3A.
 OS Betula verrucosa (White birch) (Betula pendula).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicotyledons; Rosidae;
 OC eurosids I; Fagales; Betulaceae; Betula.
 OX NCBI_TaxID=3505;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LEAF;
 RA Hilovaaara-Teijo M., Korhonen M.S., Palva T.E., Kangasjarvi J.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO CHITINASE CLASS II (FAMILY 18 OF GLYCOSYL
 CC HYDROLASES). CAB66334.1; -;
 DR EMBL; AJ279692; CAB66334.1; -;
 DR HSSP; P23472; 2HVM.
 DR InterPro; IPR001579; Chitinase_18/2.
 DR Pfam; IPR001223; Glyco_hydro_18.
 DR Pfam; PF00704; Glyco_hydro_18; 1.
 DR PROSITE; PS01095; CHITINASE_18; 1.
 KW Glycosidase; Hydrolase.
 FT NON_TER 1 1
 FT NON_TER 174 174
 SQ SEQUENCE 174 AA; 17936 MW; 834ADCC6B5C76634 CRC64;
 Query Match 70.8%; Score 34; DB 10; Length 174;
 Best Local Similarity 77.8%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 VVPXGXSYS 11
 Db ||| | | | | |
 74 VPPGGGSYS 82
 RESULT 10
 Q96CS0 PRELIMINARY; PRT; 479 AA.
 AC Q96CS0; Q96177;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Glioma tumor suppressor candidate region gene 2 (Fragment).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RA Strausberg R.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 6-479 FROM N.A.
 RC TISSUE=SKIN;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC014009; AAH14009.1; -;
 DR EMBL; BC007248; AAH07248.1; -;
 FT NON_TER 1 1
 SQ SEQUENCE 479 AA; 54529 MW; 0A6C3A8B476F7E8F CRC64;
 Query Match 70.8%; Score 34; DB 4; Length 479;
 Best Local Similarity 60.0%; Pred. No. 44;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 EWPXGXSYS 11
 Db ||| | | | | |
 240 EVAPAGASYN 249
 RESULT 11
 Q98BP5 PRELIMINARY; PRT; 541 AA.
 AC Q98BP5;
 DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Probable DNA ligase.
 GN MLL5481.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP003006; BA851927.1; -;
 DR InterPro; IPR000977; DNA_ligase.
 DR Pfam; PF01068; DNA_ligase; 1.
 DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.
 DR PROSITE; PS01060; DNA_LIGASE_A3; 1.
 KW Ligase; Complete proteome.
 SQ SEQUENCE 541 AA; 60645 MW; 2EFEF705453F28F8 CRC64;
 Query Match 70.8%; Score 34; DB 16; Length 541;
 Best Local Similarity 60.0%; Pred. No. 50;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGXSYS 10
 Db ||| | | | | |
 445 EELVPVGKAY 454
 RESULT 12
 Q9E1X6 PRELIMINARY; PRT; 678 AA.
 ID Q9E1X6

Q9E1X6;
 AC 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical 75.9 kDa protein.
 OS cercopithecine herpesvirus 7.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.
 OX NCBI_TaxID=35245;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Gray W.L., Starnes H.B., White M.W., Ashburn C.V., Mahalingam R.;
 RT "Complete Sequence of the Simian Varicella Virus Genome."
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF275348; AAC27217.1;
 KW Hypothetical protein.
 SQ SEQUENCE 678 AA; 73850 MW; A17B09E30512FE3C CRC64;

Query Match 70.8%; Score 34; DB 12; Length 678;
 Best Local Similarity 50.0%; Pred. No. 64;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSX 10
 ||::|||
 Db 147 EEIIPKGRTRY 156

RESULT 13

Q8YJ11 PRELIMINARY; PRT; 1028 AA.
 AC Q8YJ11;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE ATP-dependent DNA helicase.
 GN BMEI0275.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=16M / ATCC 23456 / BIOTYPE 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA DelVecchio V.G., Kapatal V., Redkar R.J., Patra G., Mujar C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,
 RA Jablonksi L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
 RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
 RA Haselkorn R., Kyrpides N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 Brucella melitensis";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL: AE009470; AAU51457.1;
 DR InterPro: IPR002086; Aldehyde_dehydr.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR001650; Helicase_C.
 DR Pfam: PF00271; helicase_C; 1.
 DR SMART: SM00490; HELIC_C; 1.
 DR PROSITE: PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
 KW Complete proteome.
 SQ SEQUENCE 1028 AA; 112996 MW; A752B7042572E219 CRC64;

Query Match 70.8%; Score 34; DB 16; Length 1028;
 Best Local Similarity 54.5%; Pred. No. 1e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSX 11
 ||::|||
 Db 76 EKIVPPGARYS 86

RESULT 14

Q96YH5 PRELIMINARY; PRT; 1442 AA.
 AC Q96YH5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE Hypothetical protein ST2195.
 GN ST2195.
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=111955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM 10545 / 7;
 RX PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermoacidophilic
 Crenarchaeon, Sulfolobus tokodaii strain 7";
 RL DNA Res. 8:123-140(2001).
 DR EMBL: AP000989; BAB67302.1;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 1442 AA; 156497 MW; D63EC2C35228121F CRC64;

Query Match 70.8%; Score 34; DB 17; Length 1442;
 Best Local Similarity 50.0%; Pred. No. 1.5e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSX 10
 ||::|||
 Db 863 EEITPGANY 872

RESULT 15

Q9XST4 PRELIMINARY; PRT; 78 AA.
 AC Q9XST4;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE P97 homologous protein (Fragment).
 GN P97.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=THYROID;
 RX MEDLINE=20422104; PubMed=10964405;
 RA Pichon B., Mercan D., Pouillon V., Christophe-Hobertus C.,
 RA Christophe D.;
 RT "A method for the large-scale cloning of nuclear proteins and nuclear
 targeting sequences on a functional basis";
 RL Anal. Biochem. 284:231-239(2000).
 DR EMBL: AJ388531; CAB46833.1;
 FT NON_TER 78
 SQ SEQUENCE 78 AA; 8895 MW; B62486313555FBAL CRC64;

Query Match 58.8%; Score 33; DB 6; Length 78;
 Best Local Similarity 54.5%; Pred. No. 10;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EEVVPXGXSX 11
 ||::|||
 Db 16 EDVPSGGEYS 26

RESULT 16

DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)	
DE	CG14010 protein.	
GN	CG14010.	
OS	Drosophila melanogaster (Fruit fly).	
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OC	Ephydroidea; Drosophilidae; Drosophila.	
OX	NCBI_TaxID=7227;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=BERKELEY;	
RX	MEDLINE=20196006; PubMed=10731132;	
RA	Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,	
RA	Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,	
RA	George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	
RA	Sutton G.G., Woruman J.R., Yandell M.D., Zhang Q., Chen L.X.,	
RA	Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,	
RA	Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,	
RA	Abiril J.F., Agbayani A., An H.-J., Bayraktaroglu C., Baldwin D.,	
RA	Ballem R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,	
RA	Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,	
RA	Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,	
RA	Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,	
RA	Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,	
RA	de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,	
RA	Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,	
RA	Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,	
RA	Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,	
RA	Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,	
RA	Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,	
RA	Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,	
RA	Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,	
RA	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,	
RA	Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,	
RA	Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,	
RA	Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,	
RA	Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,	
RA	Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,	
RA	Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,	
RA	Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,	
RA	Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,	
RA	Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,	
RA	Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,	
RA	Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,	
RA	Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,	
RA	Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,	
RA	Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,	
RT	Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;"	
RT	"The genome sequence of Drosophila melanogaster."	
URL	Science 287:2185-2195(2000).	
EMBL	AE003610; AAF52273.1; -	
DR	FlyBase; FBgn0031725; CG14010.	
DR	InterPro; IPR003599; Ig.	
DR	InterPro; IPR003006; Ig_MHC.	
DR	Pfam; PF00047; Ig; 1.	
DR	SMART; SM00409; Ig; 1.	
SEQ	SEQUENCE 280 AA; 30697 MW; 3705140822960D43 CRC64;	
Query Match	68.8%; Score 33; DB 5; Length 280;	
Best Local Similarity	60.0%; Pred. No. 41;	
Matches	6; Conservative 1; Mismatches 3; Indels 0; Gaps	
2y	2 EVVPGXSYS 11	
	: : :	
dbb	84 EIVPPGKGYS 93	
Q9UE9	PRELIMINARY; PRT; 299 AA.	
Q9UE9;		
AC	Q9UE9;	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	

DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE BCNT protein (CRANIOFACIAL development protein 1).
 GN Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98267221; PubMed=9602175;
 RA Takahashi I., Nobukuni T., Ohmori H., Kobayashi M., Tanaka S.,
 RA Okashima K., Okada T., Masui T., Hashimoto K., Iwashita S.;
 RT "Existence of a bovine LINE repetitive insert that appears in the
 of bovine protein BCNT in ruminant, but not in human, genomes.";
 RL Gene 211:387-394(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Strausberg R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB009285; BAA31967.1; -;
 DR EMBL; BC000991; AA00991.1; -;
 SQ SEQUENCE 299 AA; 33593 MW; F4A9E928B669451A CRC64;

Query Match 68.8%; Score 33; DB 4; Length 299;
 Best Local Similarity 54.5%; Pred. No. 44;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11
 | | | | |
 Db 16 EDVVPGGGEYS 26

RESULT 20

Q9SF93 PRELIMINARY; PRT; 815 AA.

AC Q9SF93
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Putative phosphatidylinositol-4-phosphate 5-kinase.
 GN F8A24.2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
 RA Renning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
 RT "Arabidopsis thaliana chromosome III BAC F8A24 genomic sequence.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC015985; AAF23244.1; -;
 DR InterPro; IPR003409; MORN.
 DR InterPro; IPR002498; PIP5K.
 DR Pfam; PF02493; MORN; 8.
 DR Pfam; PF01504; PIP5K; 1.
 DR SMART; SM00330; PIP5K; 1.
 KW Kinase.

SQ SEQUENCE 815 AA; 92091 MW; 3194F009D2C50130 CRC64;

Query Match 68.8%; Score 33; DB 10; Length 815;
 Best Local Similarity 63.6%; Pred. No. 1.3e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11
 | | | | |
 Db 49 ELVLPDGEYS 59

RESULT 21

Q8SS39 PRELIMINARY; PRT; 933 AA.

AC Q8SS39
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative ATP-dependent RNA helicase (SKI2 subfamily).
 GN ECU04_0910.
 OS Eucaryota; Microsporidia; Unikaryonidae; Eucephalitozoa.
 OC Eucaryota; Microsporidia; Unikaryonidae; Eucephalitozoa.
 OX NCBI_TaxID=6035;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 RA Genoscope;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GB-M1;
 RX MEDLINE=21576510; PubMed=11719806;
 RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
 RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
 RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
 RA Weissenbach J., Vivares C.P.;
 RT "Genome sequence and gene compaction of the eukaryote parasite
 Eucephalitozoa cuniculi.";
 RL Nature 414:450-453(2001).
 DR EMBL; AL590444; CAD25278.1; -;
 KW Hypothetical protein.

SQ SEQUENCE 933 AA; 106883 MW; CA400EE3A7AFF7CF CRC64;

Query Match 68.8%; Score 33; DB 5; Length 933;
 Best Local Similarity 54.5%; Pred. No. 1.5e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11
 | | | | |
 Db 43 EAVVPVGAAYT 53

RESULT 22

Q9Y855 PRELIMINARY; PRT; 96 AA.

AC Q9Y855
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE SLN1 homologue (Fragment).
 GN SLN1.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
 OX NCBI_TaxID=28985;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2359/152;
 RX MEDLINE=20136098; PubMed=10669872;
 RA Rao W.G., Fukuhara H.;
 RT "The ubiquitin-encoding genes of Kluyveromyces lactis.";
 RL Yeast 16:343-351(2000).
 DR EMBL; AJ243801; CAB50891.1; -;
 DR InterPro; IPR001789; Response_reg.
 DR Pfam; PF00072; Response_reg; 1.
 DR ProDom; PD000039; Response_reg; 1.
 DR SMART; SM00448; REC; 1.
 KW Phosphorylation; Sensory transduction.

SQ SEQUENCE 96 AA; 10971 MW; 5D86B3F852DEE8E7 CRC64;

Query Match 66.7%; Score 32; DB 3; Length 96;
 Best Local Similarity 54.5%; Pred. No. 22;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11
| | | | |
Db 6 EEILKNGESYS 16

RESULT 23

Q971S2 PRELIMINARY; PRT; 219 AA.
AC Q971S2
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Putative ribose 5-phosphate isomerase.
GN ST1302.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JCM 10545 / 7;
RX PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka K., Nakazawa H., Katamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudo H., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermophilic
RT Crenarchaeon, Sulfolobus tokodaii strain 7";
RL DNA Res. 8:123-140(2001).
DR ENBL: AP0003985; BAB6348.1; -.
DR InterPro: IPR004788; RpiA.
DR ProDom: PD005813; RpiA; 1.
KW Isomerase; Hypothetical protein; Complete proteome.
SQ SEQUENCE 219 AA; 24541 MW; A4E9A3F2C4006D90 CRC64;

Query Match 66.7%; Score 32; DB 17; Length 219;
Best Local Similarity 66.7%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EEVVPXGXSY 10
| | | | |
Db 131 EEVVPGVAY 139

RESULT 24

Q9RZ08 PRELIMINARY; PRT; 227 AA.
AC Q9RZ08
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein DRB0013.
GN DRB0013.
OS Deinococcus radiodurans.
OG Plasmid MP1.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
OC Deinococcaceae; Deinococcus.
OX NCBI_TaxID=1299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI;
RX MEDLINE=20036896; PubMed=10567266;
RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
RA Yamathavan J.J., Lam P., McDonald L., Utterback T., Zalewski C.,
RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
RA Fraser C.M.;
RT "Genome sequence of the radioresistant bacterium Deinococcus

RT radiodurans RI.";
RL Science 286:1571-1577(1999).
DR EMBL: AE001826; AAF12657.1; -.
DR TIGR: DRB0013; -.
KW Hypothetical protein; Plasmid; Complete proteome.
SQ SEQUENCE 227 AA; 24465 MW; 21C43D2CC42843B8 CRC64;

Query Match 66.7%; Score 32; DB 16; Length 227;
Best Local Similarity 54.5%; Pred. No. 55;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXSYS 11
| | | | |
Db 43 ESVLPIGHSFS 53

RESULT 25

Q96MU1 PRELIMINARY; PRT; 290 AA.
AC Q96MU1
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE CDNA FLJ31891 fis, clone NT2RP7003304, weakly similar to YceA protein
DE homolog ybfQ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK056453; BAB71188.1; -.
DR InterPro: IPR001763; Rhodanese-like.
DR Pfam: PF00581; Rhodanese; 1.
DR PIR: P00581; Rhodanese; 1.
SQ SEQUENCE 290 AA; 32972 MW; 41FB7FB0217C1421 CRC64;

Query Match 66.7%; Score 32; DB 4; Length 290;
Best Local Similarity 66.7%; Pred. No. 72;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXSY 9
| | | | |
Db 35 EEIVPMGIS 43

Search completed: June 10, 2003, 13:46:35
Job time : 26.7857 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:24:45 ; Search time 31.3571 Seconds
(without alignments)
46.744 Million cell updates/sec

Title: US-09-909-164-44
Perfect score: 52
Sequence: 1 EEVVPXGXHYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :

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2: /SIDS2/qcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
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22: /SIDS2/qcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	49	94.2	11	23	ABB80546 Hepatitis C virus
2	49	94.2	11	23	ABB80550 Hepatitis C virus
3	49	94.2	11	23	ABB80554 Hepatitis C virus
4	49	94.2	11	23	ABB80555 Hepatitis C virus
5	48	92.3	11	23	ABB80523 Hepatitis C virus
6	48	92.3	11	23	ABB80527 Hepatitis C virus
7	48	92.3	11	23	ABB80531 Hepatitis C virus
8	48	92.3	11	23	ABB80532 Hepatitis C virus
9	48	92.3	11	23	ABB80537 Hepatitis C virus
10	48	92.3	11	23	ABB80541 Hepatitis C virus

11	48	92.3	11	23	ABB80558 Hepatitis C virus
12	48	92.3	11	23	ABB80560 Hepatitis C virus
13	40	76.9	11	23	ABB80544 Hepatitis C virus
14	40	76.9	11	23	ABB80545 Hepatitis C virus
15	40	76.9	11	23	ABB80547 Hepatitis C virus
16	40	76.9	11	23	ABB80548 Hepatitis C virus
17	40	76.9	11	23	ABB80549 Hepatitis C virus
18	40	76.9	11	23	ABB80551 Hepatitis C virus
19	40	76.9	11	23	ABB80552 Hepatitis C virus
20	40	76.9	11	23	ABB80553 Hepatitis C virus
21	40	76.9	11	23	ABB80556 Hepatitis C virus
22	40	76.9	11	23	ABB80557 Hepatitis C virus
23	39	75.0	11	23	ABB80521 Hepatitis C virus
24	39	75.0	11	23	ABB80522 Hepatitis C virus
25	39	75.0	11	23	ABB80524 Hepatitis C virus
26	39	75.0	11	23	ABB80525 Hepatitis C virus
27	39	75.0	11	23	ABB80526 Hepatitis C virus
28	39	75.0	11	23	ABB80528 Hepatitis C virus
29	39	75.0	11	23	ABB80529 Hepatitis C virus
30	39	75.0	11	23	ABB80530 Hepatitis C virus
31	39	75.0	11	23	ABB80533 Hepatitis C virus
32	39	75.0	11	23	ABB80534 Hepatitis C virus
33	39	75.0	11	23	ABB80535 Hepatitis C virus
34	39	75.0	11	23	ABB80536 Hepatitis C virus
35	39	75.0	11	23	ABB80538 Hepatitis C virus
36	39	75.0	11	23	ABB80539 Hepatitis C virus
37	39	75.0	11	23	ABB80540 Hepatitis C virus
38	39	75.0	11	23	ABB80542 Hepatitis C virus
39	39	75.0	11	23	ABB80543 Hepatitis C virus
40	39	75.0	11	23	ABB80559 Hepatitis C virus
41	39	75.0	11	23	ABB80561 Hepatitis C virus
42	39	75.0	11	23	ABB80562 Hepatitis C virus
43	39	75.0	11	23	ABB80563 Hepatitis C virus
44	39	75.0	11	23	ABB80564 Hepatitis C virus
45	39	75.0	11	23	ABB80565 Hepatitis C virus
46	39	75.0	11	23	ABB80567 Hepatitis C virus
47	39	75.0	11	23	ABB80566 Hepatitis C virus
48	39	75.0	11	23	ABB80568 Hepatitis C virus
49	37	71.2	161	21	AA140435 Human ORF199
50	37	71.2	161	21	AA140435 Human ORF199
51	37	71.2	567	22	AAU39521 Propionibacterium
52	36	69.2	1037	23	ABP39949 Staphylococcus epi
53	34	65.4	126	20	AAW96145 Bovine preprotachy
54	34	65.4	150	22	AAU50013 Propionibacterium
55	34	65.4	379	21	AAV59390 Murine soluble int
56	34	65.4	381	21	AAV59390 Group B Streptococ
57	34	65.4	715	20	AAV27348 Group B Streptococ
58	34	65.4	793	20	AAV27347 Group B Streptococ
59	34	65.4	822	21	AAU91283 Streptococcus agal
60	34	65.4	822	22	AAU00028 Streptococcus agal
61	34	65.4	822	22	AAU00030 Streptococcus poly
62	34	65.4	822	23	ABP28904 Streptococcus poly
63	34	65.4	822	23	ABP29703 Streptococcus pneu
64	34	65.4	823	21	AA12746 Streptococcus pneu
65	34	65.4	824	21	AA12747 Streptococcus pneu
66	34	65.4	825	22	AAU00026 Streptococcus pyog
67	34	65.4	825	22	AAU00029 Streptococcus pyog
68	34	65.4	825	23	ABP26207 Streptococcus poly
69	33	63.5	55	23	AA150964 yeast dual substra
70	33	63.5	80	22	ABG21296 Novel human diagno
71	33	63.5	205	21	AA12726 Streptococcus pneu
72	33	63.5	205	23	AAU84025 Truncated variant
73	33	63.5	299	22	ABG00168 Novel human diagno
74	33	63.5	334	21	AA12728 Streptococcus pneu
75	33	63.5	334	23	AAU84027 Truncated variant

ALIGNMENTS

RESULT 1
ABB80546
ID ABB80546 standard; peptide: 11 AA.

XX AC ABB80546;
 XX DT 08-OCT-2002 (first entry)
 XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #26.
 XX DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX KW virucide.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Modified-site 1 /note= "N-terminal acetyl"
 XX FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 XX FT residue 7"
 XX FT Modified-site 11 /note= "C-terminal amide"
 XX PN WO200208251-A2.
 XX PD 31-JAN-2002.
 XX PE 19-JUL-2001; 2001WO-US23169.
 XX PR 21-JUL-2000; 2000US-220101P.
 XX PA (CORV-) CORVAS INT INC.
 XX PI Lim-wilby M, Levy OE, Brunck TK;
 XX DR WPI; 2002-361643/39.
 XX PT Novel peptide compound having hepatitis C virus protease inhibitory
 XX PT activity useful for treating disorders associated with hepatitis C
 XX PT virus protease
 XX PS Claim 17; Page 65; 69pp; English.
 XX CC The sequence represents a peptide compound of the invention having
 XX CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 XX CC invention are alpha-ketoamide peptide analogues. The peptides have
 XX CC virucide activity, and are useful for treating and in the manufacture of
 XX CC a medicament to treat disorders associated with HCV protease. A
 XX CC pharmaceutical composition comprising the peptide as an active ingredient
 XX CC is useful for treating disorders associated with hepatitis C virus.
 XX SQ Sequence 11 AA;
 XX Query Match 94.2%; Score 49; DB 23; Length 11;
 XX Best Local Similarity 90.9%; Pred. No. 0.0034;
 XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGXHYS 11
 Db 1 EEVVPXGXHYS 11
 RESULT 2
 ABB80550
 ID ABB80550 standard; peptide; 11 AA.
 XX AC ABB80550;
 XX DT 08-OCT-2002 (first entry)
 XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #30.
 XX DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX KW virucide.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Modified-site 1 /note= "N-terminal acetyl"
 XX FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 XX FT residue 7"

OS Synthetic.
 XX Key Location/Qualifiers
 XX FT Modified-site 1 /note= "N-terminal acetyl"
 XX FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 XX FT residue 7"
 XX FT Misc-difference 9 /note= "D-form residue"
 XX FT Modified-site 11 /note= "C-terminal amide"
 XX PN WO200208251-A2.
 XX PD 31-JAN-2002.
 XX PE 19-JUL-2001; 2001WO-US23169.
 XX PR 21-JUL-2000; 2000US-220101P.
 XX PA (CORV-) CORVAS INT INC.
 XX PI Lim-wilby M, Levy OE, Brunck TK;
 XX DR WPI; 2002-361643/39.
 XX PT Novel peptide compound having hepatitis C virus protease inhibitory
 XX PT activity useful for treating disorders associated with hepatitis C
 XX PT virus protease
 XX PS Claim 17; Page 65; 69pp; English.
 XX CC The sequence represents a peptide compound of the invention having
 XX CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 XX CC invention are alpha-ketoamide peptide analogues. The peptides have
 XX CC virucide activity, and are useful for treating and in the manufacture of
 XX CC a medicament to treat disorders associated with HCV protease. A
 XX CC pharmaceutical composition comprising the peptide as an active ingredient
 XX CC is useful for treating disorders associated with hepatitis C virus.
 XX SQ Sequence 11 AA;
 XX Query Match 94.2%; Score 49; DB 23; Length 11;
 XX Best Local Similarity 90.9%; Pred. No. 0.0034;
 XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGXHYS 11
 Db 1 EEVVPXGXHYS 11
 RESULT 3
 ABB8055A
 ID ABB8055A standard; peptide; 11 AA.
 XX AC ABB8055A;
 XX DT 08-OCT-2002 (first entry)
 XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #34.
 XX DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX KW virucide.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 XX FT Modified-site 1 /note= "N-terminal acetyl"
 XX FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 XX FT residue 7"

FT Misc-difference 8 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
FT XX

PN WO200208251-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease -

XX Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 94.2%; Score 49; DB 23; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.0034;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGXHYS 11

DB 1 EEVVPXGXHYS 11

RESULT 4

ABB80555

ID ABB80555 standard; peptide; 11 AA.

XX ABB80555;

XX 08-OCT-2002 (first entry)

XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #35.

XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with

FT residue 7"

FT Misc-difference 8 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

XX WO200208251-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease -

XX Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 94.2%; Score 49; DB 23; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.0034;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGXHYS 11

DB 1 EEVVPXGXHYS 11

RESULT 5

ABB80523

ID ABB80523 standard; peptide; 11 AA.

XX ABB80523;

XX 08-OCT-2002 (first entry)

XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #3.

XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with

FT residue 7"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

XX WO200208251-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX	Claim 17; Page 64; 69pp; English.
PS	
XX	The sequence represents a peptide compound of the invention having
CC	hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC	invention are alpha-ketoamide peptide analogues. The peptides have
CC	virucide activity, and are useful for treating and in the manufacture of
CC	a medicament to treat disorders associated with HCV protease. A
CC	pharmaceutical composition comprising the peptide as an active ingredient
CC	is useful for treating disorders associated with hepatitis C virus.
XX	
SO	Sequence 11 AA;
	Query Match 92.3%; Score 48; DB 23; Length 11;
	Best Local Similarity 90.9%; Pred. NO. 0.0054;
	Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0
Oy	1 EEVVPXGXHS 11
Dd	1 EEVVPXGMHS 11
RESULT 7	
ABB80531	ABB80531 standard; peptide; 11 AA.
ID	
XX	AC ABB80531;
AC	
XX	08-OCT-2002 (first entry)
DT	
DE	Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #11.
DE	
KW	Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
KW	
XX	Synthetic.
OS	
XX	Key Location/Qualifiers
FH	Modified-site 1 /note= "N-terminal acetyl"
FT	
FT	Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
FT	
FT	Modified-site 11 /note= "C-terminal amide"
FT	
PN	WO200208251-A2.
PN	
XX	31-JAN-2002.
PD	
XX	
XX	19-JUL-2001; 2001WO-US23169.
XX	
PR	21-JUL-2000; 2000US-220101P.
PR	
XX	(CORV-) CORVAS INT INC.
PA	
XX	Lim-wilby M, Levy OE, Brunck TK;
PI	
XX	WPI; 2002-361643/39.
DR	
XX	
PT	Novel peptide compound having hepatitis C virus protease inhibitory
PT	activity useful for treating disorders associated with hepatitis C
PT	virus protease
PT	
XX	Claim 17; Page 64; 69pp; English.
PS	
XX	The sequence represents a peptide compound of the invention having
CC	hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC	invention are alpha-ketoamide peptide analogues. The peptides have
CC	virucide activity, and are useful for treating and in the manufacture of
CC	a medicament to treat disorders associated with HCV protease. A
CC	pharmaceutical composition comprising the peptide as an active ingredient
CC	is useful for treating disorders associated with hepatitis C virus.

XX SQ Sequence 11 AA;
Query Match 92.3%; Score 48; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGXHYS 11
DB 1 EEVVPXGXHYS 11

RESULT 8
ABB80532
ID ABB80532 standard; peptide; 11 AA.
XX AC ABB80532;
XX DT 08-OCT-2002 (first entry)
XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #12.
XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX KW virucide.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
FT WO200208251-A2.
XX PN 31-JAN-2002.
XX PF 19-JUL-2001; 2001WO-US23169.
XX PR 21-JUL-2000; 2000US-220101P.
XX PA (CORV-) CORVAS INT INC.
XX PI Lim-wilby M, Levy OE, Brunck TK;
XX DR WPI; 2002-361643/39.
XX CC Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease
XX PS Claim 17; Page 64; 69pp; English.
XX CC The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.

XX SQ Sequence 11 AA;
Query Match 92.3%; Score 48; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGXHYS 11

DB 1 EEVVPXGXHYS 11
RESULT 9
ABB80537
ID ABB80537 standard; peptide; 11 AA.
XX AC ABB80537;
XX DT 08-OCT-2002 (first entry)
XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #17.
XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX KW virucide.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
FT WO200208251-A2.
XX PN 31-JAN-2002.
XX PF 19-JUL-2001; 2001WO-US23169.
XX PR 21-JUL-2000; 2000US-220101P.
XX PA (CORV-) CORVAS INT INC.
XX PI Lim-wilby M, Levy OE, Brunck TK;
XX DR WPI; 2002-361643/39.
XX CC Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease
XX PS Claim 17; Page 64; 69pp; English.
XX CC The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.

XX SQ Sequence 11 AA;
Query Match 92.3%; Score 48; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGXHYS 11
DB 1 EEVVPXGXHYS 11

RESULT 10
ABB80541
ID ABB80541 standard; peptide; 11 AA.
XX

AC ABB80541;
 XX 08-OCT-2002 (first entry)
 XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #21.
 DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX virucide.
 KW Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl"
 FT Modified-site 6
 FT /note= "Norvalyl carbonyl forming keto-amide linkage with
 OS residue 7"
 XX
 XX Modified-site 8
 FT /note= "Oxymethionine"
 FT Modified-site 11
 FT /note= "C-terminal amide"
 XX
 PN WO200208251-A2.
 XX 31-JAN-2002.
 PD
 XX 19-JUL-2001; 2001WO-US23169.
 PF
 XX 21-JUL-2000; 2000US-220101P.
 PR
 XX (CORV-) CORVAS INT INC.
 PA
 XX Lim-wilby M, Levy OE, Brunck TK;
 PI WPI; 2002-361643/39.
 XX
 DR Novel peptide compound having hepatitis C virus protease inhibitory
 XX activity useful for treating disorders associated with hepatitis C
 XX virus protease
 XX
 PS Claim 17; Page 65; 69pp; English.
 XX
 CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX
 SQ Sequence 11 AA;
 Query Match 92.3%; Score 48; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0054;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 EEVVPXGXHYS 11
 Db 1 EEVVPXGXHYS 11
 RESULT 11
 ABB80558
 ID ABB80558 standard; peptide; 11 AA.
 XX
 AC ABB80558;
 XX
 XX 08-OCT-2002 (first entry)
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #38.
 XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.

XX Synthetic.
 OS Key Location/Qualifiers
 XX Modified-site 1
 FT /note= "N-terminal acetyl"
 FT Modified-site 6
 FT /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Modified-site 8
 FT /note= "Oxymethionine"
 FT Modified-site 11
 FT /note= "C-terminal amide"
 XX
 PN WO200208251-A2.
 XX 31-JAN-2002.
 PD
 XX 19-JUL-2001; 2001WO-US23169.
 PF
 XX 21-JUL-2000; 2000US-220101P.
 PR
 XX (CORV-) CORVAS INT INC.
 PA
 XX Lim-wilby M, Levy OE, Brunck TK;
 PI WPI; 2002-361643/39.
 XX
 DR Novel peptide compound having hepatitis C virus protease inhibitory
 XX activity useful for treating disorders associated with hepatitis C
 XX virus protease
 XX
 PS Claim 17; Page 65; 69pp; English.
 XX
 CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX
 SQ Sequence 11 AA;
 Query Match 92.3%; Score 48; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0054;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 EEVVPXGXHYS 11
 Db 1 EEVVPXGXHYS 11
 RESULT 12
 ABB80560
 ID ABB80560 standard; peptide; 11 AA.
 XX
 AC ABB80560;
 XX
 XX 08-OCT-2002 (first entry)
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #40.
 XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl"
 FT Modified-site 6
 FT /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"

PA (CORV-) CORVAS INT INC.
XX Lim-wilby M, Levy OE, Brunck TK;
XX WPI; 2002-361643/39.
XX Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease
XX
PS Claim 17; Page 65; 69pp; English.
XX
CC The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
SQ Sequence 11 AA;
Query Match 76.9%; Score 40; DB 23; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 EEVVPXGXHYS 11
Db 1 EEVVPXGTYS 11
RESULT 15
ABB80547
ID ABB80547 standard; peptide; 11 AA.
XX
AC ABB80547;
XX
DT 08-OCT-2002 (first entry)
XX
DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #27.
XX
KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT Modified-site 11 residue 7"
FT Modified-site 11 /note= "C-terminal amide"
XX
PN WO200208251-A2.
XX
PD 31-JAN-2002.
XX
PF 19-JUL-2001; 2001WO-US23169.
XX
PR 21-JUL-2000; 2000US-220101P.
XX
PA (CORV-) CORVAS INT INC.
XX
PI Lim-wilby M, Levy OE, Brunck TK;
XX
DR WPI; 2002-361643/39.
XX
PT Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease
XX

PS Claim 17; Page 65; 69pp; English.
XX
CC The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
SQ Sequence 11 AA;
Query Match 76.9%; Score 40; DB 23; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 EEVVPXGXHYS 11
Db 1 EEVVPXGTYS 11
RESULT 16
ABB80548
ID ABB80548 standard; peptide; 11 AA.
XX
AC ABB80548;
XX
DT 08-OCT-2002 (first entry)
XX
DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #28.
XX
KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX
OS Synthetic.
XX
PH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT Modified-site 9 residue 7"
FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
XX
PN WO200208251-A2.
XX
PD 31-JAN-2002.
XX
PF 19-JUL-2001; 2001WO-US23169.
XX
PR 21-JUL-2000; 2000US-220101P.
XX
PA (CORV-) CORVAS INT INC.
XX
PI Lim-wilby M, Levy OE, Brunck TK;
XX
DR WPI; 2002-361643/39.
XX
PT Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease
XX
PS Claim 17; Page 65; 69pp; English.
XX
CC The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC

CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 76.9%; Score 40; DB 23; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EEVVPXGXHYS 11
||||| ||
Db 1 EEVVPXGTDYS 11

RESULT 17

ABB80549
ID ABB80549 standard; peptide; 11 AA.

XX ABB80549;

DT 08-OCT-2002 (first entry)

XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #29.

XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

FT WO200208251-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory
activity useful for treating disorders associated with hepatitis C
virus protease

XX Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having
hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
invention are alpha-ketoamide peptide analogues. The peptides have
virucide activity, and are useful for treating and in the manufacture of
a medicament to treat disorders associated with HCV protease. A
pharmaceutical composition comprising the peptide as an active ingredient
is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 76.9%; Score 40; DB 23; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EEVVPXGXHYS 11
||||| ||
Db 1 EEVVPXGSSYS 11

RESULT 18

ABB80551
ID ABB80551 standard; peptide; 11 AA.

XX ABB80551;

DT 08-OCT-2002 (first entry)

XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #31.

XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

FT WO200208251-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory
activity useful for treating disorders associated with hepatitis C
virus protease

XX Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having
hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
invention are alpha-ketoamide peptide analogues. The peptides have
virucide activity, and are useful for treating and in the manufacture of
a medicament to treat disorders associated with HCV protease. A
pharmaceutical composition comprising the peptide as an active ingredient
is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 76.9%; Score 40; DB 23; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.21;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EEVVPXGXHYS 11
||||| ||
Db 1 EEVVPXGSDYS 11

RESULT 19

ABB80552
ID ABB80552 standard; peptide; 11 AA.

XX AC ABB80552;
 XX DT 08-OCT-2002 (first entry)
 XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #32.
 XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX KW virucide.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 8 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT WO200208251-A2.
 XX PN 31-JAN-2002.
 XX PD 19-JUL-2001; 2001WO-US23169.
 XX PF 21-JUL-2000; 2000US-220101P.
 XX PR (CORV-) CORVAS INT INC.
 XX PA Lim-wilby M, Levy OE, Brunck TK;
 XX PI WPI; 2002-361643/39.
 XX DR Novel peptide compound having hepatitis C virus protease inhibitory
 XX PT activity useful for treating disorders associated with hepatitis C
 XX PT virus protease
 XX PS Claim 17; Page 65; 69pp; English.
 XX CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX SQ Sequence 11 AA;
 Query Match 76.9%; Score 40; DB 23; Length 11;
 Best Local Similarity 81.8%; Pred. NO. 0.21;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGXHYS 11
 DB 1 EEVVPXGXSSYS 11
 RESULT 20
 ABB80553
 ID ABB80553 standard; peptide; 11 AA.
 XX AC ABB80553;
 XX DT 08-OCT-2002 (first entry)
 XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #33.
 XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;

virucide.
 XX Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 8 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT WO200208251-A2.
 XX PN 31-JAN-2002.
 XX PD 19-JUL-2001; 2001WO-US23169.
 XX PF 21-JUL-2000; 2000US-220101P.
 XX PR (CORV-) CORVAS INT INC.
 XX PA Lim-wilby M, Levy OE, Brunck TK;
 XX PI WPI; 2002-361643/39.
 XX DR Novel peptide compound having hepatitis C virus protease inhibitory
 XX PT activity useful for treating disorders associated with hepatitis C
 XX PT virus protease
 XX PS Claim 17; Page 65; 69pp; English.
 XX CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX SQ Sequence 11 AA;
 Query Match 76.9%; Score 40; DB 23; Length 11;
 Best Local Similarity 81.8%; Pred. NO. 0.21;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGXHYS 11
 DB 1 EEVVPXGXSSYS 11
 RESULT 21
 ABB80556
 ID ABB80556 standard; peptide; 11 AA.
 XX AC ABB80556;
 XX DT 08-OCT-2002 (first entry)
 XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #36.
 XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX KW virucide.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1

XX PA (CORV-) CORVAS INT INC.
 XX PI Lim-wilby M, Levy OE, Brunck TK;
 XX DR WPI; 2002-361643/39.
 XX DR Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease -
 XX Claim 17; Page 64; 69pp; English.
 XX PS The sequence represents a peptide compound of the invention having
 XX hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX SQ Sequence 11 AA;
 Query Match 75.0%; Score 39; DB 23; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.33;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGXHYS 11
 ||||| ||
 Db 1 EEVVPXGMSYS 11
 RESULT 24
 ABB80522
 ID ABB80522 standard; peptide; 11 AA.
 XX AC ABB80522;
 XX DT 08-OCT-2002 (first entry)
 XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
 XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX KW virucide.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6
 FT Misc-difference 9 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Modified-site 11 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 PN WO200208251-A2.
 XX PD 31-JAN-2002.
 XX PF 19-JUL-2001; 2001WO-US23169.
 XX PR 21-JUL-2000; 2000US-220101P.
 XX PA (CORV-) CORVAS INT INC.
 XX PI Lim-wilby M, Levy OE, Brunck TK;
 XX DR WPI; 2002-361643/39.
 XX PT Novel peptide compound having hepatitis C virus protease inhibitory

PT activity useful for treating disorders associated with hepatitis C
 PT virus protease -
 XX Claim 17; Page 64; 69pp; English.
 XX PS The sequence represents a peptide compound of the invention having
 XX hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX SQ Sequence 11 AA;
 Query Match 75.0%; Score 39; DB 23; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.33;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGXHYS 11
 ||||| ||
 Db 1 EEVVPXGMSYS 11
 RESULT 25
 ABB80524
 ID ABB80524 standard; peptide; 11 AA.
 XX AC ABB80524;
 XX DT 08-OCT-2002 (first entry)
 XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
 XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX KW virucide.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 PN WO200208251-A2.
 XX PD 31-JAN-2002.
 XX PF 19-JUL-2001; 2001WO-US23169.
 XX PR 21-JUL-2000; 2000US-220101P.
 XX PA (CORV-) CORVAS INT INC.
 XX PI Lim-wilby M, Levy OE, Brunck TK;
 XX DR WPI; 2002-361643/39.
 XX PT Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease -
 XX Claim 17; Page 64; 69pp; English.
 XX PS The sequence represents a peptide compound of the invention having
 XX hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have

CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.

xx

SQ Sequence 11 AA;

Query Match 75.0%; Score 39; DB 23; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.33;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXHYS 11

|||||||

1 EEVVPXGMDYS 11

Db

Search completed: June 10, 2003, 13:39:11

Job time : 32.3571 secs

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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:31:45 ; Search time 9.64286 Seconds
(without alignments)
33.564 Million cell updates/sec

Title: US-09-909-164-44
Perfect score: 52
Sequence: 1 EEVVPXGXHYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	69.2	1037	4	US-09-134-001C-4794
2	34	65.4	126	3	US-08-879-995A-3
3	34	65.4	126	3	US-09-215-096-3
4	33	63.5	447	4	US-08-961-083-182
5	33	63.5	600	2	US-08-821-119-19
6	33	63.5	600	2	US-08-821-118-2
7	33	63.5	763	4	US-08-961-083-66
8	33	63.5	796	4	US-08-961-083-56
9	32	61.5	738	1	US-08-530-010-3
10	32	61.5	738	1	US-08-530-010-5
11	32	61.5	738	1	US-08-530-010-7
12	32	61.5	738	1	US-08-530-010-9
13	32	61.5	738	1	US-08-530-010-11
14	32	61.5	738	2	US-08-484-101B-3
15	32	61.5	738	2	US-08-484-101B-5
16	32	61.5	738	2	US-08-484-101B-7
17	32	61.5	738	2	US-08-484-101B-9
18	32	61.5	738	2	US-08-484-101B-11
19	32	61.5	738	4	US-08-714-524D-3
20	32	61.5	738	4	US-08-714-524D-5
21	32	61.5	738	4	US-08-714-524D-7
22	32	61.5	738	4	US-08-714-524D-9
23	32	61.5	738	4	US-08-714-524D-11
24	31	59.6	70	4	US-09-134-001C-3950
25	31	59.6	237	4	US-09-134-001C-4185
26	31	59.6	502	4	US-09-342-647-4
27	31	59.6	622	2	US-08-459-146-2

28	59.6	31	59.6	622	2	US-08-459-065-2	Sequence 2, Appli
29	59.6	31	59.6	630	4	US-09-342-647-2	Sequence 2, Appli
30	59.6	31	59.6	667	4	US-09-342-647-28	Sequence 28, Appli
31	58.7	30.5	58.7	268	4	US-09-085-305-8	Sequence 8, Appli
32	58.7	30.5	58.7	268	4	US-09-085-305-10	Sequence 10, Appli
33	58.7	30.5	58.7	268	4	US-09-085-305-17	Sequence 17, Appli
34	58.7	30.5	58.7	121	4	US-09-152-060-68	Sequence 68, Appli
35	57.7	30	57.7	121	4	US-09-152-060-85	Sequence 85, Appli
36	57.7	30	57.7	122	3	US-08-879-995A-1	Sequence 1, Appli
37	57.7	30	57.7	122	3	US-08-879-995A-1	Sequence 1, Appli
38	57.7	30	57.7	241	3	US-08-834-776A-2	Sequence 2, Appli
39	57.7	30	57.7	328	4	US-09-180-827-10	Sequence 10, Appli
40	57.7	30	57.7	386	4	US-09-086-483A-2	Sequence 2, Appli
41	57.7	30	57.7	386	4	US-09-130-491-6	Sequence 6, Appli
42	57.7	30	57.7	615	2	US-08-663-566A-17	Sequence 17, Appli
43	57.7	30	57.7	615	2	US-08-023-610-17	Sequence 17, Appli
44	57.7	30	57.7	615	2	US-08-288-065A-17	Sequence 17, Appli
45	57.7	30	57.7	615	2	US-08-362-240A-17	Sequence 17, Appli
46	57.7	30	57.7	615	5	PCT-US95-10245-17	Sequence 17, Appli
47	57.7	30	57.7	747	4	US-09-724-864-36	Sequence 36, Appli
48	57.7	30	57.7	1081	2	US-08-843-530B-18	Sequence 18, Appli
49	57.7	30	57.7	1117	2	US-08-843-530B-33	Sequence 33, Appli
50	57.7	30	57.7	1140	4	US-09-220-081-2	Sequence 2, Appli
51	57.7	30	57.7	1140	4	US-09-677-575-2	Sequence 2, Appli
52	56.7	29.5	56.7	501	2	US-08-408-095-31	Sequence 31, Appli
53	55.8	29	55.8	100	2	US-09-047-125-27	Sequence 27, Appli
54	55.8	29	55.8	100	3	US-07-736-335E-27	Sequence 27, Appli
55	55.8	29	55.8	261	2	US-08-879-561-1	Sequence 1, Appli
56	55.8	29	55.8	289	4	US-09-395-674B-2	Sequence 2, Appli
57	55.8	29	55.8	716	2	US-08-766-982-1	Sequence 1, Appli
58	55.8	29	55.8	716	4	US-09-296-219-1	Sequence 1, Appli
59	55.8	29	55.8	1417	2	US-08-559-303B-78	Sequence 78, Appli
60	55.8	29	55.8	1417	3	US-08-781-891-78	Sequence 78, Appli
61	55.8	29	55.8	1417	4	US-09-175-828-78	Sequence 78, Appli
62	55.8	29	55.8	2109	4	US-08-646-695-6	Sequence 6, Appli
63	55.8	29	55.8	2109	5	PCT-US96-06053-6	Sequence 6, Appli
64	53.8	28	53.8	46	5	PCT-US95-06266-112	Sequence 112, App
65	53.8	28	53.8	59	4	US-08-963-851-14	Sequence 14, Appli
66	53.8	28	53.8	102	1	US-08-469-427A-2	Sequence 2, Appli
67	53.8	28	53.8	102	2	US-08-609-443B-2	Sequence 2, Appli
68	53.8	28	53.8	102	2	US-08-569-063C-2	Sequence 2, Appli
69	53.8	28	53.8	102	4	US-08-851-896-2	Sequence 2, Appli
70	53.8	28	53.8	133	1	US-08-469-427A-9	Sequence 9, Appli
71	53.8	28	53.8	133	2	US-08-609-443B-9	Sequence 9, Appli
72	53.8	28	53.8	133	2	US-08-569-063C-9	Sequence 9, Appli
73	53.8	28	53.8	133	4	US-08-851-896-9	Sequence 9, Appli
74	53.8	28	53.8	150	2	US-08-801-105-2	Sequence 2, Appli
75	53.8	28	53.8	188	1	US-08-469-427A-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-134-001C-4794
; Sequence 4794, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GPC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4794
; LENGTH: 1037
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-4794

Query Match 69.2%; Score 36; DB 4; Length 1037;
 Best Local Similarity 63.6%; Pred. No. 37;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXHS 11
 :||| | |||
 Db 199 KEVVSNGLHYS 209

RESULT 2

US-08-879-995A-3
 ; Sequence 3, Application US/08879995A
 ; Patent No. 5985606
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Kaser, Matthew R.
 ; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/879,995A
 FILING DATE: Herewith
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0326 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 126 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 163590
 US-08-879-995A-3

Query Match 65.4%; Score 34; DB 2; Length 126;
 Best Local Similarity 66.7%; Pred. No. 9;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXH 9
 :||| | |||
 Db 28 EQVVPGGGH 36

RESULT 3

US-09-215-096-3
 ; Sequence 3, Application US/09215096
 ; Patent No. 6008194
 ; GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.
 APPLICANT: Lal, Preeti
 APPLICANT: Kaser, Matthew R.
 TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Incyte Pharmaceuticals, Inc.
 STREET: 3174 Porter Drive
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/215,096
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/879,995
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Billings, Lucy J.
 REGISTRATION NUMBER: 36,749
 REFERENCE/DOCKET NUMBER: PF-0326 US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-855-0555
 TELEFAX: 415-845-4166
 TELEX:

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 126 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 IMMEDIATE SOURCE:
 LIBRARY: GenBank
 CLONE: 163590
 US-09-215-096-3

Query Match 65.4%; Score 34; DB 3; Length 126;
 Best Local Similarity 66.7%; Pred. No. 9;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXH 9
 :||| | |||
 Db 28 EQVVPGGGH 36

RESULT 4

US-08-961-083-182
 ; Sequence 182, Application US/08961083
 ; Patent No. 6159469
 ; GENERAL INFORMATION:

APPLICANT: Choi et. al.
 TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
 NUMBER OF SEQUENCES: 452
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text
 CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/961.083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 182:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-961-083-182

Query Match 63.5%; Score 33; DB 4; Length 447;
Best Local Similarity 62.5%; Pred. No. 58;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
; : : :
Db 178 IVPHGHHY 185

RESULT 5

US-08-821-119-19
; Sequence 19, Application US/08821119
; Patent No. 5821104
; GENERAL INFORMATION:
; APPLICANT: Holm, Kaj Andre
; APPLICANT: Rasmussen, Grethe
; APPLICANT: Halkier, Torben
; APPLICANT: Lehmebeck, Jan
; TITLE OF INVENTION: Tripeptidyl Aminopeptidase
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5821104o No. 5821104disk of No. 5821104th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/821.119
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4107.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:

; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 600 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein

; FRAGMENT TYPE: internal
; US-08-821-119-19

Query Match 63.5%; Score 33; DB 2; Length 600;
Best Local Similarity 75.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 VVPXGXHY 11
; : : :
Db 31 VPKGWHYS 38

RESULT 6

US-08-821-118-2
; Sequence 2, Application US/08821118
; Patent No. 5989889
; GENERAL INFORMATION:
; APPLICANT: Rey, Michael
; APPLICANT: Golightly, Elizabeth
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYPEPTIDES
; TITLE OF INVENTION: HAVING TRIPEPTIDE AMINOPEPTIDASE
; TITLE OF INVENTION: ACTIVITY
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5989889o No. 5989889disk of No. 5989889th America, Inc.
; STREET: 405 Lexington Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10174
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/821.118
; FILING DATE: 19-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4107.400-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 600 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; US-08-821-118-2

Query Match 63.5%; Score 33; DB 2; Length 600;
Best Local Similarity 75.0%; Pred. No. 80;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 VVPXGXHY 11
; : : :
Db 31 VPKGWHYS 38

RESULT 7

US-08-961-083-66
; Sequence 66, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines

NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 763 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-083-66

Query Match 63.5%; Score 33; DB 4; Length 763;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
DB 184 IVPXGDHY 191

RESULT 8
US-08-961-083-56
Sequence 56, Application US/08961083
Patent No. 6159469
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 796 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-083-56

Query Match 63.5%; Score 33; DB 4; Length 796;
Best Local Similarity 62.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
DB 185 IVPXGDHY 192

RESULT 9
US-08-530-010-3
Sequence 3, Application US/08530010
Patent No. 5689055
GENERAL INFORMATION:
APPLICANT: Meyerowitz, Elliott M.
APPLICANT: Chang, Caren
APPLICANT: Bleecker, Anthony B.
TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO ETHYLENE
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Trecartin
STREET: 3400 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/530,010
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/086,555
FILING DATE: 01-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-57515/RFT
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-530-010-3

Query Match 61.5%; Score 32; DB 1; Length 738;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10

TELEFAX: (415) 398-3249

COUNTRY: USA

; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-530-010-9

Query Match 61.5%; Score 32; DB 1; Length 738;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
Db 498 VVPTGSHF 505

RESULT 13

US-08-530-010-11
; Sequence 11, Application US/08530010
; Patent No. 5689055

; GENERAL INFORMATION:
; APPLICANT: Meyerowitz, Elliott M.
; APPLICANT: Chang, Caren
; APPLICANT: Blecker, Anthony B.
; TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO ETHYLENE
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecartin
; STREET: 3400 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/530,010
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/086,555
; FILING DATE: 01-JUL-1993

; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-57515/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-530-010-11

Query Match 61.5%; Score 32; DB 1; Length 738;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
Db 498 VVPTGSHF 505

RESULT 14

US-08-484-101B-3
; Sequence 3, Application US/08484101B

; Patent No. 5824868
; GENERAL INFORMATION:
; APPLICANT: California Institute of Technology
; TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO
; TITLE OF INVENTION: ETHYLENE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecartin
; STREET: 3400 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,101B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/
; FILING DATE: 01-JUL-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/086,555
; FILING DATE: 01-JUL-1993

; ATTORNEY/AGENT INFORMATION:
; NAME: Trecartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-57515-2/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-101B-3

Query Match 61.5%; Score 32; DB 2; Length 738;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
Db 498 VVPTGSHF 505

RESULT 15

US-08-484-101B-5
; Sequence 5, Application US/08484101B
; Patent No. 5824868
; GENERAL INFORMATION:

; APPLICANT: California Institute of Technology
; TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO
; TITLE OF INVENTION: ETHYLENE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Trecartin
; STREET: 3400 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/484,101B
APPLICATION NUMBER: US/08/484,101B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/
FILING DATE: 01-JUL-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/086,555
FILING DATE: 01-JUL-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-57515-2/RFT
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 5:
LENGTH: 738 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-101B-5

Query Match 61.5%; Score 32; DB 2; Length 738;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
||| | |
Db 498 VVPTGSHF 505

RESULT 16
US-08-484-101B-7
Sequence 7, Application US/08484101B
Patent No. 5824868
GENERAL INFORMATION:
APPLICANT: California Institute of Technology
TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO
ETHYLENE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Trecartin
STREET: 3400 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,101B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/
FILING DATE: 01-JUL-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/086,555
FILING DATE: 01-JUL-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.

REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-57515-2/RFT
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-101B-7

Query Match 61.5%; Score 32; DB 2; Length 738;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
||| | |
Db 498 VVPTGSHF 505

RESULT 17
US-08-484-101B-9
Sequence 9, Application US/08484101B
Patent No. 5824868
GENERAL INFORMATION:
APPLICANT: California Institute of Technology
TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO
ETHYLENE
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard F. Trecartin
STREET: 3400 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,101B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/
FILING DATE: 01-JUL-1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/086,555
FILING DATE: 01-JUL-1993
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: A-57515-2/RFT
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-484-101B-9

Query Match 61.5%; Score 32; DB 2; Length 738;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
||| | | |
Db 498 VVPTGSHF 505

RESULT 18

US-08-484-101B-11
; Sequence 11, Application US/08484101B
; Patent No. 5824868
; GENERAL INFORMATION:
; APPLICANT: California Institute of Technology
; TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO
; TITLE OF INVENTION: ETHYLENE
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Richard F. Treccartin
; STREET: 3400 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,101B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/
; FILING DATE: 01-JUL-1994
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/086,555
; FILING DATE: 01-JUL-1993
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Treccartin, Richard F.
; REGISTRATION NUMBER: 31,801
; REFERENCE/DOCKET NUMBER: A-57515-2/RFT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-101B-11

Query Match 61.5%; Score 32; DB 2; Length 738;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
||| | | |
Db 498 VVPTGSHF 505

RESULT 19

US-08-714-524D-3
; Sequence 3, Application US/08714524D
; Patent No. 6294716
; GENERAL INFORMATION:
; APPLICANT: Meyerowitz, Elliott M
; APPLICANT: Chang, Caren
; APPLICANT: Blecker, Anthony B
; TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO ETHYLENE
; FILE REFERENCE: a-57515-4

; CURRENT APPLICATION NUMBER: US/08/714,524D
; CURRENT FILING DATE: 1996-09-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-08-714-524D-3

Query Match 61.5%; Score 32; DB 4; Length 738;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
||| | | |
Db 498 VVPTGSHF 505

RESULT 20

US-08-714-524D-5
; Sequence 5, Application US/08714524D
; Patent No. 6294716
; GENERAL INFORMATION:
; APPLICANT: Meyerowitz, Elliott M
; APPLICANT: Chang, Caren
; APPLICANT: Blecker, Anthony B
; TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO ETHYLENE
; FILE REFERENCE: a-57515-4
; CURRENT APPLICATION NUMBER: US/08/714,524D
; CURRENT FILING DATE: 1996-09-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-08-714-524D-5

Query Match 61.5%; Score 32; DB 4; Length 738;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
||| | | |
Db 498 VVPTGSHF 505

RESULT 21

US-08-714-524D-7
; Sequence 7, Application US/08714524D
; Patent No. 6294716
; GENERAL INFORMATION:
; APPLICANT: Meyerowitz, Elliott M
; APPLICANT: Chang, Caren
; APPLICANT: Blecker, Anthony B
; TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO ETHYLENE
; FILE REFERENCE: a-57515-4
; CURRENT APPLICATION NUMBER: US/08/714,524D
; CURRENT FILING DATE: 1996-09-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-08-714-524D-7

Query Match 61.5%; Score 32; DB 4; Length 738;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10

Db 498 VVPTGSHF 505
||| | | |

RESULT 22

US-08-714-524D-9
; Sequence 9, Application US/08714524D
; Patent No. 6294716
; GENERAL INFORMATION:
; APPLICANT: Meyerowitz, Elliott M
; APPLICANT: Chang, Caren
; APPLICANT: Blecker, Anthony B
; TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO ETHYLENE
; FILE REFERENCE: a-57515-4
; CURRENT APPLICATION NUMBER: US/08/714,524D
; CURRENT FILING DATE: 1996-09-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-08-714-524D-9

Query Match 61.5%; Score 32; DB 4; Length 738;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 VVPXGXHY 10
||| | | |
Db 498 VVPTGSHF 505

RESULT 23

US-08-714-524D-11
; Sequence 11, Application US/08714524D
; Patent No. 6294716
; GENERAL INFORMATION:
; APPLICANT: Meyerowitz, Elliott M
; APPLICANT: Chang, Caren
; APPLICANT: Blecker, Anthony B
; TITLE OF INVENTION: PLANTS HAVING MODIFIED RESPONSE TO ETHYLENE
; FILE REFERENCE: a-57515-4
; CURRENT APPLICATION NUMBER: US/08/714,524D
; CURRENT FILING DATE: 1996-09-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 738
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-08-714-524D-11

Query Match 61.5%; Score 32; DB 4; Length 738;
Best Local Similarity 62.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 VVPXGXHY 10
||| | | |
Db 498 VVPTGSHF 505

RESULT 24

US-09-134-001C-3950
; Sequence 3950, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3950
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3950

Query Match 59.6%; Score 31; DB 4; Length 70;
Best Local Similarity 62.5%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 VVPXGXHY 11
: | | | | |
Db 36 MPKGFHYS 43

RESULT 25

US-09-134-001C-4185
; Sequence 4185, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 4185
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4185

Query Match 59.6%; Score 31; DB 4; Length 237;
Best Local Similarity 43.8%; Pred. No. 73;
Matches 7; Conservative 1; Mismatches 2; Indels 6; Gaps 1;

Qy 1 EEV-----PXGXHY 10
||| | | | |
Db 106 EEIVKEKVPSPGDHY 121

Search completed: June 10, 2003, 13:51:36
Job time : 10.6429 secs

FILE REFERENCE: 8331-9002
CURRENT APPLICATION NUMBER: US/09/252,088
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: US/60/075,425
EARLIER FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16
LENGTH: 715
TYPE: PRT
ORGANISM: group B streptococcus
US-09-252-088-16

Query Match 65.4%; Score 34; DB 9; Length 715;
Best Local Similarity 75.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
||| | |
DB 243 VVPHGDHY 250

RESULT 2

US-09-252-088-15
Sequence 15, Application US/09252088
Publication No. US20030031682A1
GENERAL INFORMATION:
APPLICANT: BRODEUR, Bernard R.
APPLICANT: RIOUX, Clment
APPLICANT: BOYER, Martine
APPLICANT: CHARLEBOIS, Isabelle
APPLICANT: HAMEL, Jose
APPLICANT: MARTIN, Denis
TITLE OF INVENTION: NOVEL GROUP B STREPTOCOCCUS ANTIGENS
FILE REFERENCE: 8331-9002
CURRENT APPLICATION NUMBER: US/09/252,088
CURRENT FILING DATE: 1999-02-18
EARLIER APPLICATION NUMBER: US/60/075,425
EARLIER FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 793
TYPE: PRT
ORGANISM: group B streptococcus
US-09-252-088-15

Query Match 65.4%; Score 34; DB 9; Length 793;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
||| | |
DB 321 VVPHGDHY 328

RESULT 3

US-09-765-272-182
Sequence 182, Application US/09765272
Patent No. US20020061545A1
GENERAL INFORMATION:
APPLICANT: Choi et. al.
TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/961,083
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 182:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 182:
US-09-765-272-182

Query Match 63.5%; Score 33; DB 10; Length 447;
Best Local Similarity 62.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
||| | |
DB 178 IVPHGGHY 185

RESULT 4

US-09-769-787-38
Sequence 38, Application US/09769787
Publication No. US20030091577A1
GENERAL INFORMATION:
APPLICANT: Microbial Technics Limited
APPLICANT: Gilbert, Christophe FG
APPLICANT: Hansbro, Philip M
TITLE OF INVENTION: Proteins
FILE REFERENCE: PWC/P21129WO
CURRENT APPLICATION NUMBER: US/09/769,787
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: GB 9816337.1
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60/125164
PRIOR FILING DATE: 1999-03-19
NUMBER OF SEQ ID NOS: 388
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 38
LENGTH: 484
TYPE: PRT
ORGANISM: Streptococcus pneumoniae
US-09-769-787-38

Query Match 63.5%; Score 33; DB 9; Length 484;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
||| | |
DB 202 IVPHGGHY 209

RESULT 5

US-09-765-272-66
Sequence 66, Application US/09765272
Patent No. US20020061545A1

[illegible]

; TITLE OF INVENTION: Streptococcus Antigens
 ; FILE REFERENCE: 055190-0044
 ; CURRENT APPLICATION NUMBER: US/09/884,465A
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: 60/212,683
 ; NUMBER OF SEQ ID NOS: 384
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 838
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 US-09-884-465A-8

Query Match 63.5%; Score 33; DB 9; Length 838;
 Best Local Similarity 62.5%; Pred. No. 2.5e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
 :|||
 Db 203 IVPXGDHY 210

RESULT 9

US-09-884-465A-7
 ; Sequence 7, Application US/09884465A
 ; Publication No. US20030077293A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shire Biochem, Inc.
 ; APPLICANT: Hamel, Josee
 ; APPLICANT: Brodeur, Bernard
 ; APPLICANT: Martin, Denis
 ; APPLICANT: Charland, Nathalie
 ; APPLICANT: Ouellet, Catherine
 ; TITLE OF INVENTION: Streptococcus Antigens
 ; FILE REFERENCE: 055190-0044
 ; CURRENT APPLICATION NUMBER: US/09/884,465A
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: 60/212,683
 ; NUMBER OF SEQ ID NOS: 384
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 7
 ; LENGTH: 840
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 US-09-884-465A-7

Query Match 63.5%; Score 33; DB 9; Length 840;
 Best Local Similarity 62.5%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
 :|||
 Db 205 IVPXGDHY 212

RESULT 10

US-09-884-465A-10
 ; Sequence 10, Application US/09884465A
 ; Publication No. US20030077293A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shire Biochem, Inc.
 ; APPLICANT: Hamel, Josee
 ; APPLICANT: Brodeur, Bernard
 ; APPLICANT: Martin, Denis
 ; APPLICANT: Charland, Nathalie
 ; APPLICANT: Ouellet, Catherine
 ; TITLE OF INVENTION: Streptococcus Antigens
 ; FILE REFERENCE: 055190-0044
 ; CURRENT APPLICATION NUMBER: US/09/884,465A
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: 60/212,683

; PRIOR FILING DATE: 2000-06-20
 ; NUMBER OF SEQ ID NOS: 384
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 840
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 US-09-884-465A-10

Query Match 63.5%; Score 33; DB 9; Length 840;
 Best Local Similarity 62.5%; Pred. No. 2.6e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
 :|||
 Db 182 IVPXGDHY 189

RESULT 11

US-09-884-465A-6
 ; Sequence 6, Application US/09884465A
 ; Publication No. US20030077293A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shire Biochem, Inc.
 ; APPLICANT: Hamel, Josee
 ; APPLICANT: Brodeur, Bernard
 ; APPLICANT: Martin, Denis
 ; APPLICANT: Charland, Nathalie
 ; APPLICANT: Ouellet, Catherine
 ; TITLE OF INVENTION: Streptococcus Antigens
 ; FILE REFERENCE: 055190-0044
 ; CURRENT APPLICATION NUMBER: US/09/884,465A
 ; PRIOR FILING DATE: 2001-06-20
 ; PRIOR APPLICATION NUMBER: 60/212,683
 ; NUMBER OF SEQ ID NOS: 384
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 6
 ; LENGTH: 1039
 ; TYPE: PRT
 ; ORGANISM: Streptococcus pneumoniae
 US-09-884-465A-6

Query Match 63.5%; Score 33; DB 9; Length 1039;
 Best Local Similarity 62.5%; Pred. No. 3.2e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
 :|||
 Db 202 IVPXGDHY 209

RESULT 12

US-10-176-847-22
 ; Sequence 22, Application US/10176847
 ; Publication No. US20030068636A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Velby, Petter Ole
 ; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
 ; IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF BREAST
 ; TITLE OF INVENTION: AND OVARIAN CANCER
 ; FILE REFERENCE: MRI-039
 ; CURRENT APPLICATION NUMBER: US/10/176,847
 ; CURRENT FILING DATE: 2002-06-21
 ; NUMBER OF SEQ ID NOS: 112
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 22
 ; LENGTH: 1463
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-176-847-22

Query Match 61.5%; Score 32; DB 9; Length 1463;

Best Local Similarity 45.5%; Pred. No. 7.3e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EEVVPXGXHYS 11
|||:
Db 438 EEVIQTSSHYT 448

RESULT 13

US-09-881-752A-292
; Sequence 292, Application US/09881752A
; Patent No. US20020115078A1
; GENERAL INFORMATION:
; APPLICANT: Kleantous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Omen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020115078A1 Helicobacter Polypeptides in the
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/041002
; CURRENT APPLICATION NUMBER: US/09/881,752A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/833,457
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 292
; LENGTH: 44
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-881-752A-292

Query Match 59.6%; Score 31; DB 10; Length 44;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 VVPXGXHYS 11
|||:
Db 34 VVPTGTHAS 42

RESULT 14

US-09-815-242-10416
; Sequence 10416, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10416
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-815-242-10416

Query Match 59.6%; Score 31; DB 10; Length 387;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EEVVPXGXH 9
|||:
Db 188 EEIPTGGH 195

RESULT 15

US-09-738-626-4919
; Sequence 4919, Application US/09738626
; Publication No. US20020197603A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIALI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAOKO
; APPLICANT: SENO, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4919
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4919

Query Match 59.6%; Score 31; DB 9; Length 622;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 EEVVPXG--XHY 10
|||:
Db 46 EEIPIGVPNHY 57

RESULT 16

US-09-820-843A-26
; Sequence 26, Application US/09820843A
; Publication No. US20030039963A1
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE
; TITLE OF INVENTION: USEFUL AS ANTI-INFECTIVES
; FILE REFERENCE: Q63915
; CURRENT APPLICATION NUMBER: US/09/820,843A
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 118

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Vibrio cholerae
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Iron(III) ABC transporter, permease protein
; NAME/KEY: misc_feature
; OTHER INFORMATION: gi|9654609
US-09-820-843A-26

Query Match 59.6%; Score 31; DB 9; Length 653;
Best Local Similarity 85.7%; Pred. No. 4.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
|:|:|:|:|
Db 300 EEVVPXG 306

RESULT 17

US-09-942-447-2
; Sequence 2, Application US/09942447
; Patent No. US20020127567A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: A NOVEL HUMAN TRANSPORTER AND USES
; FILE REFERENCE: 38155-20032.00
; CURRENT APPLICATION NUMBER: US/09/942,447
; PRIOR FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: US 60/229,036
; PRIOR FILING DATE: 2000-08-31
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-447-2

Query Match 59.6%; Score 31; DB 10; Length 665;
Best Local Similarity 62.5%; Pred. No. 4.9e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EEVVPXGXH 9
|:|:|:|:|
Db 632 EEVVPXGXH 639

RESULT 18

US-10-027-806-4
; Sequence 4, Application US/10027806
; Patent No. US20020160476A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCOIP.002A
; CURRENT APPLICATION NUMBER: US/10/027,806
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3472
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-806-4

Query Match 59.6%; Score 31; DB 9; Length 3472;
Best Local Similarity 45.5%; Pred. No. 2.9e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXHYS 11
|:|:|:|:|:|
Db 2294 EEVVPXGXHYS 2304

RESULT 19

US-10-034-623-4
; Sequence 4, Application US/10034623
; Publication No. US20020198365A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCOIP.002A
; CURRENT APPLICATION NUMBER: US/10/034,623
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/408,020
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/102,294
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3472
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-034-623-4

Query Match 59.6%; Score 31; DB 9; Length 3472;
Best Local Similarity 45.5%; Pred. No. 2.9e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXHYS 11
|:|:|:|:|:|
Db 2294 EEVVPXGXHYS 2304

RESULT 20

US-10-027-801-4
; Sequence 4, Application US/10027801
; Publication No. US20030054364A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCOIP.002A
; CURRENT APPLICATION NUMBER: US/10/027,801
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3472
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-801-4

Query Match 59.6%; Score 31; DB 9; Length 3472;
Best Local Similarity 45.5%; Pred. No. 2.9e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXHYS 11
|:|:|:|:|:|
Db 2294 EEVVPXGXHYS 2304

RESULT 21
US-09-909-062-1
; Sequence 1, Application US/09909062
; Publication No. US20030036501A1
; GENERAL INFORMATION:
; APPLICANT: Saksena, Anil K
; APPLICANT: Girijavaliabhan, Viyyor M
; APPLICANT: Lovey, Raymond G
; APPLICANT: Jao, Edwin
; APPLICANT: Bennett, Frank
; APPLICANT: McCormick, Jinping L
; APPLICANT: Pike, Russell E
; APPLICANT: Bogen, Stephane L
; APPLICANT: Liu, Yi-Tsung
; APPLICANT: Arasappan, Ashok
; APPLICANT: Pinto, Patrick A
; APPLICANT: Njoroge, F George
; APPLICANT: Ganguly, Ashit
; TITLE OF INVENTION: NOVEL PEPTIDES AS NS3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
; FILE REFERENCE: IN01157K-US
; CURRENT APPLICATION NUMBER: US/09/909,062
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/220,109
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: norvaline-C(=O)
US-09-909-062-1

Query Match 57.7%; Score 30; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEVVPXG 7
Db 1 EEVVPXG 7

RESULT 22
US-09-909-062-9
; Sequence 9, Application US/09909062
; Publication No. US20030036501A1
; GENERAL INFORMATION:
; APPLICANT: Saksena, Anil K
; APPLICANT: Girijavaliabhan, Viyyor M
; APPLICANT: Lovey, Raymond G
; APPLICANT: Jao, Edwin
; APPLICANT: Bennett, Frank
; APPLICANT: McCormick, Jinping L
; APPLICANT: Pike, Russell E
; APPLICANT: Bogen, Stephane L
; APPLICANT: Liu, Yi-Tsung
; APPLICANT: Arasappan, Ashok
; APPLICANT: Pinto, Patrick A
; APPLICANT: Njoroge, F George
; APPLICANT: Ganguly, Ashit
; TITLE OF INVENTION: NOVEL PEPTIDES AS NS3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
; FILE REFERENCE: IN01157K-US
; CURRENT APPLICATION NUMBER: US/09/909,062

; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/220,109
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: norvaline-C(=O)
US-09-909-062-9

Query Match 57.7%; Score 30; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EEVVPXG 7
Db 1 EEVVPXG 7

RESULT 23
US-09-909-062-130
; Sequence 130, Application US/09909062
; Publication No. US20030036501A1
; GENERAL INFORMATION:
; APPLICANT: Saksena, Anil K
; APPLICANT: Girijavaliabhan, Viyyor M
; APPLICANT: Lovey, Raymond G
; APPLICANT: Jao, Edwin
; APPLICANT: Bennett, Frank
; APPLICANT: McCormick, Jinping L
; APPLICANT: Pike, Russell E
; APPLICANT: Bogen, Stephane L
; APPLICANT: Arasappan, Ashok
; APPLICANT: Pinto, Patrick A
; APPLICANT: Njoroge, F George
; APPLICANT: Ganguly, Ashit
; TITLE OF INVENTION: NOVEL PEPTIDES AS NS3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
; FILE REFERENCE: IN01157K-US
; CURRENT APPLICATION NUMBER: US/09/909,062
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/220,109
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: AMIDATION
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (6)..(6)

; OTHER INFORMATION: norvaline-(C=O)
US-09-909-062-130

Query Match 57.7%; Score 30; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
 |||||
Db 1 EEVVPXG 7

RESULT 24

US-09-925-297-664
; Sequence 664, Application US/09925297
; Patent No. US20020081659A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA105
; CURRENT APPLICATION NUMBER: US/09/925,297
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05989
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 928
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 664
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-297-664

Query Match 57.7%; Score 30; DB 10; Length 72;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
 :| | |
Db 5 IMPEGXHY 12

RESULT 25

US-09-852-797-68
; Sequence 68, Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05

; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-68

Query Match 57.7%; Score 30; DB 9; Length 121;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EEVVPXG 7
 |||||
Db 28 EEVVPXG 34

Search completed: June 10, 2003, 14:35:45
Job time : 15.0714 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:31:15 ; Search time 11.2143 Seconds
(without alignments)
94.297 Million cell updates/sec

Title: US-09-909-164-44
Perfect score: 52
Sequence: 1 EEVVPXGXHY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_73:*

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	67.3	233	2 T02590	DNA binding protei
2	35	67.3	308	2 A72207	ftsh proteinase ac
3	35	67.3	360	2 E69086	cell division prot
4	35	67.3	1028	2 AF3286	ATP-dependent DNA
5	35	67.3	1396	2 S36851	L-shaped tail fibe
6	34	65.4	102	2 A42452	V1 protein - tobac
7	34	65.4	126	2 A25905	tachykinin B precu
8	34	65.4	279	2 C75538	hypothetical prote
9	34	65.4	495	2 T28717	hypothetical prote
10	34	65.4	534	2 A69284	coenzyme F420-quin
11	34	65.4	822	2 T46758	hypothetical 92.4K
12	34	65.4	1057	2 F98992	carbamoyl-phosphat
13	33	63.5	46	2 E97985	hypothetical prote
14	33	63.5	124	1 VKLJ51	trans-regulatory s
15	33	63.5	156	2 D82618	conserved hypoteth
16	33	63.5	252	2 AE2001	hypothetical prote
17	33	63.5	412	2 A48702	2-methyl-branched-
18	33	63.5	460	2 E98046	hypothetical prote
19	33	63.5	510	2 G86430	T518.1 protein - A
20	33	63.5	743	2 S38143	hypothetical prote
21	33	63.5	802	2 C95136	conserved domain p
22	33	63.5	819	2 B95136	conserved domain p
23	33	63.5	828	2 E98004	hypothetical prote
24	33	63.5	839	2 G95115	conserved hypoteth
25	33	63.5	853	2 C97985	hypothetical prote
26	33	63.5	855	2 D98004	histidine Motif-Co
27	33	63.5	1039	2 H95115	conserved hypoteth
28	33	63.5	1039	2 D97985	hypothetical prote
29	32	61.5	162	2 A70939	probable monooxygen

30	32	61.5	225	2 S57810	hypothetical prote
31	32	61.5	286	2 C86169	prohibitin 2 [impo
32	32	61.5	311	2 H69194	GMP synthetase, su
33	32	61.5	322	2 AF3211	hypothetical prote
34	32	61.5	364	2 S47540	fructose-bisphosph
35	32	61.5	369	2 T17267	hypothetical prote
36	32	61.5	374	2 G69119	probable aspartate
37	32	61.5	425	2 T24111	hypothetical prote
38	32	61.5	454	2 G96568	probable non-photo
39	32	61.5	519	2 G84598	probable bzrp tran
40	32	61.5	536	2 AI3544	aldehyde dehydroge
41	32	61.5	627	2 A69663	DNA mismatch repai
42	32	61.5	696	2 A91247	phage transposase
43	32	61.5	701	2 S61239	hypothetical prote
44	32	61.5	716	1 JC5061	macrophage-stimula
45	32	61.5	738	2 A48446	ethylene-response
46	32	61.5	902	2 AH2999	conserved hypoteth
47	32	61.5	903	2 A96284	hypothetical prote
48	32	61.5	905	2 A54654	centromere protein
49	32	61.5	1374	2 T16129	hypothetical prote
50	32	61.5	1378	1 I48751	protein-tyrosine k
51	31.5	60.6	126	2 F69305	conserved hypoteth
52	31	59.6	61	2 T40544	probable centromer
53	31	59.6	61	2 G83958	hypothetical prote
54	31	59.6	125	2 C97134	hypothetical prote
55	31	59.6	212	2 E82061	peptide methionine
56	31	59.6	284	2 G69117	diphthine synthase
57	31	59.6	319	2 S03833	hypothetical prote
58	31	59.6	364	1 ADHUB	fructose-bisphosph
59	31	59.6	379	2 A69516	probable aspartate
60	31	59.6	387	1 XUEC	acetyl-CoA C-acylt
61	31	59.6	387	2 E91225	acetyl-CoA transfe
62	31	59.6	387	2 C86072	acetyl-CoA transfe
63	31	59.6	387	2 A10914	small (beta) chain
64	31	59.6	426	2 S58132	Sisi protein precu
65	31	59.6	427	2 F64064	tolB protein - Hae
66	31	59.6	441	2 G82253	conserved hypoteth
67	31	59.6	487	2 S65811	finger protein (cl
68	31	59.6	545	2 T08564	hypothetical prote
69	31	59.6	622	2 S15009	hypothetical prote
70	31	59.6	653	2 D82352	iron(III) ABC tran
71	31	59.6	668	2 C96501	hypothetical prote
72	31	59.6	704	2 T29996	hypothetical prote
73	31	59.6	761	2 T33816	hypothetical prote
74	31	59.6	772	2 T02098	probable phosphati
75	31	59.6	991	2 S43891	dna exoribonucleas

ALIGNMENTS

RESULT 1

T02590
DNA binding protein EREBP-2 - common tobacco

C;Species: Nicotiana tabacum (common tobacco)

C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 21-Jul-2000

C;Accession: T02590

R;Onme-Takagi, M.; Shinshi, H.

Plant Cell 7, 173-182, 1995

A;Title: Ethylene-inducible DNA binding proteins that interact with an ethylene re:

A;Reference number: Z14671; MUID:95276459; PMID:7756828

A;Accession: T02590

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-233 <OHM>

A;Cross-references: EMBL:D38126; NID:G790362; PIDN:BAA07324.1; PID:g1208498

A;Experimental source: strain BY4; tissue-type leaf

Query Match 67.3%; Score 35; DB 2; Length 233;
Best Local Similarity 60.0%; Pred. No. 9.7;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXHY 10

```

Db      90 QAVVPKGRHY 99
      : ||| | ||
RESULT 2
A72207
ftsh proteinase activity modulator HflK - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: A72207
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A>Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: A72207
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-308 <ARN>
A:Cross-references: GB:AE001819; GB:AE000512; NID:g4982396; PIDN:AAD36885.1; PID:g498240
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TMI822
C:Superfamily: erythrocyte band 7 integral membrane protein

Query Match      67.3%; Score 35; DB 2; Length 308;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 VVPXGXHY 10
      ||| | ||
Db      41 VVPSGIHY 48

RESULT 3
E69086
cell division protein - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C:Accession: E69086
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicalre, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A>Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: E69086
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-360 <MTH>
A:Cross-references: GB:AE000923; GB:AE000666; NID:g2622766; PIDN:AAB86115.1; PID:g262277
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1642
C:Superfamily: cell division protein MJ0174

Query Match      67.3%; Score 35; DB 2; Length 360;
Best Local Similarity 45.5%; Pred. No. 16;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1 EEVVPXGXHY 11
      ||:| | ||:
Db      98 EDLVPMSGSHY 108

RESULT 4
AF3286
ATP-dependent DNA helicase BMEI0275 [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C:Accession: AF3286
R:DelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova,

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.: Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; i
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A>Title: The genome sequence of the facultative intracellular pathogen Brucella m
A:Reference number: AD3252; PMID:11756688
A:Accession: AF3286
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1028 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL51457.1; PID:g17982167; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI0275
A:Map position: 1

Query Match      67.3%; Score 35; DB 2; Length 1028;
Best Local Similarity 54.5%; Pred. No. 48;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 EEVVPXGXHY 11
      ||:| | ||
Db      76 EKIVPPGARYS 86

RESULT 5
S36851
L-shaped tail fiber protein - phage T5
N:Alternate names: ltf protein
C:Species: phage T5
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000
C:Accession: S65934; S01984; S36851
R:Kallman, A.V.; Kuishin, V.E.; Shlyapnikov, M.G.; Ksenzenko, V.N.; Kryukov, V.M.
FEBS Lett. 366, 46-48, 1995
A>Title: The nucleotide sequence of the bacteriophage T5 ltf gene.
A:Reference number: S65934; MUID:95309401; PMID:7789514
A:Accession: S65934
A:Molecule type: DNA
A:Residues: 1-1396 <KAL>
A:Cross-references: EMBL:X69460; NID:g15415; PIDN:CAA49220.1; PID:g15416
R:Kallman, A.V.; Kryukov, V.M.; Bayev, A.A.
Nucleic Acids Res. 16, 6230, 1988
A>Title: The nucleotide sequence of bacteriophage T5 DNA at the region between earl
A:Reference number: S01984; MUID:88289370; PMID:3267228
A:Accession: S01984
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 934-985, 'A', 987-1396 <KA2>
A:Cross-references: EMBL:X07559
C:Genetics:
A:Gene: ltf
C:Keywords: late protein; tail fiber

Query Match      67.3%; Score 35; DB 2; Length 1396;
Best Local Similarity 50.0%; Pred. No. 67;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      2 EVVPXGXHY 11
      : || | |||
Db      1360 KTIPAGDHY 1369

RESULT 6
A42452
VI protein - tobacco yellow dwarf virus (strain Australia)
C:Species: tobacco yellow dwarf virus
C>Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
C:Accession: A42452
R:Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
Virology 187, 633-642, 1992
A>Title: The nucleotide sequence of the infectious cloned DNA component of tobacco
A:Reference number: A42452; MUID:92188538; PMID:1546458
A:Accession: A42452
A:Molecule type: DNA
A:Residues: 1-102 <MOR>

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A;Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284

Query Match 65.4%; Score 34; DB 2; Length 102;

Best Local Similarity 60.0%; Pred. No. 6.5;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVVPXGXHS 11

Db 7 QVVPXGXHS 16

RESULT 7

A25905

tachykinin B precursor - bovine

N;Alternate names: neuromedin K

C;Species: Bos primigenius taurus (cattle)

C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 16-Jul-1999

C;Accession: A25905

R;Kotani, H.; Hoshimaru, M.; Nawa, H.; Nakanishi, S.

Proc. Natl. Acad. Sci. U.S.A. 83, 7074-7078, 1986

A;Title: Structure and gene organization of bovine neuromedin K precursor.

A;Reference number: A25905; MUID:86313713; PMID:3462746

A;Accession: A25905

A;Molecule type: DNA

A;Residues: 1-126 <KOT>

A;Cross-references: GB:M14351; NID:g163587; PIDN:AAA30723.1; PID:g163590

C;Superfamily: neurokinin B precursor

F;1-26/Domain: signal sequence #status predicted <SIG>

F;27-126/Product: protachykinin B #status predicted <MAT>

Query Match 65.4%; Score 34; DB 2; Length 126;

Best Local Similarity 66.7%; Pred. No. 8.2;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXH 9

Db 28 EQVVPXGXH 36

RESULT 8

C75538

hypothetical protein - Deinococcus radiodurans (strain R1)

C;Species: Deinococcus radiodurans

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000

C;Accession: C75538

R;Whiter, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;

M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.

Science 286, 1571-1577, 1999

A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266

A;Accession: C75538

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-279 <WHI>

A;Cross-references: GB:AE001889; GB:AE000513; NID:g6457944; PIDN:AAF09867.1; PID:g645795

A;Experimental source: strain R1

C;Genetics:

A;Gene: DR0271

A;Map position: 1

C;Superfamily: Deinococcus radiodurans hypothetical protein DR0271

Query Match 65.4%; Score 34; DB 2; Length 279;

Best Local Similarity 75.0%; Pred. No. 19;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 VFXGXHS 11

Db 100 VPLGRHS 107

RESULT 9

T28717

hypothetical 92.4K protein - Streptococcus agalactiae

C;Species: Streptococcus agalactiae

C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 21-Jul-2000

hypothetical protein F10D2.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999

C;Accession: T28717

R;Graves, T.; Wohlmann, P.; Gillam, B.

submitted to the EMBL Data Library, September 1997

A;Description: The sequence of C. elegans cosmid F10D2.

A;Reference number: Z20515

A;Accession: T28717

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-495 <GRA>

A;Cross-references: EMBL:AF022972; PIDN:AAC48234.1; GSPDB:GN00023; CESP:F10D2.3

A;Experimental source: strain Bristol N2; clone F10D2

C;Genetics:

A;Gene: CESP:F10D2.3

A;Map position: 5

A;Introns: 37/2; 90/1; 113/1; 183/3; 356/3; 380/3; 428/2

Query Match 65.4%; Score 34; DB 2; Length 495;

Best Local Similarity 50.0%; Pred. No. 36;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXHY 10

Db 218 ENIVPTGKHH 227

RESULT 10

A69284

coenzyme F420-quinone oxidoreductase (EC 1.6.5.-) 56K chain - Archaeoglobus fulgidus

N;Alternate names: sarcosine oxidase alpha chain soxa homolog

C;Species: Archaeoglobus fulgidus

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 19-May-2000

C;Accession: A69284; S45665

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.;

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiaich, P.; Kaine, B.P.; Syk

Smith, H.O.; Woese, C.R.; Venter, J.C.

A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing a

A;Reference number: A69250; MUID:98049343; PMID:9389475

A;Accession: A69284

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-534 <KLE>

A;Cross-references: GB:AE001086; GB:AE000782; NID:g2689409; PIDN:AAB90959.1; PID:g

R;Kunow, J.; Linder, D.; Stetter, K.O.; Thauer, R.K.

Eur. J. Biochem. 223, 503-511, 1994

A;Title: F(420)H(2): quinone oxidoreductase from Archaeoglobus fulgidus. Character

A;Reference number: S45665; MUID:94333340; PMID:8055920

A;Accession: S45665

A;Molecule type: protein

A;Residues: 2,'X',4,'X',6-7,'X',9-10,'XX',13-14 <KUN>

A;Note: the authors could not distinguish between glutamate and cysteine for residu

C;Superfamily: glutamate synthase small chain

C;Keywords: oxidoreductase

Query Match 65.4%; Score 34; DB 2; Length 534;

Best Local Similarity 45.5%; Pred. No. 39;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXHS 11

Db 119 DKVFPXGSHYT 129

C:Accession: T46758
 R:Spellerberg, B.; Rordzinski, E.; Martin, S.; Weber-Heynemann, J.; Schnitzler, N.; Luet
 Infect. Immun. 67, 871-878, 1999
 A:Title: Lmb, a protein with similarities to the Lrai adhesin family, mediates attachment
 A:Reference number: 224091; MUID:99115568; PMID:9916102
 A:Accession: T46758
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-822 <SPE>
 A:Cross-references: EMBL:AF062533; NID:g4249622; PIDN:AAD13797.1; PID:g4249624
 A:Experimental source: strain R268
 C:Superfamily: Streptococcus agalactiae hypothetical 92.4K protein

Query Match 65.4%; Score 34; DB 2; Length 822;
 Best Local Similarity 75.0%; Pred. No. 62;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
 ||| |||
 DB 350 VVPHGDHY 357

RESULT 12
 F89892
 carbamoyl-phosphate synthase large chain [imported] - Staphylococcus aureus (strain N315
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: F89892
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: F89892
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1057 <KUR>
 A:Cross-references: GB:BA000018; PID:g13701002; PIDN:BAB42298.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: pyrAB
 C:Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain; biotin

Query Match 65.48%; Score 34; DB 2; Length 1057;
 Best Local Similarity 60.0%; Pred. No. 81;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVPXGXHY 11
 ||| |||
 DB 190 EIVSNGHY 199

RESULT 13
 E97985
 hypothetical protein spr0909 [imported] - Streptococcus pneumoniae (strain R6)
 C:Species: Streptococcus pneumoniae
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001
 C:Accession: E97985
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A:Reference number: A97872; MUID:21429245; PMID:11544234
 A:Accession: E97985
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-46 <KUR>
 A:Cross-references: GB:AE007317; PIDN:AAK99713.1; PID:g15458516; GSPDB:GN00174
 C:Genetics:
 A:Gene: spr0909

Query Match 63.5%; Score 33; DB 2; Length 46;
 Best Local Similarity 62.5%; Pred. No. 4.5;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
 :|| |||
 DB 21 IVPHGGHY 28

RESULT 14
 VRLJ51
 trans-regulatory splicing protein - simian immunodeficiency virus SIVcpz
 N:Alternate names: anti-repression trans-activator; art protein; rev protein; trs
 C:Species: simian immunodeficiency virus SIVcpz
 A:Note: host Pan troglodytes (Chimpanzee)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
 C:Accession: S09988
 R:Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
 Nature 345, 356-359, 1990
 A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
 A:Reference number: S09983; MUID:90259077; PMID:2188136
 A:Accession: S09988
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-124 <HUE>
 A:Cross-references: EMBL:X52154; NID:g58866; PIDN:CAA36405.1; PID:g763085
 C:Genetics:
 A:Gene: rev; trs; art
 A:Introns: 27/1
 C:Superfamily: AIDS trans-regulatory splicing protein
 C:Keywords: AIDS; immunodeficiency; splicing protein; transcription regulation

Query Match 63.5%; Score 33; DB 1; Length 124;
 Best Local Similarity 60.0%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVPXGXHY 11
 ||| |||
 DB 107 ETVPAGGNY 116

RESULT 15
 D82618
 conserved hypothetical protein XF1950 [imported] - Xylella fastidiosa (strain 9a5c)
 C:Species: Xylella fastidiosa
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
 C:Accession: D82618
 R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide S
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A82515; MUID:20365717; PMID:10910347
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: D82618
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-156 <SIN>
 A:Cross-references: GB:AE004014; GB:AE003849; NID:g9107044; PIDN:AAF84752.1; GSPDB:
 R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga,
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Car
 a-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.;
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.;
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Marti
 A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki,
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sa
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Si
 M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.
 A:Reference number: A59328
 A:Contents: annotation

10

A:Reference number: S38130
A:Accession: S38143
A:Molecule type: DNA
A:Residues: 1-743 <VAN>
A:Cross-references: EMBL:Z28292; NID:g486537; MIPS:YKR0674
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:GPT2
A:Cross-references: SGD:S0001775
A:Map position: 11R
C:Keywords: transmembrane protein

Query Match 63.5%; Score 33; DB 2; Length 743;
Best Local Similarity 75.0%; Pred. No. 91;
Matches 6; Conservative 0; Mismatches 0; Indels 2; Gaps 0;

QY 3 VVPXGXHY 10
||| |
Db 294 VVPCGLHY 301

RESULT 21

C95136
conserved domain protein Sp1175 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: C95136
R:Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzap
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: C95136
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-802 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK75284.1; PID:g14972655; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:
A:Gene: Sp1175
C:Superfamily: Streptococcus agalactiae hypothetical 92.4K protein

Query Match 63.5%; Score 33; DB 2; Length 802;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 1; Mismatches 2; Indels 2; Gaps 0;

QY 3 VVPXGXHY 10
||| |
Db 191 IVPXGDHY 198

RESULT 22

B95136
conserved domain protein Sp1174 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: B95136
R:Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzap
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: B95136
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-819 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK75283.1; PID:g14972654; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:

A:Gene: Sp1174

C:Superfamily: Streptococcus agalactiae hypothetical 92.4K protein

Query Match 63.5%; Score 33; DB 2; Length 819;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
||| |
Db 203 IVPXGDHY 210

RESULT 23

E98004
hypothetical protein phtA [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C:Accession: E98004
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren,
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas,
A:Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A:Reference number: A97872; MUID:21429245; PMID:11544234
A:Accession: E98004
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-828 <KUR>
A:Cross-references: GB:AE007317; PIDN:AAK99865.1; PID:g15458683; GSPDB:GN00174
C:Genetics:
A:Gene: phtA
C:Superfamily: Streptococcus agalactiae hypothetical 92.4K protein

Query Match 63.5%; Score 33; DB 2; Length 828;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
||| |
Db 217 IVPXGDHY 224

RESULT 24

G95115
conserved hypothetical protein SPI003 [imported] - Streptococcus pneumoniae (strain
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001
C:Accession: G95115
R:Tetelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.;
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzap
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A:Reference number: A95000; MUID:21357209; PMID:11463916
A:Accession: G95115
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-839 <KUR>
A:Cross-references: GB:AE005672; PIDN:AAK75120.1; PID:g14972476; GSPDB:GN00164; TIGR:SP4
A:Experimental source: strain TIGR4
C:Genetics:

C:Superfamily: Streptococcus agalactiae hypothetical 92.4K protein

Query Match 63.5%; Score 33; DB 2; Length 839;
Best Local Similarity 62.5%; Pred. No. 1e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
||| |
Db 204 IVPXGDHY 211

RESULT 25

C97985
 hypothetical protein phtD [imported] - Streptococcus pneumoniae (strain R6)
 C:Species: Streptococcus pneumoniae
 C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
 C:Accession: C97985
 R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E
 e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
 y, P.; Sun, P.M.; Winkler, M.E.
 J. Bacteriol. 183, 5709-5717, 2001
 A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
 A:title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A:Reference number: A97872; MUID:21429245; PMID:11544234
 A:Accession: C97985
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-853 <KUR>
 A:Cross-references: GB:AE007317; PIDN:AAK99711.1; PID:g15458514; GSPDB:GN00174
 C:Genetics:
 A:Gene: phtD
 C:Superfamily: Streptococcus agalactiae hypothetical 92.4K protein

Query Match 63.5%; Score 33; DB 2; Length 853;
 Best Local Similarity 62.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
 :|||
 Db 203 IVPHGHHY 210

Search completed: June 10, 2003, 13:49:17
 Job time : 12.2143 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model
Run on: June 10, 2003, 13:25:04 ; Search time 4.5 Seconds
(without alignments)
101.387 Million cell updates/sec

Title: US-09-909-164-44
Perfect score: 52
Sequence: 1 EEWVPGXHYHS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	35	67.3	1058	1	CARB_FUSNN	Q8f986 fusbacteri
2	35	67.3	1396	1	VITF_BPT5	P13390 bacterioph
3	34	65.4	102	1	Y11K_TYDVA	P31619 tobacco yel
4	34	65.4	126	1	TKNK_BOVIN	P08858 bos taurus
5	34	65.4	1057	1	CARB_STAAM	Q99ur5 staphylococ
6	34	65.4	1057	1	CARB_STAAM	P58940 staphylococ
7	33	63.5	124	1	REV_SIVCZ	P17280 chimpanzee
8	33	63.5	460	1	UMEL_YEAST	Q03010 saccharomyc
9	33	63.5	743	1	YK47_YEAST	P36148 saccharomyc
10	32	61.5	308	1	GAAB_METH	O26806 methanobact
11	32	61.5	363	1	ALFB_SHEEP	P52210 ovine aries
12	32	61.5	627	1	MUTL_BACSU	P49850 bacillus su
13	32	61.5	735	1	ETRL_BRAOL	O49230 brassica ol
14	32	61.5	738	1	ETRL_ARATH	P49333 arabidopsis
15	32	61.5	906	1	CNMC_MOUSE	P49452 mus musculu
16	32	61.5	1374	1	Y056_CAEEL	Q09541 caenorhabdi
17	32	61.5	1378	1	RON_MOUSE	O62190 mus musculu
18	31	59.6	130	1	S205_RAT	P97885 rattus norv
19	31	59.6	212	1	MSRA_VIBCH	Q9kp30 vibrio chol
20	31	59.6	319	1	YHAI_CRYPA	P10941 cryptonectr
21	31	59.6	363	1	ALFB_HUMAN	P05062 homo sapien
22	31	59.6	363	1	ALFB_RABIT	P79226 oryctolagus
23	31	59.6	387	1	THIK_ECOLI	P21151 escherichia
24	31	59.6	426	1	SUSL_YARLI	Q99158 yarrowia li
25	31	59.6	427	1	TOLH_HAEIN	P44677 haemophilus
26	31	59.6	991	1	DHP1_SCHPO	P40848 schizosacch
27	31	59.6	1188	1	KPBA_CAEEL	P34335 caenorhabdi
28	31	59.6	1410	1	PDRB_YEAST	P40550 saccharomyc
29	31	59.6	1499	1	A10C_HUMAN	O60312 homo sapien
30	31	59.6	3099	1	POUG_FEMVN	O56075 p genome po
31	30.5	58.7	268	1	ILIA_BOVIN	P08831 bos taurus
32	30.5	58.7	268	1	ILIA_CAPHI	P79161 capra hircu
33	30.5	58.7	268	1	ILIA_SHEEP	Q28579 ovine aries

34	30	57.7	121	1	TKNK_HUMAN	Q9uhf0 homo sapien
35	30	57.7	152	1	Y16D_BPT4	P22917 bacterioph
36	30	57.7	160	1	Y201_METJA	Q57654 methanococc
37	30	57.7	223	1	COAT_CIV36	Q00686 citrus tris
38	30	57.7	232	1	SCOA_HELPJ	Q2le33 helicobacte
39	30	57.7	232	1	SCOA_HELPJ	P56006 helicobacte
40	30	57.7	316	1	COQ3_YEAST	P27680 s hexapreny
41	30	57.7	328	1	ROPA_BORPE	P37368 bordetella
42	30	57.7	353	1	T2BA_BACAR	P19887 bacillus an
43	30	57.7	386	1	T10D_HUMAN	Q9ubn6 homo sapien
44	30	57.7	394	1	NUCC_SYNY3	P27724 synecocyst
45	30	57.7	427	1	TRBI_AERPE	Q9y8t5 aeropyrum p
46	30	57.7	430	1	FOLC_BACSU	Q05865 bacillus su
47	30	57.7	513	1	PHSL_DESBA	P13065 desulfovibr
48	30	57.7	541	1	LNT_CHLPN	Q9z7q1 chlamydia p
49	30	57.7	695	1	VNUC_MABVP	P35263 marburg vir
50	30	57.7	960	1	CSEL_YEAST	P33307 saccharomyc
51	29.5	56.7	526	1	NADB_MYCLE	Q49617 mycobacteri
52	29.5	56.7	527	1	NADB_MYCTU	O06595 mycobacteri
53	29.5	56.7	847	1	CD22_HUMAN	P20273 homo sapien
54	29	55.8	223	1	Y864_THEVO	Q97ae6 thermoplas
55	29	55.8	224	1	Y764_THEAC	Q9hk42 thermoplas
56	29	55.8	227	1	ID11_MESAU	O35586 mesocricetu
57	29	55.8	231	1	FLGH_PSEPU	Q52081 pseudomonas
58	29	55.8	238	1	GLO2_HAEIN	P1374 haemophilus
59	29	55.8	242	1	PSB4_XENLA	P28024 xenopus lae
60	29	55.8	263	1	CANS_BOVIN	P31335 bos taurus
61	29	55.8	285	1	IF2A_PYRAE	Q82ty5 pyrobaculum
62	29	55.8	276	1	PRXC_SYNY3	Q55921 synecocyst
63	29	55.8	293	1	YD11_METJA	Q58707 methanococc
64	29	55.8	341	1	HYPE_AZQVI	P04595 azotobacter
65	29	55.8	354	1	VGLI_VZVD	P09258 varicella-z
66	29	55.8	360	1	ALF_DROME	P07664 drosophila
67	29	55.8	363	1	ALFB_CHICK	P07341 gallus gall
68	29	55.8	363	1	ALFB_RAT	P00684 rattus norv
69	29	55.8	363	1	ALF_SCHMA	P53442 schistosoma
70	29	55.8	394	1	MNN9_YEAST	P39107 saccharomyc
71	29	55.8	404	1	YJ9N_YEAST	P47177 saccharomyc
72	29	55.8	421	1	ACDM_HUMAN	P11310 homo sapien
73	29	55.8	421	1	ACDM_PIG	P41367 sus scrofa
74	29	55.8	450	1	Y325_HAEIN	P44640 haemophilus
75	29	55.8	471	1	TMLH_NEUCR	Q96ub1 neurospora

ALIGNMENTS

RESULT 1		STANDARD:		PRT: 1058 AA.	
CARB_FUSNN		CARB_FUSNN		ID	
AC		Q8RG86:		AC	
DT		15-JUN-2002 (Rel. 41, Created)		DT	
DT		15-JUN-2002 (Rel. 41, Last sequence update)		DT	
DE		15-JUN-2002 (Rel. 41, Last annotation update)		DE	
DE		Carbamoyl-phosphatase synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain)		DE	
GN		CARB OR FN0422.		GN	
OS		Fusobacterium nucleatum (subsp. nucleatum).		OS	
OC		Bacteria; Fusobacteria; Fusobacterium.		OC	
OX		NCBI_TaxID=76856;		OX	
RN		[1]		RN	
RP		SEQUENCE FROM N.A.		RP	
RC		MEDLINE-21886394; PubMed-11889109;		RC	
RX		Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chou L., Kogan Y., Chaga O., Goltzman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyripides N., Overbeek R.;		RX	
RA		Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586.		RA	
RT		J. Bacteriol. 184:2005-2018(2002).		RT	
RL		-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O -> 2 ADP +		RL	
CC				CC	

phosphate + L-glutamate + carbamoyl phosphate.
 -1- COFACTOR: Binds three manganese ions (By similarity).
 -1- PATHWAY: Arginine biosynthesis.
 -1- PATHWAY: Pyrimidine biosynthesis; first step.
 -1- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).
 -1- SIMILARITY: BELONGS TO THE CARB FAMILY.

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EMBL; AE010554; AAL94625.1; ALT_INIT.
 InterPro; IPR005483; CPase_L.
 InterPro; IPR005479; CPase_L_D2.
 InterPro; IPR005480; CPase_L_D3.
 InterPro; IPR005481; CPase_L_N.
 InterPro; IPR004362; MGS_like.
 Pfam; PF00289; CPase_L_chain; 2.
 Pfam; PF02786; CPase_L_D2; 2.
 Pfam; PF02787; CPase_L_D3; 1.
 Pfam; PF02142; MGS; 1.
 PRINTS; PR00098; CPASE.
 PROSITE; PS00866; CPASE_1; 2.
 PROSITE; PS00867; CPASE_2; 2.
 Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
 ATP-binding; Manganese; Complete proteome.
 FT DOMAIN 1 401 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
 FT DOMAIN 402 546 OLIGOMERIZATION DOMAIN.
 FT DOMAIN 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
 FT DOMAIN 930 1058 ALLOSTERIC DOMAIN.
 FT REPEAT 1 546
 FT REPEAT 547 1058
 FT NP_BIND 153 210 ATP (POTENTIAL).
 FT NP_BIND 302 352 ATP (POTENTIAL).
 FT METAL 284 284 MANGANESE 1 (BY SIMILARITY).
 FT METAL 298 298 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 300 300 MANGANESE 2 (BY SIMILARITY).
 FT METAL 820 820 MANGANESE 3 (BY SIMILARITY).
 FT METAL 832 832 MANGANESE 3 (BY SIMILARITY).
 SQ SEQUENCE 1058 AA; 117451 MW; ED7037AF77C1E39F CRC64;

Query Match 67.3%; Score 35; DB 1; Length 1058;
 Best Local Similarity 60.0%; Pred. No. 20;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGXHYS 11
 Db 190 EIVPGLNYS 199

RESULT 2
 VLTF_BPT5 STANDARD; PRT; 1396 AA.
 AC P13390; O48502;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE L-shaped tail fiber protein (LTF protein).
 GN LTF.
 OS Bacteriophage T5.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
 OC T5-like viruses.
 OX NCBI_TaxID=10726;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95309401; PubMed=7789514;

Kallman A.V., Kulshin V.E., Shlyapnikov M.G., Ksenzenko V.N.,
 RA Kryukov V.M.;
 RA "The nucleotide sequence of the bacteriophage T5 ltf gene.";
 RT FEBS Lett. 366:46-48(1995).
 RL [2]
 RN SEQUENCE FROM N.A.
 RP Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RA Kallman A.V.;
 RL [3]
 RN PRELIMINARY PARTIAL SEQUENCE FROM N.A.
 RX MEDLINE=88289370; PubMed=3267228;
 RA Kallman A.V., Kryukov V.M., Bayev A.A.;
 RT "The nucleotide sequence of bacteriophage T5 DNA at the region
 RT between early and late genes.";
 RL Nucleic Acids Res. 16:6230-6230(1988).
 CC -1- FUNCTION: NONESSENTIAL PROTEIN THAT MEDIATES BINDING TO THE
 CC POLYMANNOSE O ANTIGEN.
 CC -----
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 CC -----

EMBL; X69460; CAA49220.1; -
 DR EMBL; AJ001191; CAA04591.1; -
 DR PIR; S01982; S01982.
 KW Late protein.
 FT CONFLICT 986
 FT SEQUENCE 1396 AA; 147989 MW; 18CD2192FG5FFFC1 CRC64;
 SQ

Query Match 67.3%; Score 35; DB 1; Length 1396;
 Best Local Similarity 50.0%; Pred. No. 26;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVPXGXHYS 11
 Db 1360 KTIAPGDHYS 1369

RESULT 3
 YLIK_TYDVA STANDARD; PRT; 102 AA.
 ID P31619;
 AC P31619;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE Hypothetical 11.2 kDa protein.
 GN VI.
 OS Tobacco yellow dwarf virus (strain Australia) (TYDV).
 OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
 OX NCBI_TaxID=31599;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92188538; PubMed=1546458;
 RA Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
 RT "The nucleotide sequence of the infectious cloned DNA component of
 RT tobacco yellow dwarf virus reveals features of geminiviruses
 RT infecting monocotyledonous plants.";
 RL Virology 187:633-642(1992).
 CC -----
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 CC -----

EMBL; M81103; AAA47947.1; -
 DR PIR; A42452; A42452.


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FT REPEAT      547 1057
FT NP_BIND     153 210
FT NP_BIND     302 352
FT METAL       284 284
FT METAL       284 284
FT METAL       298 298
FT METAL       300 300
FT METAL       820 820
FT METAL       832 832
FT METAL       832 832
SQ SEQUENCE    1057 AA; 117171 MW; E3E179EF0591F0F8 CRC64;

Query Match      65.4%; Score 34; DB 1; Length 1057;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVPXGXHYS 11
   |:| |::|
Db 190 EIVSNGLHYS 199

RESULT 6
CARB_STAAR
ID CARB_STAAR STANDARD; PRT; 1057 AA.
AC P58940;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-
DE phosphate synthetase ammonia chain).
GN CARB OR PYRAB OR MW1086.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamanoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA";
RL Lancet 359:1819-1827(2002).
CC -|- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +
CC phosphate + L-glutamate + carbamoyl phosphate
CC -|- COFACTOR: Binds three manganese ions (By similarity).
CC -|- PATHWAY: Arginine biosynthesis; first step.
CC -|- SUBUNIT: Composed of two chains; the small (or glutamine) chain
CC promotes the hydrolysis of glutamine to ammonia, which is used by
CC the large (or ammonia) chain to synthesize carbamoyl phosphate (By
CC similarity).
CC -|- SIMILARITY: BELONGS TO THE CARB FAMILY.
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-----
EMBL; AP0084825; BAB94951.1; -.
DR PROSITE; PS00866; CPSASE.1; 2.
DR PROSITE; PS00867; CPSASE.2; 2.
KW Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
KW ATP-binding; Manganese.
FT DOMAIN 1 401 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
FT DOMAIN 402 546 OLIGOMERIZATION DOMAIN.
FT DOMAIN 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
FT DOMAIN 930 1057 ALLOSTERIC DOMAIN.
FT REPEAT 1 546
FT REPEAT 547 1057
FT NP_BIND 153 210 ATP (POTENTIAL).
FT NP_BIND 302 352 ATP (POTENTIAL).

```

```

FT METAL       284 284 MANGANESE 1 (BY SIMILARITY).
FT METAL       298 298 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL       300 300 MANGANESE 2 (BY SIMILARITY).
FT METAL       820 820 MANGANESE 3 (BY SIMILARITY).
FT METAL       832 832 MANGANESE 3 (BY SIMILARITY).
FT METAL       832 832 MANGANESE 3 (BY SIMILARITY).
SQ SEQUENCE    1057 AA; 117185 MW; DBE3B09F9BC6F152 CRC64;

Query Match      65.4%; Score 34; DB 1; Length 1057;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVPXGXHYS 11
   |:| |::|
Db 190 EIVSNGLHYS 199

RESULT 7
REV_SIVCZ
ID REV_SIVCZ STANDARD; PRT; 124 AA.
AC P17280;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE REV Protein (Anti-repression transactivator protein) (ART/TRS).
GN REV.
OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11723;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90259077; PubMed=2188136;
RA Huet T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
RT "Genetic organization of a chimpanzee lentivirus related to HIV-1.";
RL Nature 345:356-359(1990).
CC -|- FUNCTION: REV APPEARS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE
CC NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.
CC -|- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.
CC -|- PTM: PHOSPHOPROTEIN WHOSE STATE OF PHOSPHORYLATION IS MEDIATED
CC BY A SPECIFIC SERINE KINASE ACTIVITY PRESENT IN THE NUCLEUS.
-----
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-----
EMBL; X52154; CAA36405.1; -.
DR PIR; S09988; VKLJS1.
DR HIV; X52154; REVSCPZ.
DR InterPro; IPR000625; REV_protein.
DR Pfam; PF00424; REV; 1.
KW Transcription regulation; AIDS; Phosphorylation; Nuclear protein.
SQ SEQUENCE    124 AA; 13701 MW; F5877D1BDF65A7B2 CRC64;

Query Match      63.5%; Score 33; DB 1; Length 124;
Best Local Similarity 60.0%; Pred. No. 5.5;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVPXGXHYS 11
   |:| |::|
Db 107 ETVPAGGNYS 116

RESULT 8
UMEL_YEAST
ID UMEL_YEAST STANDARD; PRT; 460 AA.
AC Q03010; P87330;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Melosis negative regulator UMEL.

```


RT deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 CC -1- CATALYTIC ACTIVITY: ATP + xanthosine 5'-phosphate + L-glutamine +
 CC H(2)O = AMP + diphosphate + GMP + L-glutamate.
 CC -1- PATHWAY: GMP biosynthesis.
 CC -1- SUBUNIT: HETERODIMER COMPOSED OF A GLUTAMINE AMIDOTRANSFERASE
 CC SUBUNIT (A) AND A GMP SYNTHASE SUBUNIT (B) (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE GMP SYNTHASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AE00850; AAB85215.1; ALT_INIT.
 CC HSSP; P04079; IGP.
 CC InterPro: IPR001674; GMP_synt_C.
 CC Pfam; PF00958; GMP_synt_C; 1.
 CC TIGRfams; TIGR00884; guaA_Cterm; 1.
 CC Ligase; GMP biosynthesis; Purine biosynthesis; ATP-binding;
 CC Complete proteome.
 CC FT DOMAIN 33 184 GMP-BINDING (BY SIMILARITY).
 CC FT NP_BIND 29 35 ATP (BY SIMILARITY).
 CC SEQUENCE 308 AA; 34403 MW; F2DCFOED202CAEC1 CRC64;
 CC -----
 CC Query Match 61.5%; Score 32; DB 1; Length 308;
 CC Best Local Similarity 63.6%; Pred. No. 23;
 CC Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 CC -----
 CC QY 1 EFWPVGXHYIS 11
 CC ||||| | | | |
 CC DB 216 EYVESGLHRS 226
 CC -----
 CC RESULT 11
 CC ALPB_SHEEP
 CC ID ALPB_SHEEP STANDARD; PRT; 363 AA.
 CC AC P52210;
 CC DT 01-OCT-1996 (Rel. 34, Created)
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Fructose-bisphosphate aldolase B (EC 4.1.2.13) (Liver-type aldolase).
 CC GN ALDOB.
 CC OS Ovis aries (Sheep).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC OC Bovidae; Caprinae; Ovis.
 CC OX NCBI_TaxID=9940;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Mesonephros;
 CC RX MEDLINE=94368863; PubMed=8086469;
 CC RA Giallanto L., Pailhoux E.A., Bezard J., Servel N., Kirzenbaum M.,
 CC RA Cotinot C.;
 CC RT "Cloning and characterization of a full-length cDNA coding for ovine
 CC aldolase B from fetal mesonephros.";
 CC RL Biochim. Biophys. Acta 1219:223-227(1994).
 CC CC -1- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycero-
 CC phosphate + D-glyceraldehyde 3-phosphate.
 CC CC -1- PATHWAY: Glycolysis; sixth step.
 CC CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC CC -1- MISCELLANEOUS: IN VERTEBRATES, THREE FORMS OF THIS UBIQUITOUS
 CC GLYCOLYTIC ENZYME ARE FOUND, ALDOLASE A IN MUSCLE, ALDOLASE B IN
 CC LIVER, & ALDOLASE C IN BRAIN.
 CC CC -1- SIMILARITY: BELONGS TO CLASS I FRUCTOSE-BISPHOSPHATE ALDOLASE
 CC FAMILY.
 CC -----
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 CC -----
 CC EMBL; Z29372; CAA82563.1; -.
 CC HSSP; P00883; IADO.
 CC InterPro: IPR000741; Aldolase_I.
 CC Pfam; PF00274; glycolytic_enz; 1.
 CC ProDom; PD001128; Aldolase_I; 1.
 CC PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
 CC KW Lyase; Schiff base; Glycolysis; Multigene family.
 CC FT INIT_MET 0 0 BY SIMILARITY.
 CC FT BINDING 55 55 C-1-PHOSPHATE GROUP OF THE SUBSTRATE.
 CC FT BINDING 146 146 C-1-PHOSPHATE GROUP OF THE SUBSTRATE.
 CC FT BINDING 229 229 SCHIFF-BASE WITH DIHYDROXYACETONE-P.
 CC FT ACT_SITE 363 363 ESSENTIAL FOR ENHANCED ACTIVITY OF THE
 CC ENZYME TOWARD FRUCTOSE 1,6-BISPHOSPHATE.
 CC FT AS COMPARED WITH FRUCTOSE 1-PHOSPHATE.
 CC SQ SEQUENCE 363 AA; 39500 MW; FC8B4566821E2BD CRC64;
 CC -----
 CC Query Match 61.5%; Score 32; DB 1; Length 363;
 CC Best Local Similarity 62.5%; Pred. No. 28;
 CC Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 CC -----
 CC QY 2 EWPVGXGH 9
 CC ||| | | | |
 CC DB 189 EVIDPGSH 196
 CC -----
 CC RESULT 12
 CC MUTL_BACSU
 CC ID MUTL_BACSU STANDARD; PRT; 627 AA.
 CC AC P49850;
 CC DT 01-OCT-1996 (Rel. 34, Created)
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE DNA mismatch repair protein mutL.
 CC GN MUTL.
 CC OS Bacillus subtilis.
 CC OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CC OX NCBI_TaxID=1423;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=168;
 CC RX MEDLINE=96349107; PubMed=8760914;
 CC RA Ginetti F., Perego M., Albertini A.M., Galizzi A.;
 CC RT "Bacillus subtilis mutL operon: identification, nucleotide
 CC sequence and mutagenesis.";
 CC RL Microbiology 142:2021-2029(1996).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=168;
 CC RX MEDLINE=98044033; PubMed=9384377;
 CC RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 CC RA Avevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 CC RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 CC RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 CC RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 CC RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 CC RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 CC RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 CC RA Gim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 CC RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 CC RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
 CC RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 CC RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 CC RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 CC RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 CC RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 CC RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 CC RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 CC RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,

RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenberg M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
 RT *subtilis*.";
 RL Nature 390:249-256(1997).
 CC -1- FUNCTION: THIS PROTEIN IS INVOLVED IN THE REPAIR OF MISMATCHES IN
 CC DNA. IT IS REQUIRED FOR DAM-DEPENDENT METHYL-DIRECTED DNA MISMATCH
 CC REPAIR. MAY ACT AS A "MOLECULAR MATCHMAKER". A PROTEIN THAT
 CC PROMOTES THE FORMATION OF A STABLE COMPLEX BETWEEN TWO OR MORE
 CC DNA-BINDING PROTEINS IN AN ATP-DEPENDENT MANNER WITHOUT ITSELF
 CC BEING PART OF A FINAL EFFECTOR COMPLEX (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTL/HEXB FAMILY.
 CC -----
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 CC -----
 CC EMBL: U7343; AAB19236.1; -;
 DR EMBL: Z99112; CAB13578.1; -;
 DR HSP: P23367; IBKN.
 DR Subtilist; BG11402; mutL.
 DR InterPro: IPR003594; ATPbind_ATPase.
 DR InterPro: IPR002099; DNA_mis_repair.
 DR InterPro: IPR004359; HIS_KIN_sig.
 DR Pfam: PF02518; HATPase_c; 1.
 DR Pfam: PF01590; GAF; 1.
 DR TIGRams: TIGR00585; mutL; 1.
 DR PROSITE: PS00058; DNA_MISMATCH_REPAIR_1; 1.
 DR DNA repair; Complete proteome.
 KW SEQUENCE 627 AA; 70431 MW; 068A0509CC265343 CRC64;
 SQ
 Query Match 61.5%; Score 32; DB 1; Length 627;
 Best Local Similarity 54.5%; Pred. No. 49;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EEVVPXGXHY 11
 | : || |||
 DB 488 EMIVPLTFHY 498
 RESULT 13
 ETR1_BRAOL STANDARD; PRT; 735 AA.
 ID ETR1_BRAOL
 AC 049230;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ethylene receptor (EC 2.7.3.-).
 GN ETR1.
 OS Brassica oleracea (Cauliflower).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Brassica.
 OX NCBI_TaxID=3712;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98344657; PubMed=9687267;
 RA Chen H.-H., Chong Y.-Y., Yang S.F., Shaw J.-F.;
 RT "Molecular cloning and sequencing of a broccoli cDNA encoding an ETR-
 RT type ethylene receptor.";
 RL (in) Plant Gene Register PGR98-088.
 CC -1- FUNCTION: May act early in the ethylene signal transduction

CC pathway, possibly as an ethylene receptor, or as a regulator of
 CC the pathway (By similarity).
 CC -1- COFACTOR: Binds 1 copper ion per dimer (By similarity).
 CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum (By similarity).
 CC -1- PTM: Activation probably requires a transfer of a phosphate group
 CC between a His in the transmitter domain and a Asp of the receiver
 CC domain (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE ETHYLENE RECEPTOR FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
 CC -----
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 CC -----
 CC EMBL: AF047476; AAC39497.1; -;
 DR InterPro: IPR003594; ATPbind_ATPase.
 DR InterPro: IPR003018; GAF.
 DR InterPro: IPR003661; His_KinA.
 DR InterPro: IPR004359; HIS_KIN_sig.
 DR InterPro: IPR001789; Response_reg.
 DR Pfam: PF01590; GAF; 1.
 DR Pfam: PF02518; HATPase_c; 1.
 DR Pfam: PF00072; response_reg; 1.
 DR Pfam: PF00512; signal; 1.
 DR ProDom: PD000039; Response_reg; 1.
 DR SMART: SM00065; GAF; 1.
 DR SMART: SM00387; HATPase_c; 1.
 DR SMART: SM00388; HisKA; 1.
 DR SMART: SM00448; REC; 1.
 DR PROSITE: PS0109; HIS_KIN; 1.
 DR PROSITE: PS0110; RESPONSE_REGULATORY; 1.
 DR Receptor; Sensory transduction; Phosphorylation; Transmembrane;
 KW Transferase; Kinase; Copper; Metal-binding
 FT DOMAIN 350 586 HISTIDINE KINASE.
 FT DOMAIN 609 726 RESPONSE REGULATORY.
 FT TRANSMEM 23 43 POTENTIAL.
 FT TRANSMEM 54 74 POTENTIAL.
 FT TRANSMEM 92 112 POTENTIAL.
 FT METAL 65 65 COPPER (BY SIMILARITY).
 FT METAL 69 69 COPPER (BY SIMILARITY).
 FT DISULFID 4 4 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 6 6 INTERCHAIN (BY SIMILARITY).
 FT MOD_RES 353 353 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 657 657 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 735 AA; 82240 MW; 520B77291CF2BCC6 CRC64;
 Query Match 61.5%; Score 32; DB 1; Length 735;
 Best Local Similarity 62.5%; Pred. No. 58;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 VVPXGXHY 10
 ||| | |
 DB 499 VVPTGSHF 506
 RESULT 14
 ETR1_ARATH STANDARD; PRT; 738 AA.
 ID ETR1_ARATH
 AC P49333;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Ethylene receptor (EC 2.7.3.-).
 GN ETR1 OR AT1G66340 OR T27F4.9.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

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```
CC EMBL; X74736; CA52754.1; -.
CC EMBL; U65949; AAC39953.1; -.
CC HSSP; P11362; IFGK.
CC MGD; MGI:99614; Mst1r.
CC InterPro; IPR000719; Euk_pkinase.
CC InterPro; IPR002909; IPT_TIG.
CC InterPro; IPR00165; Plexin_repeat.
CC InterPro; IPR001627; Sema.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC InterPro; IPR001245; Tyr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC Pfam; PF01403; Sema; 1.
CC Pfam; PF01437; PSI; 1.
CC Pfam; PF01833; TIG; 3.
CC ProDom; PD000001; Euk_pkinase; 1.
CC SMART; SM00220; S_TKC; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
CC Transferrase; Tyrosine-protein kinase; Receptor; Transmembrane;
CC Glycoprotein; Signal; Phosphorylation; ATP-binding.
CC SIGNAL 1 23
CC CHAIN 24 1378
CC CHAIN 25 305
CC CHAIN 311 1378
CC DOMAIN 25 960
CC TRANSMEM 961 981
CC DOMAIN 982 1378
CC DOMAIN 60 509
CC DOMAIN 1059 1322
CC NP_BIND 1065 1073
CC BINDING 1091 1091
CC ACT_SITE 1185 1185
CC MOD_RES 1330 1330
CC MOD_RES 1337 1337
CC CARBOHYD 91 91
CC CARBOHYD 391 391
CC CARBOHYD 460 460
CC CARBOHYD 490 490
CC CARBOHYD 656 656
CC CARBOHYD 722 722
CC CARBOHYD 845 845
CC CARBOHYD 901 901
CC CONFLICT 713 714
CC CONFLICT 719 719
CC SEQUENCE 1378 AA; 150538 MW; FC5P932377B57009 CRC64;
Query Match 61.5%; Score 32; DB 1; Length 1378;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 EEVVPXGXH 9
DB 601 DDVPEGTH 609
RESULT 18
SZ05_RAT SZ05_RAT STANDARD; PRT; 130 AA.
AC P97855;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Small inducible cytokine B5 precursor (CXCL5) (Cytokine LIX).
GN SCYB5.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
CC NCBI_TaxID=101116;
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CC SEQUENCE FROM N.A.
CC STRAIN-Sprague-Dawley;
CC Kelnor G.S., Maciejewski-Lenoir D., Lee E.D., Maki R.A.;
CC Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY PARTICIPATE IN THE RECRUITMENT OF INFLAMMATORY CELLS
CC BY INJURED OR INFECTED TISSUE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
CC
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EMBL; U90448; AAB61460.1; -.
HSSP; P10889; IMI2.
InterPro; IPR001089; CXC_chemokine_sml.
InterPro; IPR001811; Chemokine_IL8.
Pfam; PF00048; IL8; 1.
PRINTS; PR00437; SMALLCYTCKXC.
SMART; SM00199; SCY; 1.
PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW CYTOKINE; Signal.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 130 SMALL INDUCIBLE CYTOKINE B5.
FT DISULFID 50 76 BY SIMILARITY.
FT DISULFID 52 93 BY SIMILARITY.
SQ SEQUENCE 130 AA; 14263 MW; C00F6B3605524F4E CRC64;
Query Match 59.6%; Score 31; DB 1; Length 130;
Best Local Similarity 62.5%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 EVVPXGXH 9
DB 68 EVIPAGPH 75
RESULT 19
MSRA_VIBCH STANDARD; PRT; 212 AA.
ID MSRA_VIBCH AC Q9KP30;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Peptide methionine sulfoxide reductase msra (EC 1.8.4.6) (Protein-
DE methionine-S-oxide reductase) (Peptide Met(O) reductase).
GN MSRA OR VC2549.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
CC NCBI_TaxID=686;
CC
CC SEQUENCE FROM N.A.
CC STRAIN=El Tor N16961 / Serotype O1;
CC MEDLINE=20406833; PubMed=10952301;
CC Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
CC Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
CC Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
CC Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
CC McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
CC Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
CC Fraser C.M.;
CC "DNA sequence of both chromosomes of the cholera pathogen Vibrio
CC cholerae";
CC Nature 406:477-483(2000).
CC -!- FUNCTION: Has an important function as a repair enzyme for
CC proteins that have been inactivated by oxidation. Catalyzes the
CC reversible oxidation-reduction of methionine sulfoxide in proteins
CC to methionine (By similarity).


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CC -1- CATALYTIC ACTIVITY: Protein L-methionine + oxidized thioredoxin =
 CC protein L-methionine S-oxide + reduced thioredoxin.
 CC -1- SIMILARITY: BELONGS TO THE MSRA MET SULFOXIDE REDUCTASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; AE004324; AAF95690.1; -
 CC HGSP; P54149; 1FVA.
 CC TIGR; VC2549; -
 CC InterPro; IPR002569; PMSR.
 CC Pfam; PF01625; PMSR; 1.
 CC ProDom; PD003489; PMSR; 1.
 CC TIGRFAMs; TIGR00401; msrA; 1.
 CC OXfoldreductase; Complete proteome.
 CC ACT_SITE 51 51 BY SIMILARITY.
 CC SEQUENCE 212 AA; 23360 MW; AD50686E8BFF13016 CRC64;
 CC
 CC Query Match 59.6%; Score 31; DB 1; Length 212;
 CC Best Local Similarity 44.4%; Pred. No. 26;
 CC Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 CC
 CC QY 2 EVVPGXHY 10
 CC |::| |:
 CC 171 EILPAGAYY 179
 CC
 CC DB
 CC
 CC RESULT 20
 CC YHAI_CRYPA STANDARD; PRT; 319 AA.
 CC ID YHAI_CRYPA
 CC AC P10941;
 CC DT 01-JUL-1989 (Rel. 11, Created)
 CC DT 01-JUL-1989 (Rel. 11, Last sequence update)
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
 CC DE Hypothetical protein 1 in hypovirulence-associated DS-RNA genetic
 CC element [contains: P29 proteinase].
 CC OS Cryphonectria parasitica (Chestnut blight fungus) (Endothia
 CC parasitica).
 CC OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC OC Diaporthales; Valsaceae; Cryphonectria.
 CC OX NCBI_TaxID=5116;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=EP713;
 CC RX MEDLINE=89251594; PubMed=2721496;
 CC RA Rae B.P., Hillman B.I., Tartaglia J., Nuss D.L.;
 CC RT "Characterization of double-stranded RNA genetic elements associated
 CC with biological control of chestnut blight: organization of terminal
 CC domains and identification of gene products.";
 CC RL EMBO J. 8:657-663(1989).
 CC CC -1- MISCELLANEOUS: DOUBLE-STRANDED RNA GENETIC ELEMENTS ARE ASSOCIATED
 CC WITH BIOLOGICAL CONTROL OF THE FUNGAL DISEASE CHESTNUT BLIGHT.
 CC THIS DS-RNA ARE ASSOCIATED WITH HYPOVIRULENCE. THEY ARE LOCALIZED
 CC IN THE CYTOPLASM.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C7.
 CC -----
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 CC -----
 CC EMBL; X14524; CAA32666.1; -
 CC PIR; S03833; S03833.
 CC MEROPS; C07.001; -
 CC InterPro; IPR002704; Peptidase_C7.

DR Pfam; PF01830; Peptidase_C7; 1.
 DR ProDom; PD040949; Peptidase_C7; 1.
 KW Hypothetical protein; Hydrolase; Thiol protease.
 SQ SEQUENCE 319 AA; 35443 MW; A1F5F775F9ACE7A CRC64;
 CC
 CC Query Match 59.6%; Score 31; DB 1; Length 319;
 CC Best Local Similarity 85.7%; Pred. No. 40;
 CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC QY 1 EEVVPXG 7
 CC |::| |:
 CC 31 EEVVPAG 37
 CC
 CC DB
 CC
 CC RESULT 21
 CC ALPB_HUMAN STANDARD; PRT; 363 AA.
 CC ID ALPB_HUMAN
 CC AC P05062; Q13741; Q13742;
 CC DT 13-AUG-1987 (Rel. 05, Created)
 CC DT 13-AUG-1987 (Rel. 05, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Fructose-bisphosphate aldolase B (EC 4.1.2.13) (Liver-type aldolase).
 CC GN ALDOB OR ALDB.
 CC OS Homo sapiens (Human).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC OX NCBI_TaxID=9606;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=85037920; PubMed=6548561;
 CC RA Paolella G., Santamaria R., Izso P., Costanzo P., Salvatore F.;
 CC RT "Isolation and nucleotide sequence of a full-length cDNA coding for
 CC aldolase B from human liver.";
 CC RL Nucleic Acids Res. 12:7401-7410(1984).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=85269627; PubMed=2410860;
 CC RA Sakakibara M., Mukai T., Yatsuki H., Hori K.;
 CC RT "Human aldolase isozyme gene: the structure of multispecies aldolase
 CC B mRNAs.";
 CC RL Nucleic Acids Res. 13:5055-5069(1985).
 CC RN [3]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=84194081; PubMed=6585824;
 CC RA Rottmann W.H., Toland D.R., Penhoet E.E.;
 CC RT "Complete amino acid sequence for human aldolase B derived from cDNA
 CC and genomic clones.";
 CC RL Proc. Natl. Acad. Sci. U.S.A. 81:2738-2742(1984).
 CC RN [4]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=88139255; PubMed=2830249;
 CC RA Mukai T., Yatsuki H., Arai Y., Joh K., Matsuhashi S., Hori K.;
 CC RT "Human aldolase B gene: characterization of the genomic aldolase B
 CC gene and analysis of sequences required for multiple
 CC polyadenylations.";
 CC RL J. Biochem. 102:1043-1051(1987).
 CC RN [5]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=86284198; PubMed=3016456;
 CC RA Toland D.R., Penhoet E.E.;
 CC RT "Characterization of the human aldolase B gene.";
 CC RL Mol. Biol. Med. 3:245-264(1986).
 CC RN [6]
 CC RP SEQUENCE OF 238-364 FROM N.A.
 CC RX MEDLINE=84104270; PubMed=6689266;
 CC RA Besmond C., Dreyfus J.-C., Gregori C., Frain M., Zakim M.M.,
 CC RA Sala Trepat J., Kahn A.;
 CC RT "Nucleotide sequence of a cDNA clone for human aldolase B.";
 CC RL Biochem. Biophys. Res. Commun. 117:601-609(1983).
 CC RN [7]
 CC RP REVIEW ON VARIANTS.
 CC RX MEDLINE=96121610; PubMed=8535439;
 CC RA Toland D.R.;

RT "Molecular basis of hereditary fructose intolerance: mutations and polymorphisms in the human aldolase B gene.";

RL Hum. Mutat. 6:210-218(1995).

RN [8]

RP VARIANT HFI.

RX MEDLINE-88253408; PubMed-3383242;

RA Cross N.C.P., Tolan D.R., Cox T.M.;

RT "Catalytic deficiency of human aldolase B in hereditary fructose intolerance caused by a common missense mutation.";

RL Cell 53:881-885(1988).

RN [9]

RP VARIANT HFI.

RX MEDLINE-90135738; PubMed-1967768;

RA Cross N.C.P., de Franchis R., Sebastio G., Dazzo C., Tolan D.R.,

RA Gregori C., Odievre M., Vidailhet M., Romano V., Mascali G.,

RA Romano C., Musumeci S., Steinmann B., Gitzelmann R., Cox T.;

RT "Molecular analysis of aldolase B genes in hereditary fructose intolerance.";

RL Lancet 335:306-309(1990).

RN [10]

RP VARIANT HFI ARG-134.

RX MEDLINE-94131206; PubMed-8299883;

RA Brooks C.C., Tolan D.R.;

RT "A partially active mutant aldolase B from a patient with hereditary fructose intolerance.";

RL FASEB J. 8:107-113(1994).

RN [11]

RP VARIANT HFI ARG-147.

RX MEDLINE-95233426; PubMed-7717389;

RA Ali M., Cox T.M.;

RT "Diverse mutations in the aldolase B gene that underlie the prevalence of hereditary fructose intolerance.";

RL Am. J. Hum. Genet. 56:1002-1005(1995).

RN [12]

RP VARIANT HFI PRO-256.

RX MEDLINE-94214447; PubMed-8162030;

RA Ali M., Sebastio G., Cox T.M.;

RT "Identification of a novel mutation (Leu 256->Pro) in the human aldolase B gene associated with hereditary fructose intolerance.";

RL Hum. Mol. Genet. 3:203-204(1994).

RN [13]

RP VARIANT HFI LYS-334.

RX MEDLINE-90245619; PubMed-2336380;

RA Cross N.C.P., Stojanov L.M., Cox T.M.;

RT "A new aldolase B variant, N334K, is a common cause of hereditary fructose intolerance in Yugoslavia.";

RL Nucleic Acids Res. 18:1925-1925(1990).

CC -1- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glyceralone phosphate + D-glyceraldehyde 3-phosphate.

CC -1- PATHWAY: glycolysis; sixth step.

CC -1- SUBUNIT: HOMOTETRAMER.

CC -1- DISEASE: DEFECTS IN ALDOB ARE THE CAUSE OF HEREDITARY FRUCTOSE INTOLERANCE (HFI); AN AUTOSOMAL RECESSIVE DISEASE THAT RESULTS IN AN INABILITY TO METABOLIZE FRUCTOSE AND RELATED SUGARS. COMPLETE EXCLUSION OF FRUCTOSE RESULTS IN DRAMATIC RECOVERY; HOWEVER, IF NOT TREATED PROPERLY, HFI SUBJECTS SUFFER EPISODES OF HYPOGLYCEMIA, GENERAL ILL HEALTH, AND RISK OF DEATH THE REMAINDER OF LIFE.

CC -1- MISCELLANEOUS: IN VERTEBRATES, THREE FORMS OF THIS UBIQUITOUS GLYCOLYTIC ENZYME ARE FOUND, ALDOLASE A IN MUSCLE, ALDOLASE B IN LIVER, & ALDOLASE C IN BRAIN.

CC -1- SIMILARITY: BELONGS TO CLASS I FRUCTOSE-BISPHOSPHATE ALDOLASE FAMILY.

CC -----

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CC -----

CC EMBL; X02747; CAA26526.1; .

DR EMBL; X01098; CAA25572.1; .

DR EMBL; K01177; AAB59377.1; .

DR EMBL; D00183; BAA00125.1; .

DR EMBL; D00176; BAA00125.1; JOINED.

DR EMBL; D00177; BAA00125.1; JOINED.

DR EMBL; D00178; BAA00125.1; JOINED.

DR EMBL; D00179; BAA00125.1; JOINED.

DR EMBL; D00180; BAA00125.1; JOINED.

DR EMBL; D00181; BAA00125.1; JOINED.

DR EMBL; D00182; BAA00125.1; JOINED.

DR EMBL; M15656; AAA51691.1; .

DR EMBL; X00270; CAA25072.1; .

DR EMBL; X00270; CAA25072.1; JOINED.

DR PIR; A23788; ADHUB.

DR HSP; P00883; LADO.

DR Genew; HGNC:417; ALDOB.

DR MIM; 229600; .

DR InterPro; IPR000741; Aldolase_I.

DR Pfam; PF00274; glycolytic_enzy; 2.

DR ProDom; PD001128; Aldolase_I; 1.

DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.

DR Lyase; Schiff base; Glycolysis; Multigene family; Disease mutation.

FT INIT_MET 0

FT BINDING 55

FT BINDING 146

FT BINDING 229

FT ACT_SITE 363

FT VARIANT 134

FT VARIANT 147

FT VARIANT 149

FT VARIANT 174

FT VARIANT 256

FT VARIANT 303

FT VARIANT 334

FT VARIANT 337

FT CONFLICT 53

FT CONFLICT 249

FT CONFLICT 277

FT CONFLICT 308

FT CONFLICT 347

FT SEQUENCE 363 AA; 39342 MW; B3371B012B2DBA8 CRC64;

SQ

Query Match 59.6%; Score 31; DB 1; Length 363;

Best Local Similarity 62.5%; Pred. No. 45;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPGXGH 9

DB 189 EVIPDGDH 196

RESULT 22

ID ALFB_RABIT STANDARD; PRT; 363 AA.

AC P79226;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Fructose-bisphosphate aldolase B (EC 4.1.2.13) (Liver-type aldolase).

GN ALDOB OR ALDB.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OX Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN NCBI_TaxID=9986;
 [1]
 RP SEQUENCE FROM N.A.
 RA Berardini T.Z., Amsden A.B., Penhoet E.E., Tolan D.R.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: D-fructose 1,6-bisphosphate = glycerone
 CC phosphate + D-glyceraldehyde 3-phosphate.
 CC -1- PATHWAY: Glycolysis; sixth step.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- MISCELLANEOUS: IN VERTEBRATES, THREE FORMS OF THIS UBIQUITOUS
 CC GLYCOLYTIC ENZYME ARE FOUND, ALDOLASE A IN MUSCLE, ALDOLASE B IN
 CC LIVER, & ALDOLASE C IN BRAIN.
 CC -1- SIMILARITY: BELONGS TO CLASS I FRUCTOSE-BISPHOSPHATE ALDOLASE
 CC FAMILY.
 CC
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 CC
 DR EMBL; U85645; AAB42087.1; -
 DR HSP; P00883; IADO.
 DR InterPro; IPR000741; Aldolase_I.
 DR Pfam; PF00274; glycolytic_enz; 1.
 DR ProDom; PD001128; Aldolase_I; 1.
 DR PROSITE; PS00158; ALDOLASE_CLASS_I; 1.
 KW Lyase; Schiff base; Glycolysis; Multigene family.
 FT INIT_MET 0 BY SIMILARITY.
 FT BINDING 55 55 C-1-PHOSPHATE GROUP OF THE SUBSTRATE.
 FT BINDING 146 146 C-1-PHOSPHATE GROUP OF THE SUBSTRATE.
 FT BINDING 229 229 SCHIFF-BASE WITH DIHYDROXYACETONE-P.
 FT ACT_SITE 363 363 ESSENTIAL FOR ENHANCED ACTIVITY OF THE
 FT ENZYME TOWARD FRUCTOSE 1,6-BISPHOSPHATE.
 FT AS COMPARED WITH FRUCTOSE 1-PHOSPHATE.
 SQ SEQUENCE 363 AA; 39474 MW; 0A7185A7E89F436 CRC64;
 Query Match 59.6%; Score 31; DB 1; Length 363;
 Best Local Similarity 62.5%; Pred. NO. 45;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 EVVPXGXH 9
 ||:|:|
 Db 189 EVIPDGDH 196
 RESULT 23
 THIK_ECOLI
 ID THIK_ECOLI STANDARD; PRT; 387 AA.
 AC P21151; P78130;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE 3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Fatty oxidation complex beta
 DE subunit) (beta-ketothiolase) (Acetyl-CoA acyltransferase).
 GN FADA OR OLDA OR B3845.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE-92358234; PubMed-1379743;
 RA Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
 RT "Analysis of the Escherichia coli genome: DNA sequence of the region
 RL from 84.5 to 86.5 minutes."
 RL Science 257:771-778(1992).
 RN [2]

RP SEQUENCE FROM N.A.
 RA MEDLINE-91035260; PubMed-1699931;
 RX Dirusso C.C.;
 RT "Primary sequence of the Escherichia coli fadBA operon, encoding the
 RT fatty acid-oxidizing multienzyme complex, indicates a high degree of
 RT homology to eucaryotic enzymes."
 RL J. Bacteriol. 172:6459-6468(1990).
 RN [3]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-10.
 RC STRAIN-K12;
 RX MEDLINE-90285166; PubMed-2191949;
 RA Yang S.-Y., Yang X.-Y.H., Healy-Louie G., Schulz H., Elzinga M.;
 RT "Nucleotide sequence of the fadA gene. Primary structure of
 RT 3-ketoacyl-coenzyme A thiolase from Escherichia coli and the
 RT structural organization of the fadAB operon."
 RL J. Biol. Chem. 265:10424-10429(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / W3110;
 RX MEDLINE-90370500; PubMed-2204034;
 RA Nakahigashi K., Inokuchi H.;
 RT "Nucleotide sequence of the fadA and fadB genes from Escherichia
 RT coli."
 RL Nucleic Acids Res. 18:4937-4937(1990).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE-97426617; PubMed-9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12."
 RL Science 277:1453-1474(1997).
 CC -1- FUNCTION: FADB AND FADA ARE THE ALPHA AND BETA SUBUNITS OF THE
 CC MULTIFUNCTIONAL ENZYME COMPLEX OF THE FATTY ACID DEGRADATION
 CC CYCLE.
 CC -1- CATALYTIC ACTIVITY: Acyl-CoA + acetyl-CoA = CoA + 3-oxoacyl-CoA.
 CC -1- PATHWAY: Fatty acid beta-oxidation cycle.
 CC -1- SUBUNIT: Tetramer of two alpha chains and two beta chains.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE THIOLEASE FAMILY.
 CC
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 CC
 DR EMBL; M87049; AAA67642.1; -
 DR EMBL; M59368; AAA23751.1; -
 DR EMBL; X52837; CAB40810.1; -
 DR EMBL; M74164; AAA62778.1; -
 DR EMBL; AE000460; AAC76848.1; -
 DR PIR; A35436; XUCF.
 DR PIR; JQ0655; JQ0655.
 DR PIR; JY0109; JY0109.
 DR PIR; S30736; S30736.
 DR HSP; P27796; IAFY.
 DR ECO2DBASE; H038.6; 6TH EDITION.
 DR ECO2DBASE; H038.7; 6TH EDITION.
 DR EcoGene; EG10278; fada.
 DR InterPro; IPR002155; Thiolase.
 DR Pfam; PF00108; thiolase; 1.
 DR Pfam; PF02803; thiolase_C; 1.
 DR PROSITE; PS00098; THIOLEASE_1; 1.
 DR PROSITE; PS00099; THIOLEASE_3; 1.
 DR PROSITE; PS00737; THIOLEASE_2; 1.
 KW Fatty acid metabolism; Transferase; Acyltransferase;
 KW Complete proteome.
 ACT_SITE 91 SUBSTRATE BINDING (BY SIMILARITY).
 FT ACT_SITE 91

FT ACT_SITE 373 373 BASE (BY SIMILARITY).
 FT CONFLICT 37 37 T -> S (IN REF. 2 AND 3).
 FT CONFLICT 119 119 E -> G (IN REF. 4).
 FT CONFLICT 371 374 TNCI -> DGCVS (IN REF. 3).
 SQ SEQUENCE 387 AA; 40890 MW; CB0FF8EF4597D8BA CRC64;
 Query Match 59.6%; Score 31; DB 1; Length 387;
 Best Local Similarity 50.0%; Pred. No. 48;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 EVVPXGXH 9
 Db 188 EIIPTGGH 195

RESULT 24
 SLS1_YARLI STANDARD; PRT; 426 AA.
 AC Q9158;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SLS1 protein precursor.
 GN SLS1.
 OS Yarrowia lipolytica (Candida lipolytica).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Dipodascaceae; Yarrowia.
 OX NCBI_TaxID=4952;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 20460 / W29;
 RX MEDLINE=96216076; PubMed=8662639;
 RA Boistame A., Beckerich J.-M., Gaillardin C.;
 RT "Sisip, an endoplasmic reticulum component, is involved in the
 protein translocation process in the yeast Yarrowia lipolytica.";
 RL J. Biol. Chem. 271:11668-11675(1996).
 CC -1- FUNCTION: INVOLVED IN THE PROTEIN TRANSLOCATION PROCESS. MAY
 INTERACT DIRECTLY WITH TRANSLATING POLYPEPTIDES TO FACILITATE
 THEIR TRANSFER AND/OR HELP THEIR FOLDING IN THE ER. IT IS NOT
 REQUIRED FOR VIABILITY BUT IS ESSENTIAL FOR OPTIMAL GROWTH AT
 ELEVATED TEMPERATURES.
 CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
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 CC -----
 DR EMBL; Z50154; CAA90516.1; .
 DR InterPro; IPR000886; ER_target.
 DR PROSITE; PS00014; ER_TARGET; 1.
 KW Endoplasmic reticulum; Signal.
 FT SIGNAL 1 17 POTENTIAL.
 FT CHAIN 18 426 SLS1 PROTEIN.
 FT SITE 423 426 PREVENT SECRETION FROM ER (POTENTIAL).
 SQ SEQUENCE 426 AA; 47201 MW; 0ACD7EF17540B8E2 CRC64;
 Query Match 59.6%; Score 31; DB 1; Length 426;
 Best Local Similarity 44.4%; Pred. No. 54;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGXH 9
 Db 52 DQVIPAGLH 60

RESULT 25
 TOLB_HAEIN STANDARD; PRT; 427 AA.
 ID TOLB_HAEIN
 AC P44677; P94811;

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE TOLB protein precursor.
 GN TOLB OR HI0382.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 Scott J.D., Shirley R., Liu L.-L., Glodek A., Kelley J.M.,
 Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 Venter J.C.;
 RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
 Rd.";
 RT Science 269:496-512(1995).
 RL [2]
 RN RP SEQUENCE FROM N.A.
 RC STRAIN=1479;
 RX MEDLINE=97080550; PubMed=8921895;
 RA Sen K., Sikkema D.J., Murphy T.F.;
 RT "Isolation and characterization of the Haemophilus influenzae tolQ,
 tolR, tolA and tolB genes.";
 RL Gene 178:75-81(1996).
 CC -1- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
 (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Periplasmic (Potential).
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U32722; AAC22040.1; .
 DR EMBL; U32470; AAC44597.1; .
 DR HSPSP; P19935; ICRZ.
 DR TIGR; HI0382; .
 KW Transport; Protein transport; Periplasmic; Signal; Complete proteome.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 427 TOLB PROTEIN.
 FT VARIANT 6 6 R -> H (IN STRAIN 1479).
 FT VARIANT 14 14 V -> I (IN STRAIN 1479).
 FT VARIANT 17 19 VGS -> ITH (IN STRAIN 1479).
 FT VARIANT 21 21 A -> V (IN STRAIN 1479).
 FT VARIANT 79 79 R -> H (IN STRAIN 1479).
 FT VARIANT 129 129 T -> A (IN STRAIN 1479).
 FT VARIANT 160 160 A -> G (IN STRAIN 1479).
 FT VARIANT 237 237 A -> T (IN STRAIN 1479).
 FT VARIANT 322 322 S -> N (IN STRAIN 1479).
 FT VARIANT 326 326 A -> V (IN STRAIN 1479).
 FT VARIANT 328 328 A -> S (IN STRAIN 1479).
 SQ SEQUENCE 427 AA; 44967 MW; 0882201AE9254B9 CRC64;
 Query Match 59.6%; Score 31; DB 1; Length 427;
 Best Local Similarity 60.0%; Pred. No. 54;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 EVVPXGXHS 11
 Db 103 QVPSGNGYS 112

Wed Jun 11 15:43:14 2003

us-09-909-164-44.rsp

Page 15

Search completed: June 10, 2003, 13:40:24
Job time : 5.5 secs

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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:30:25 ; Search time 25.7857 Seconds
(without alignments)
87.898 Million cell updates/sec

Title: US-09-909-164-44
Perfect score: 52
Sequence: 1 EEVVPXGXHYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :

SPTREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.rvirus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	69.2	208	2	Q46486
2	35	67.3	233	10	Q40479
3	35	67.3	237	10	Q9LW50
4	35	67.3	285	16	Q98HU6
5	35	67.3	308	16	Q9X2E2
6	35	67.3	317	9	Q38317
7	35	67.3	350	17	Q27679
8	35	67.3	678	12	Q9EIX6
9	35	67.3	1028	16	Q8YJ11
10	35	67.3	1063	16	Q8RG86
11	34	65.4	279	16	Q9RXN9
12	34	65.4	322	17	Q9HLH8
13	34	65.4	495	5	Q16912
14	34	65.4	534	17	Q29966
15	34	65.4	822	2	Q9ZHG7
16	34	65.4	825	16	Q99XV4

17	34	65.4	1057	16	Q99UR5
18	34	65.4	1442	17	Q96YH5
19	33	63.5	78	6	Q9XST4
20	33	63.5	139	2	Q57489
21	33	63.5	156	16	Q9PC35
22	33	63.5	217	4	Q00404
23	33	63.5	252	16	Q8YWP1
24	33	63.5	299	4	Q9UEE9
25	33	63.5	412	5	Q08523
26	33	63.5	480	5	Q95NK1
27	33	63.5	510	10	Q9SA71
28	33	63.5	722	12	Q9QTC7
29	33	63.5	748	12	Q9YR01
30	33	63.5	795	5	Q9V8K6
31	33	63.5	802	16	Q97QM8
32	33	63.5	816	2	Q9AHT9
33	33	63.5	819	2	Q9ANY3
34	33	63.5	819	10	Q9AVK4
35	33	63.5	819	16	Q97QM9
36	33	63.5	839	16	Q9ANY2
37	33	63.5	844	2	Q9AG74
38	33	63.5	848	16	Q8P6S4
39	33	63.5	1039	16	Q9ANY1
40	32	61.5	132	2	Q9SIN2
41	32	61.5	135	4	Q9UBD2
42	32	61.5	143	17	Q8TX62
43	32	61.5	162	16	Q53667
44	32	61.5	201	16	Q9L2F0
45	32	61.5	225	10	Q40129
46	32	61.5	246	5	Q9N366
47	32	61.5	280	5	Q9VMN9
48	32	61.5	286	10	Q9ZNT7
49	32	61.5	327	16	Q8UJ05
50	32	61.5	372	16	Q8XQH7
51	32	61.5	374	17	Q27916
52	32	61.5	387	2	Q9ROM6
53	32	61.5	425	5	Q9XVK4
54	32	61.5	432	4	Q75528
55	32	61.5	432	11	Q8R0L9
56	32	61.5	439	2	Q9R9H4
57	32	61.5	454	10	Q9C941
58	32	61.5	471	11	Q8R126
59	32	61.5	484	11	Q8VD18
60	32	61.5	505	10	Q8S300
61	32	61.5	519	10	Q9SIG8
62	32	61.5	536	16	Q8YD95
63	32	61.5	573	5	Q9VWP4
64	32	61.5	637	5	Q9Y0Y6
65	32	61.5	696	16	Q8X344
66	32	61.5	701	12	Q65568
67	32	61.5	716	11	P70521
68	32	61.5	728	12	Q9ELH4
69	32	61.5	728	12	Q9DPR8
70	32	61.5	729	12	Q9BEQ0
71	32	61.5	735	10	Q49230
72	32	61.5	743	12	Q91BV8
73	32	61.5	903	16	Q8U9X3
74	32	61.5	1435	11	Q9JIZ2
75	32	61.5	1444	11	Q9JLP0

ALIGNMENTS

RESULT 1
Q46486
ID Q46486
AC Q46486
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE Hypothetical 23.0 kDa protein (Gcra).
GN GCRA.

Q99ur5 staphylococ
Q96yh5 sulfolobus
Q9xst4 canis famil
Q57489 bacteroides
Q9pc35 xylella fas
Q00404 homo sapien
Q8ywp1 anabaena sp
Q9uee9 homo sapien
Q08523 ascaris suu
Q95nk1 plasmodium
Q9sa71 arabidopsis
Q9qtc7 marek's dis
Q9yr01 ranid herpe
Q9v8k6 drosophila
Q9v8k6 drosophila
Q9ah9 streptococ
Q9any3 streptococ
Q9avk4 pisum sativ
Q97qm9 streptococ
Q9any2 streptococ
Q9ag74 streptococ
Q8p6s4 thermoanaer
Q9any1 streptococ
Q9sin2 streptococ
Q9ubd2 homo sapien
Q8tx62 methanopyru
Q53667 mycobacteri
Q9l2f0 streptomyce
Q40129 lycopersico
Q9n366 caenorhabdi
Q9vmn9 drosophila
Q9znt7 arabidopsis
Q8uj05 agrobacteri
Q8xqh7 rälstonia s
Q27916 methanobact
Q9rm6 agrobacteri
Q9xvk4 caenorhabdi
Q75528 homo sapien
Q8r0l9 mus musculu
Q9r9h4 pseudomonas
Q9c941 arabidopsis
Q8r126 mus musculu
Q8vdl8 mus musculu
Q8s300 arabidopsis
Q9sig8 arabidopsis
Q8yds5 brucella me
Q9vwp4 drosophila
Q9y0y6 drosophila
Q8x344 escherichia
Q65568 bovine herp
P70521 rattus norv
Q9elh4 meleagrid h
Q9dpr8 meleagrid h
Q9beq0 turkey herp
Q49230 brassica ol
Q9ibv8 turkey herp
Q8u9x3 agrobacteri
Q9jiz2 mus musculu
Q9jlp0 mus musculu

OS Corynebacterium xerosis, and
 OS Corynebacterium striatum.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Corynebacteriaceae;
 OC Corynebacterium.
 OX NCBI_TaxID=1725, 43770;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=C.xerosis; STRAIN=M82B;
 RX MEDLINE=96117603; PubMed=8559800;
 RA Tauch A., Kassing F., Kalinowski J., Puhler A.;
 RT "The Corynebacterium xerosis composite transposon Tn5432 consists of
 RT two identical insertion sequences, designated IS1249, flanking the
 RT erythromycin resistance gene ermCX.";
 RL Plasmid 34:119-131(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=C.striatum; STRAIN=M82B;
 RX MEDLINE=20194806; PubMed=10732668;
 RA Tauch A., Krieff S., Kalinowski J., Puhler A.;
 RT "The 51,409-bp R-plasmid pTP10 from the multidrug-resistant clinical
 RT isolate Corynebacterium striatum M82B is composed of DNA segments
 RT initially identified in soil bacteria and in plant, animal, and human
 RT pathogens.";
 RL Mol. Gen. Genet. 263:1-11(2000).
 DR EMBL; U21300; AAC95478.1; -.
 DR EMBL; AF024666; AAG03390.1; -.
 KW Hypothetical protein; Plasmid.
 SQ SEQUENCE 208 AA; 23012 MW; F1504BE1ECD8E5A6 CRC64;
 Query Match 59.28; Score 36; DB 2; Length 208;
 Best Local Similarity 50.0%; Pred. No. 8.6;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 EVVPXGXHY 11
 Db 130 DVIPEKHVA 139
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 RESULT 2
 Q40479 PRELIMINARY; PRT; 233 AA.
 ID Q40479
 AC Q40479
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE EREP-2.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BY4; TISSUE=LEAF;
 RX MEDLINE=95276459; PubMed=7756828;
 RA Ohme-Takagi M., Shinshi H.;
 RT "Ethylene-inducible DNA binding proteins that interact with an
 RT ethylene responsive element.";
 RL Plant Cell 7:173-182(1995).
 DR EMBL; D38126; BAA07324.1; -.
 DR HSP; O80337; 2GCC.
 DR TRANSFAC; T02654; -.
 DR InterPro; IPR001471; TF_ERF.
 DR Pfam; PF00847; AP2-domain; 1.
 DR PRINTS; PD00367; ETHRSPELEMT.
 DR ProDom; PD001423; TF_AP2; 1.
 DR SMART; SM00380; AP2; 1.
 SQ SEQUENCE 233 AA; 25563 MW; 6CD16783582C0CB5 CRC64;
 Query Match 67.3%; Score 35; DB 10; Length 233;
 Best Local Similarity 60.0%; Pred. No. 16;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 130 DVIPEKHVA 139
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 RESULT 2
 Q40479 PRELIMINARY; PRT; 233 AA.
 ID Q40479
 AC Q40479
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE EREP-2.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4097;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BY4; TISSUE=LEAF;
 RX MEDLINE=95276459; PubMed=7756828;
 RA Ohme-Takagi M., Shinshi H.;
 RT "Ethylene-inducible DNA binding proteins that interact with an
 RT ethylene responsive element.";
 RL Plant Cell 7:173-182(1995).
 DR EMBL; D38126; BAA07324.1; -.
 DR HSP; O80337; 2GCC.
 DR TRANSFAC; T02654; -.
 DR InterPro; IPR001471; TF_ERF.
 DR Pfam; PF00847; AP2-domain; 1.
 DR PRINTS; PD00367; ETHRSPELEMT.
 DR ProDom; PD001423; TF_AP2; 1.
 DR SMART; SM00380; AP2; 1.
 SQ SEQUENCE 233 AA; 25563 MW; 6CD16783582C0CB5 CRC64;
 Query Match 67.3%; Score 35; DB 10; Length 237;
 Best Local Similarity 60.0%; Pred. No. 16;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EEVVPXGXHY 10
 Db 94 QAVVPKGRHY 103
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 RESULT 4
 Q98HU6 PRELIMINARY; PRT; 285 AA.
 ID Q98HU6
 AC Q98HU6
 DT 01-OCT-2001 (TRENBLrel. 18, Created)
 DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Cytochrome c1.
 GN MLL2705.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Igesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP003000; BAB49770.1; -.
 DR InterPro; IPR000345; CytC_heme_bind.
 DR InterPro; IPR002326; Cyt_C1.

QY 1 EEVVPXGXHY 10
 Db 94 QAVVPKGRHY 99
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 RESULT 3
 Q9LW50 PRELIMINARY; PRT; 237 AA.
 ID Q9LW50
 AC Q9LW50
 DT 01-OCT-2000 (TRENBLrel. 15, Created)
 DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Ethylene-responsive element binding factor.
 GN NSERF2.
 OS Nicotiana sylvestris (Wood tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
 OX NCBI_TaxID=4096;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20399450; PubMed=10945353;
 RX Kicajima S., Koyama T., Ohme-Takagi M., Shinshi H., Sato F.;
 RT "Characterization of gene expression of NSERFs, transcription factors
 RT of basic PR genes from Nicotiana sylvestris.";
 RL Plant Cell Physiol. 41:817-824(2000).
 DR EMBL; AB016264; BAA97122.1; -.
 DR HSP; O80337; 2GCC.
 DR InterPro; IPR001471; TF_ERF.
 DR Pfam; PF00847; AP2-domain; 1.
 DR PRINTS; PD00367; ETHRSPELEMT.
 DR ProDom; PD001423; TF_AP2; 1.
 DR SMART; SM00380; AP2; 1.
 SQ SEQUENCE 237 AA; 26243 MW; 01BC3EB51E46298 CRC64;
 Query Match 67.3%; Score 35; DB 10; Length 237;
 Best Local Similarity 60.0%; Pred. No. 16;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EEVVPXGXHY 10
 Db 94 QAVVPKGRHY 103
 :|:|:|:
 RESULT 4
 Q98HU6 PRELIMINARY; PRT; 285 AA.
 ID Q98HU6
 AC Q98HU6
 DT 01-OCT-2001 (TRENBLrel. 18, Created)
 DT 01-OCT-2001 (TRENBLrel. 18, Last sequence update)
 DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
 DE Cytochrome c1.
 GN MLL2705.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Igesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-338(2000).
 DR EMBL; AP003000; BAB49770.1; -.
 DR InterPro; IPR000345; CytC_heme_bind.
 DR InterPro; IPR002326; Cyt_C1.


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DR Pfam: PF02167; Cytochrome_C1; 1.
DR PRINTS; PR00603; CYTOCHROME_C1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 285 AA; 30961 MW; 31D9CDE27111747EE CRC64;

Query Match 67.3%; Score 35; DB 16; Length 285;
Best Local Similarity 55.6%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 11
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Db 194 VPEGTHYN 202

RESULT 5
Q9X2E2 SEQUENCE FROM N.A.
ID Q9X2E2 PRELIMINARY; PRT; 308 AA.
AC Q9X2E2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE FTSH protease activity modulator HFLK.
GN TM1822.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;

RN SEQUENCE FROM N.A.
RP STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Hart D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
DR EMBL; AE001819; AAD36885.1; -.
DR TIGR; TM1822; -.
DR InterPro; IPR001107; Band_7.
DR InterPro; IPR003130; GED.
DR InterPro; IPR001972; Stomatin.
DR Pfam; PF01145; Band_7; 1.
DR PRINTS; PR00721; STOMATIN.
DR SMART; SM00302; GED; 1.
DR SMART; SM00244; PHB; 1.
KW Protease; Complete proteome.
SQ SEQUENCE 308 AA; 34778 MW; ADE03603E5101A9D CRC64;

Query Match 67.3%; Score 35; DB 16; Length 308;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
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Db 41 VVPSGIHY 48

RESULT 6
Q38317 SEQUENCE FROM N.A.
ID Q38317 PRELIMINARY; PRT; 317 AA.
AC Q38317;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Lysin.
GN Lys.
OS Lactobacillus bacteriophage phi adh.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
OX NCBI_TaxID=12417;

RN SEQUENCE FROM N.A.
RP Altermann E.;
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
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deltaH: functional analysis and comparative genomics.";
J. Bacteriol. 179:7135-7155(1997).
EMBL; AE000923; AAB86115.1; -
InterPro; IPR005140; eRF1_1;
InterPro; IPR005141; eRF1_2;
InterPro; IPR005142; eRF1_3;
InterPro; IPR004405; PeIa;
Pfam; PF03463; eRF1_1; 1;
Pfam; PF03464; eRF1_2; 1;
Pfam; PF03465; eRF1_3; 1;
TIGRfams; TIGR00111; peIa; 1;
Cell division; Complete proteome.
KW COMPLETE PROTEOME.
SQ SEQUENCE 360 AA; 40814 MW; 2A000CB4B3CEFA69 CRC64;

Query Match 67.3%; Score 35; DB 17; Length 360;
Best Local Similarity 45.5%; Pred. No. 26;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEWVPXGXHY 11
|::||| |::|
Db 98 EDLVPMSGSHHT 108

RESULT 8

Q9E1X6 PRELIMINARY; PRT; 678 AA.
ID Q9E1X6
AC Q9E1X6
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical 75.9 kba protein.
OS Cercopithecine herpesvirus 7.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
OX NCBI_TaxID=35245;
RN [1]
RP SEQUENCE FROM N.A.
RA Gray W.L., Starnes H.B., White M.W., Ashburn C.V., Mahalingam R.;
RT "Complete Sequence of the Simian Varicella Virus Genome.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RW EMBL; AF275348; AAG27217.1; -
KW Hypothetical protein.
SQ SEQUENCE 678 AA; 75850 MW; A17B09E30512FE3C CRC64;

Query Match 67.3%; Score 35; DB 12; Length 678;
Best Local Similarity 50.0%; Pred. No. 52;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEWVPXGXHY 10
|::||| |::|
Db 147 EEIIPKGTGY 156

RESULT 9

Q8YJ11 PRELIMINARY; PRT; 1028 AA.
ID Q8YJ11
AC Q8YJ11
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE ATP-dependent DNA helicase.
GN BMEI0275.
OS Brucella melitensis.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29459;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-16M / ATCC 23456 / BIOTYPE 1;
RX MEDLINE-2002109; PubMed-11756688;
RA DelVecchio V.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G.,

RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
RA Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
RA Haselkorn R., Kyrpides N., Overbeek R.;
RT "The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
DR EMBL; AE009470; AAL51457.1; -
DR InterPro; IPR002086; Aldehyde_dehydr.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001650; Helicase_C.
DR Pfam; PF00271; helicase_C; 1.
DR SMART; SM00490; HELIC; 1.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 1028 AA; 112996 MW; A752B704257E219 CRC64;

Query Match 67.3%; Score 35; DB 16; Length 1028;
Best Local Similarity 54.5%; Pred. No. 81;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEWVPXGXHY 11
|::||| |::|
Db 76 EKIVPPGARYS 86

RESULT 10

Q8RG86 PRELIMINARY; PRT; 1063 AA.
ID Q8RG86
AC Q8RG86
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Carbamoyl-phosphate synthase large chain (EC 6.3.5.5).
GN FN0422
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteriia; Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 25586;
RX MEDLINE-21886394; PubMed-11889109;
RA Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Shaleva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fongstein M., Kyrpides N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
nucleatum strain ATCC 25586.";
RL J. Bacteriol. 184:2005-2018(2002).
DR EMBL; AE010554; AAL94625.1; -
KW Ligase; Complete proteome.
SQ SEQUENCE 1063 AA; 118008 MW; 39700E10B7CCE411 CRC64;

Query Match 67.3%; Score 35; DB 16; Length 1063;
Best Local Similarity 60.0%; Pred. No. 84;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EEWVPXGXHY 11
|::||| |::|
Db 195 EIVPGLNYS 204

RESULT 11

Q9RXN9 PRELIMINARY; PRT; 279 AA.
ID Q9RXN9
AC Q9RXN9
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Hypothetical protein DR0271.
GN DR0271.
OS Deinococcus radiodurans.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;

OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RI;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Uterback T., Zaleski C.,
 RA Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome sequence of the radioresistant bacterium Deinococcus
 RT radiodurans R1.";
 RL Science 286:1571-1577(1999).
 DR EMBL: AE001889; AAF09867.1; -
 DR TIGR: DR0271; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 279 AA; 31140 MW; DCEA100E0AE8831 CRC64;
 Query Match 65.4%; Score 34; DB 16; Length 279;
 Best Local Similarity 75.0%; Pred. No. 32;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 4 VPGXHY 11
 Db 100 VPLGRHY 107
 RESULT 12
 Q9HLH8
 ID Q9HLH8 PRELIMINARY; PRT; 322 AA.
 AC Q9HLH8
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Glucose-fructose oxidoreductase related protein.
 GN TA0250.
 OS Thermoplasma acidophilum.
 OC Archaea; Euryarchaeota; Thermoplasmatia; Thermoplasmatiales;
 OC Thermoplasmataceae; Thermoplasma.
 OX NCBI_TaxID=2303;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1728;
 RX MEDLINE=20479972; PubMed=11029001;
 RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
 RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
 RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
 RT acidophilum".
 RL Nature 407:508-513(2000).
 DR EMBL: AL445063; CAC11395.1; -
 DR InterPro: IPR00683; GFO_IDH_MocA.
 DR Pfam: PF01408; GFO_IDH_MocA; 1.
 KW Complete proteome.
 SQ SEQUENCE 322 AA; 36918 MW; B8C239E71009D167 CRC64;
 Query Match 65.4%; Score 34; DB 17; Length 322;
 Best Local Similarity 75.0%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 VVPXGHY 10
 Db 66 VVPGLHY 73
 RESULT 13
 O16912
 ID O16912 PRELIMINARY; PRT; 495 AA.
 AC O16912;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE F10D2.3 protein.
 GN F10D2.3
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=941150718; PubMed=7906398;
 RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
 RA Crawford J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins J., Hillier L., Jier M., Johnston L.,
 RA Jones M., Kersey J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkneen R.,
 RA Smalton N., Smith A., Sontheimer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Woldman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Graves T., Woldman P., Gillam B.;
 RT "The sequence of C. elegans cosmid F10D2.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF022972; AAC48234.1; -
 DR InterPro: IPR004151; Sre.
 DR Pfam: PF03125; Sre; 1
 DR SEQUENCE 495 AA; 58190 MW; 0C61139C138EE4C CRC64;
 Query Match 65.4%; Score 34; DB 5; Length 495;
 Best Local Similarity 50.0%; Pred. No. 61;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EEVVPXGHY 10
 Db 218 ENIVPTGKH 227
 RESULT 14
 O29966
 ID O29966 PRELIMINARY; PRT; 534 AA.
 AC O29966;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Sarcosine oxidase, subunit alpha (SOXA).
 GN AF0273.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uterback T.,
 RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
 RA Sadov P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-

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RT reducing archaeon Archaeoglobus fulgidus."
RL Nature 390:364-370(1997).
CC -I- COFACTOR: FAD (BY SIMILARITY).
CC -I- COFACTOR: BINDS A 2FE-2S CLUSTER (BY SIMILARITY).
DR EMBL; AE01086; AAB90959.1; -.
DR TIGR; AF0273; -.
DR InterPro; IPR000564; 2Fe2S_ferredoxin.
DR InterPro; IPR001327; FAD_Pyr_redox.
DR InterPro; IPR001041; Ferredoxin.
DR InterPro; IPR000205; NAD_binding.
DR Pfam; PF00111; ferr2; 1.
DR Pfam; PF00070; pyr_redox; 1.
DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
KW FAD; Flavoprotein; Hypothetical protein; Iron-sulfur; Oxidoreductase;
KW Complete proteome.
SQ SEQUENCE 534 AA; 59352 MW; A9DB03174F95093F CRC64;

Query Match 65.4%; Score 34; DB 17; Length 534;
Best Local Similarity 45.5%; Pred. No. 66;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EVVPXGXHYS 11
Db :||| |||
119 DKVFPGHSHVT 129

RESULT 15
Q9ZHG7 PRELIMINARY; PRT; 822 AA.
AC Q9ZHG7;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 92.4 kDa protein.
OS Streptococcus agalactiae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1311;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R268;
RX MEDLINE=99115568; PubMed=9916102;
RA Spellerberg B., Rozdzinski E., Martin S., Weber-Heynemann J.,
RA Schnitzler N., Luetticken R., Podbielski A.;
RT "Lmb, a protein with similarities to the lraI adhesin family, mediates
attachment of Streptococcus agalactiae to human laminin.";
RL Infect. Immun. 67:871-878(1999).
DR EMBL; AF062533; AAD13797.1; -.
KW Hypothetical protein.
SQ SEQUENCE 822 AA; 80E4EDF313481F98 CRC64;

Query Match 65.4%; Score 34; DB 2; Length 822;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
Db :||| |||
350 VVPXGXHY 357

RESULT 16
Q9XV4 PRELIMINARY; PRT; 825 AA.
AC Q9XV4;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical protein SpY2006.
GN SpY2006.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
OC Streptococcaceae; Streptococcus.
OX NCBI_TaxID=1314;

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RN SEQUENCE FROM N.A.
RP STRAIN=SF370 / ATCC 700294 / SEROTYPE M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL; AE006623; AAK34688.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 825 AA; 92649 MW; 57DF50969E6D50F4 CRC64;

Query Match 65.4%; Score 34; DB 16; Length 825;
Best Local Similarity 75.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHY 10
Db :||| |||
352 VVPXGXHY 359

RESULT 17
Q99UR5 PRELIMINARY; PRT; 1057 AA.
AC Q99UR5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Carbamoyl-phosphate synthase large chain.
GN PYRAB OR SAVI203 OR SA1046.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBI_TaxID=158878, 158879;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003361; BAB57365.1; -.
DR EMBL; AP003132; BAB42298.1; -.
DR HSP; P00968; 1CS0.
DR InterPro; IPR000901; CPSase.
DR InterPro; IPR004362; MGS_like.
DR InterPro; IPR001169; SHprot_acsite.
DR Pfam; PF00289; CPSase_L_chain; 2.
DR Pfam; PF02786; CPSase_L_D2; 2.
DR Pfam; PF02787; CPSase_L_D3; 1.
DR Pfam; PF02142; MGS; 1.
DR PRINTS; PR00098; CPSASE.
DR PROSITE; PS00866; CPSASE_1; 2.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_2.
DR PROSITE; PS00639; THIOI_PROTEASE_HIS; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 1057 AA; 117171 MW; E3E179EF0591F0F8 CRC64;

Query Match 65.4%; Score 34; DB 16; Length 1057;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVPXGXHYS 11

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Db 190 EIVSNGLHYS 199
||| | |||

RESULT 18

Q96YH5 PRELIMINARY; PRT; 1442 AA.
AC Q96YH5
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Hypothetical protein S72195.
GN S72195.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JCM 10545 / 7;
RX PubMed=11572479;
RA Kawabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankaï A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
KW EMBL; AP000989; BAB67302.1; -;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 1442 AA; 156497 MW; D63EC2C35228121F CRC64;

Query Match 65.4%; Score 34; DB 17; Length 1442;

Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXHY 10
||| | |||

Db 863 EEITPTGANY 872

RESULT 19

Q9XST4 PRELIMINARY; PRT; 78 AA.
AC Q9XST4
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE P97 homologous protein (Fragment).
GN P97.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=THYROID;
RX MEDLINE=20422104; PubMed=10964405;
RA Pichon B., Mercan D., Pouillon V., Christophe-Hobertus C.,
RA Christophe D.;
RT "A method for the large-scale cloning of nuclear proteins and nuclear
RT targeting sequences on a functional basis.";
RL Anal. Biochem. 284:231-239(2000).
DR EMBL; AJ388531; CAB46833.1; -;
FT NON_TER 78
SQ SEQUENCE 78 AA; 8895 MW; B62486313555FBAL CRC64;

Query Match 63.5%; Score 33; DB 6; Length 78;

Best Local Similarity 54.5%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EEVVPXGXHYS 11
||| | |||

Db 16 EDYVPSGGEYS 26

RESULT 20

Q57489 PRELIMINARY; PRT; 139 AA.
AC Q57489
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE DNA ligase (Fragment).
GN Bacteroides nodosus (Dichelobacter nodosus).
OS Bacteria; Proteobacteria; gamma subdivision; Cardiobacteriaceae;
OC Dichelobacter.
OX NCBI_TaxID=870;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96020672; PubMed=7476204;
RX Moses E.K., Good R.T., Sinistaj M., Billington S.J., Langford C.J.,
RA Rood J.I.;
RT "A multiple site-specific DNA-inversion model for the control of Omp1
RT phase and antigenic variation in Dichelobacter nodosus.";
RL Mol. Microbiol. 17:183-196(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96257263; PubMed=8654969;
RA Billington S.J., Sinistaj M., Cheetham B.F., Ayres A., Moses E.K.,
RA Katz M.E., Rood J.I.;
RT "Identifications of a native Dichelobacter nodosus plasmid and
RT implications for the evolution of the vap regions.";
RL Gene 172:111-116(1996).
DR EMBL; U02462; AAB12366.1; -;
DR InterPro; IPR001357; BRCT.
DR Pfam; PF00533; BRCT; 1.
DR SMART; SM00292; BRCT; 1.
DR PROSITE; PS50172; BRCT; 1.
KW Ligase.
FT NON_TER 1
SQ SEQUENCE 139 AA; 15052 MW; E0E110AA4B7D4708 CRC64;

Query Match 63.5%; Score 33; DB 2; Length 139;

Best Local Similarity 55.6%; Pred. No. 25;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXHYS 11
||| | |||

Db 21 IVPAGVHWS 29

RESULT 21

Q9PC35 PRELIMINARY; PRT; 156 AA.
AC Q9PC35
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Hypothetical protein Xfi950.
GN Xfi950.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Bordin S., Bove J.M., Briones M.R.S.,
RA Barros M.R.P., Bonaccorsi E.D., Carraro D.M., Carrer H.,
RA Bueno M.R.P., Camargo L.A., Camargo L.E.A., Costa F.F., Costa C.M.,
RA Colauto N.B., Colombo C.,

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RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Frega J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Pelxoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.W., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AE004014; AAF84752.1; -.
DR InterPro: IPR002545; ChwP.
DR SMART; SM00260; ChwP; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 156 AA; 17144 MW; D8358619C6671A5D CRC64;

Query Match 63.5%; Score 33; DB 16; Length 156;
Best Local Similarity 55.6%; Pred. No. 29;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXH 9
Db 119 EEILPQGVH 127

RESULT 22
O00404 PRELIMINARY; PRT; 217 AA.
AC O00404;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE P37 homologous protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX MEDLINE=97160586; PubMed=9006920;
RA Nobukuni T., Kobayashi M., Omori A., Ichinose S., Iwanaga T.,
RA Takahashi I., Hashimoto K., Hattori S., Kaibuchi K., Miyata Y.;
RT "An Alu-linked repetitive sequence corresponding to 280 amino acids is
expressed in a novel bovine protein, but not in its human homologue.";
RL J. Biol. Chem. 272:2801-2807(1997).
DR EMBL; D85939; BAA20069.1; -.
SQ SEQUENCE 217 AA; 24061 MW; E404BA2E35497828 CRC64;

Query Match 63.5%; Score 33; DB 4; Length 217;
Best Local Similarity 54.5%; Pred. No. 41;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EEVVPXGXHS 11
Db 16 EDVPSGGEYS 26

RESULT 23
Q8YWP1 PRELIMINARY; PRT; 252 AA.
AC Q8YWP1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein ALR1563.
GN ALR1563.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
OX NCBI_TaxID=103690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21595285; PubMed=11759840;
RA Kato T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
RA Watanabe A., Iriiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120.";
RL DNA Res. 8:205-213(2001).
DR EMBL; AP003586; BAB77929.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 252 AA; 28831 MW; 925572DA5D1CA519 CRC64;

Query Match 63.5%; Score 33; DB 16; Length 252;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXHY 10
Db 235 EMIVPAGLHF 244

RESULT 24
Q9UEE9 PRELIMINARY; PRT; 299 AA.
AC Q9UEE9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE BCNT protein (CRANIOFACIAL development protein 1).
GN BCNT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98267221; PubMed=9602175;
RA Takahashi I., Nobukuni T., Ohmori H., Kobayashi M., Tanaka S.,
RA Ohshima K., Okada N., Masui T., Hashimoto K., Iwashita S.;
RT "Existence of a bovine LINE repetitive insert that appears in the cDNA
of bovine protein BCNT in ruminant, but not in human, genomes.";
RL Gene 211:387-394(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RX Strausberg R.;
RA Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB009285; BAA31867.1; -.
DR EMBL; BC000991; AAH00991.1; -.
SQ SEQUENCE 299 AA; 33593 MW; F4A9E28B669451A CRC64;

Query Match 63.5%; Score 33; DB 4; Length 299;
Best Local Similarity 54.5%; Pred. No. 58;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EEVVPXGXHS 11
Db 16 EDVPSGGEYS 26

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RESULT 25
Q08523 ID Q08523 PRELIMINARY; PRT; 412 AA.
AC Q08523; 1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE 2-methyl branched-chain enoyl CoA reductase precursor.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
OX NCBI_TaxID=6253;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=MUSCLE;
RX MEDLINE=94042988; PubMed=7693666;
RA Duran E.; Komuniecki R.W.; Komuniecki P.R.; Wheelock M.J.;
RA Klingbeil M.M.; Ma Y.C.; Johnson K.R.;
RT "Characterization of cDNA clones for the 2-methyl branched-chain
RT enoyl-CoA reductase. An enzyme involved in branched-chain fatty acid
RT synthesis in anaerobic mitochondria of the parasitic nematode Ascaris
RT suum.";
RL J. Biol. Chem. 268:22391-22396(1993).
DR EMBL; L22165; AA16096.1; -.
DR HSP; P11310; 1EGE.
DR InterPro: IPR001552; Acyl-CoA_dh.
DR Pfam: PF00441; Acyl-CoA_dh; 1.
DR Pfam: PF02770; Acyl-CoA_dh_M; 1.
DR Pfam: PF02771; Acyl-CoA_dh_N; 1.
DR PROSITE; PS00073; ACYL_COA_DH_2; 1.
KW Mitochondrion; Transit peptide.
FT TRANSIT 1 16 MITOCHONDRION.
FT CHAIN 17 412 2-METHYL BRANCHED-CHAIN ENOYL COA
FT REDUCTASE
SQ SEQUENCE 412 AA; 44849 MW; 31173867DD6E0C40 CRC64;

Query Match 63.5%; Score 33; DB 5; Length 412;
Best Local Similarity 50.0%; Pred. No. 83;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGXY 10
Db 47 EEVIPKAAHH 56

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Search completed: June 10, 2003, 13:46:37
Job time : 27.7857 secs

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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:24:45 ; Search time 31.3571 Seconds
(without alignments)
46.744 Million cell updates/sec

Title: US-09-909-164-45
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Scoring table: BLOSUM62
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Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

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Listing first 75 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	94.0	11	23	ABB80547
2	47	94.0	11	23	ABB80548
3	47	94.0	11	23	ABB80551
4	47	94.0	11	23	ABB80556
5	47	94.0	11	23	ABB80557
6	46	92.0	11	23	ABB80524
7	46	92.0	11	23	ABB80528
8	46	92.0	11	23	ABB80529
9	46	92.0	11	23	ABB80533
10	46	92.0	11	23	ABB80534

11	46	92.0	11	23	ABB80538	Hepatitis C virus
12	46	92.0	11	23	ABB80542	Hepatitis C virus
13	46	92.0	11	23	ABB80543	Hepatitis C virus
14	46	92.0	11	23	ABB80561	Hepatitis C virus
15	46	92.0	11	23	ABB80562	Hepatitis C virus
16	41	82.0	11	23	ABB80544	Hepatitis C virus
17	41	82.0	11	23	ABB80545	Hepatitis C virus
18	41	82.0	11	23	ABB80549	Hepatitis C virus
19	41	82.0	11	23	ABB80552	Hepatitis C virus
20	41	82.0	11	23	ABB80553	Hepatitis C virus
21	40	80.0	11	23	ABB80521	Hepatitis C virus
22	40	80.0	11	23	ABB80522	Hepatitis C virus
23	40	80.0	11	23	ABB80525	Hepatitis C virus
24	40	80.0	11	23	ABB80526	Hepatitis C virus
25	40	80.0	11	23	ABB80530	Hepatitis C virus
26	40	80.0	11	23	ABB80535	Hepatitis C virus
27	40	80.0	11	23	ABB80536	Hepatitis C virus
28	40	80.0	11	23	ABB80539	Hepatitis C virus
29	40	80.0	11	23	ABB80540	Hepatitis C virus
30	40	80.0	11	23	ABB80546	Hepatitis C virus
31	40	80.0	11	23	ABB80550	Hepatitis C virus
32	40	80.0	11	23	ABB80554	Hepatitis C virus
33	40	80.0	11	23	ABB80555	Hepatitis C virus
34	40	80.0	11	23	ABB80559	Hepatitis C virus
35	40	80.0	11	23	ABB80563	Hepatitis C virus
36	40	80.0	11	23	ABB80564	Hepatitis C virus
37	40	80.0	11	23	ABB80565	Hepatitis C virus
38	40	80.0	11	23	ABB80566	Hepatitis C virus
39	40	80.0	11	23	ABB80567	Hepatitis C virus
40	40	80.0	11	23	ABB80568	Hepatitis C virus
41	39	78.0	11	23	ABB80523	Hepatitis C virus
42	39	78.0	11	23	ABB80527	Hepatitis C virus
43	39	78.0	11	23	ABB80531	Hepatitis C virus
44	39	78.0	11	23	ABB80532	Hepatitis C virus
45	39	78.0	11	23	ABB80537	Hepatitis C virus
46	39	78.0	11	23	ABB80541	Hepatitis C virus
47	39	78.0	11	23	ABB80558	Hepatitis C virus
48	39	78.0	11	23	ABB80560	Hepatitis C virus
49	35	70.0	143	22	ABB60256	Drosophila melanog
50	35	70.0	150	21	ACG28379	Arabidopsis thalia
51	35	70.0	299	22	ABG00168	Novel human diagno
52	35	70.0	587	21	AAV74287	Neisseria meningit
53	35	70.0	692	22	ABG64835	Drosophila melanog
54	34	68.0	150	22	AA887623	Bovine mammary tis
55	34	68.0	175	21	ACG10069	Arabidopsis thalia
56	34	68.0	283	22	ACG91127	C glutamic prote
57	34	68.0	576	22	AA887272	Novel central nerv
58	34	68.0	1022	22	ABG03621	Novel human diagno
59	34	68.0	1022	22	ABG05826	Novel human diagno
60	34	68.0	1022	22	ABG08173	Novel human diagno
61	34	68.0	2778	22	AB858683	Drosophila melanog
62	33	66.0	25	23	ABG52372	Eubacterial DNA po
63	33	66.0	140	16	AA864232	MAB L243 VH region
64	33	66.0	140	16	AA864235	Humanized antibody
65	33	66.0	140	16	AA864265	CDR-grafted L243-g
66	33	66.0	140	16	AA864257	MHC-II MAB L243 he
67	33	66.0	165	23	AB848059	Listeria monocytog
68	33	66.0	222	22	AAU03629	Group B Streptococ
69	33	66.0	222	23	ABP26468	Streptococcus poly
70	33	66.0	244	21	AA812881	Murine JNK3 bindin
71	33	66.0	484	21	AA812882	Murine JNK3 bindin
72	33	66.0	563	23	ABP27069	Streptococcus poly
73	32	64.0	139	23	ABP40279	Staphylococcus epi
74	32	64.0	150	22	AAU43140	Propionibacterium
75	32	64.0	275	22	AB863063	Drosophila melanog

ALIGNMENTS

RESULT 1
ABB80547
ID ABB80547 standard; peptide; 11 AA.

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XX AC ABB80547;
XX DT 08-OCT-2002 (first entry)
XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #27.
XX DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX KW virucide.
XX OS Synthetic.
XX OS Key Location/Qualifiers
XX FH Modified-site 1 /note= "N-terminal acetyl"
XX FT Modified-site 6
XX FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
XX FT residue 7"
XX FT Misc-difference 9
XX FT /note= "D-form residue"
XX FT Modified-site 11
XX FT /note= "C-terminal amide"
XX FT WO200208251-A2.
XX PN 31-JAN-2002.
XX PD 19-JUL-2001; 2001WO-US23169.
XX PF 21-JUL-2000; 2000US-220101P.
XX PR (CORV-) CORVAS INT INC.
XX PA Lim-wilby M, Levy OE, Brunck TK;
XX PI WPI; 2002-361643/39.
XX DR Novel peptide compound having hepatitis C virus protease inhibitory
XX PT activity useful for treating disorders associated with hepatitis C
XX PT virus protease
XX XX Claim 17; Page 65; 69pp; English.
XX CC The sequence represents a peptide compound of the invention having
XX CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
XX CC invention are alpha-ketoamide peptide analogues. The peptides have
XX CC virucide activity, and are useful for treating and in the manufacture of
XX CC a medicament to treat disorders associated with HCV protease. A
XX CC pharmaceutical composition comprising the peptide as an active ingredient
XX CC is useful for treating disorders associated with hepatitis C virus.
XX SQ Sequence 11 AA;
XX Query Match 94.0%; Score 47; DB 23; Length 11;
XX Best Local Similarity 90.9%; Pred. No. 0.0081;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1 EEVVPXGXDYS 11
XX Db 1 EEVVPXGTDYS 11
XX RESULT 2
XX ABB80548
XX ID ABB80548 standard; peptide; 11 AA.
XX XX
XX AC ABB80548;
XX DT 08-OCT-2002 (first entry)
XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #28.
XX DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX KW virucide.
XX OS Synthetic.
XX OS Key Location/Qualifiers
XX FH Modified-site 1 /note= "N-terminal acetyl"
XX FT Modified-site 6
XX FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
XX FT residue 7"
XX FT Misc-difference 9
XX FT /note= "D-form residue"
XX FT Modified-site 11
XX FT /note= "C-terminal amide"
XX FT WO200208251-A2.
XX PN 31-JAN-2002.
XX PD 19-JUL-2001; 2001WO-US23169.
XX PF 21-JUL-2000; 2000US-220101P.
XX PR (CORV-) CORVAS INT INC.
XX PA Lim-wilby M, Levy OE, Brunck TK;
XX PI WPI; 2002-361643/39.
XX DR Novel peptide compound having hepatitis C virus protease inhibitory
XX PT activity useful for treating disorders associated with hepatitis C
XX PT virus protease
XX XX Claim 17; Page 65; 69pp; English.
XX CC The sequence represents a peptide compound of the invention having
XX CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
XX CC invention are alpha-ketoamide peptide analogues. The peptides have
XX CC virucide activity, and are useful for treating and in the manufacture of
XX CC a medicament to treat disorders associated with HCV protease. A
XX CC pharmaceutical composition comprising the peptide as an active ingredient
XX CC is useful for treating disorders associated with hepatitis C virus.
XX SQ Sequence 11 AA;
XX Query Match 94.0%; Score 47; DB 23; Length 11;
XX Best Local Similarity 90.9%; Pred. No. 0.0081;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1 EEVVPXGXDYS 11
XX Db 1 EEVVPXGTDYS 11
XX RESULT 3
XX ABB80551
XX ID ABB80551 standard; peptide; 11 AA.
XX XX
XX AC ABB80551;
XX DT 08-OCT-2002 (first entry)
XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #31.
XX DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX KW virucide.
XX OS Synthetic.
XX OS Key Location/Qualifiers
XX FH Modified-site 1 /note= "N-terminal acetyl"
XX FT Modified-site 6
XX FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
XX FT residue 7"

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OS Synthetic.
XX Key Location/Qualifiers
XX FH Modified-site 1 /note= "N-terminal acetyl"
XX FT Modified-site 6
XX FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
XX FT residue 7"
XX FT Misc-difference 9
XX FT /note= "D-form residue"
XX FT Modified-site 11
XX FT /note= "C-terminal amide"
XX FT WO200208251-A2.
XX PN 31-JAN-2002.
XX PD 19-JUL-2001; 2001WO-US23169.
XX PF 21-JUL-2000; 2000US-220101P.
XX PR (CORV-) CORVAS INT INC.
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XX PT activity useful for treating disorders associated with hepatitis C
XX PT virus protease
XX XX Claim 17; Page 65; 69pp; English.
XX CC The sequence represents a peptide compound of the invention having
XX CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
XX CC invention are alpha-ketoamide peptide analogues. The peptides have
XX CC virucide activity, and are useful for treating and in the manufacture of
XX CC a medicament to treat disorders associated with HCV protease. A
XX CC pharmaceutical composition comprising the peptide as an active ingredient
XX CC is useful for treating disorders associated with hepatitis C virus.
XX SQ Sequence 11 AA;
XX Query Match 94.0%; Score 47; DB 23; Length 11;
XX Best Local Similarity 90.9%; Pred. No. 0.0081;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1 EEVVPXGXDYS 11
XX Db 1 EEVVPXGTDYS 11
XX RESULT 3
XX ABB80551
XX ID ABB80551 standard; peptide; 11 AA.
XX XX
XX AC ABB80551;
XX DT 08-OCT-2002 (first entry)
XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #31.
XX DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX KW virucide.
XX OS Synthetic.
XX OS Key Location/Qualifiers
XX FH Modified-site 1 /note= "N-terminal acetyl"
XX FT Modified-site 6
XX FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
XX FT residue 7"

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FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
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XX WO200208251-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease

XX Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 94.0%; Score 47; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0081;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXGXDXYS 11

Db 1 EEVVPXGXSDYS 11

RESULT 4

ID ABB80556 standard; peptide; 11 AA.

XX ABB80556;

XX 08-OCT-2002 (first entry)

XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #36.

XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"

FT Misc-difference 8 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

XX WO200208251-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease

XX Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 94.0%; Score 47; DB 23; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.0081;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXGXDXYS 11

Db 1 EEVVPXGXSDYS 11

RESULT 5

ID ABB80557 standard; peptide; 11 AA.

XX ABB80557;

XX 08-OCT-2002 (first entry)

XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #37.

XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"

FT Misc-difference 8 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

XX WO200208251-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease
 XX Claim 17; Page 65; 69pp; English.
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX SQ Sequence 11 AA;
 Query Match 94.0%; Score 47; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0081;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDYS 11
 Db 1 EEVVPXGSDYS 11
 RESULT 6
 ABB80524
 ID ABB80524 standard; peptide; 11 AA.
 XX AC ABB80524;
 XX 08-OCT-2002 (first entry)
 DT Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
 DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX virucide.
 KW Synthetic.
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT W0200208251-A2.
 PN 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 XX 21-JUL-2000; 2000US-220101P.
 XX (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease

XX Claim 17; Page 64; 69pp; English.
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX SQ Sequence 11 AA;
 Query Match 92.0%; Score 46; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDYS 11
 Db 1 EEVVPXGMDYS 11
 RESULT 7
 ABB80528
 ID ABB80528 standard; peptide; 11 AA.
 XX AC ABB80528;
 XX 08-OCT-2002 (first entry)
 DT Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
 DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX virucide.
 KW Synthetic.
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 8 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT W0200208251-A2.
 PN 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 XX 21-JUL-2000; 2000US-220101P.
 XX (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease
 XX Claim 17; Page 64; 69pp; English.
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A

ID XX ABB80534 standard; peptide; 11 AA.
 AC ABB80534;
 XX
 DT 08-OCT-2002 (first entry)
 XX
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #14.
 XX
 KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl"
 FT Modified-site 6
 FT /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 9
 FT /note= "D-form residue"
 FT Modified-site 11
 FT /note= "C-terminal amide"
 XX
 PN WO200208251-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 19-JUL-2001; 2001WO-US23169.
 PR
 XX 21-JUL-2000; 2000US-220101P.
 XX
 PA (CORV-) CORVAS INT INC.
 XX
 PI Lim-wilby M, Levy OE, Brunck TK;
 XX
 DR WPI; 2002-361643/39.
 XX
 PT Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease
 XX
 PS Claim 17; Page 64; 69pp; English.
 XX
 CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX
 SQ Sequence 11 AA;
 Query Match 92.0%; Score 46; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGDYS 11
 Db 1 EEVVPXGDYS 11
 RESULT 11
 ABB80538
 ID ABB80538 standard; peptide; 11 AA.
 XX
 AC ABB80538;
 XX
 DT 08-OCT-2002 (first entry)
 XX
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #18.

KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl"
 FT Modified-site 6
 FT /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 9
 FT /note= "D-form residue"
 FT Modified-site 11
 FT /note= "C-terminal amide"
 XX
 PN WO200208251-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 19-JUL-2001; 2001WO-US23169.
 PR
 XX 21-JUL-2000; 2000US-220101P.
 XX
 PA (CORV-) CORVAS INT INC.
 XX
 PI Lim-wilby M, Levy OE, Brunck TK;
 XX
 DR WPI; 2002-361643/39.
 XX
 PT Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease
 XX
 PS Claim 17; Page 64; 69pp; English.
 XX
 CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX
 SQ Sequence 11 AA;
 Query Match 92.0%; Score 46; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGDYS 11
 Db 1 EEVVPXGDYS 11
 RESULT 12
 ABB80542
 ID ABB80542 standard; peptide; 11 AA.
 XX
 AC ABB80542;
 XX
 DT 08-OCT-2002 (first entry)
 XX
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #22.
 XX
 KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminal acetyl"

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT residue 7"
FT
FT Misc-difference 8 /note= "D-form residue"
FT Modified-site 11
FT /note= "C-terminal amide"
XX
XX WO200208251-A2.
XX
XX 31-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-US23169.
XX
XX 21-JUL-2000; 2000US-220101P.
XX
XX (CORV-) CORVAS INT INC.
XX
XX Lim-wilby M, Levy OE, Brunck TK;
XX WPI; 2002-361643/39.
XX
XX Novel peptide compound having hepatitis C virus protease inhibitory
FT activity useful for treating disorders associated with hepatitis C
FT virus protease
XX
XX Claim 17; Page 65; 69pp; English.
XX
XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
XX Sequence 11 AA;
SQ
Query Match 92.0%; Score 46; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.013; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EEVVPXGXDYS 11
DB 1 EEVVPXGQDYS 11
RESULT 13
ABB80543
ID ABB80543 standard; peptide; 11 AA.
XX
XX ABB80543;
XX
XX 08-OCT-2002 (first entry)
XX
XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #23.
XX
XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT residue 7"
FT Misc-difference 8 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 11 /note= "D-form residue"
FT

FT /note= "C-terminal amide"
XX WO200208251-A2.
XX
XX 31-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-US23169.
XX
XX 21-JUL-2000; 2000US-220101P.
XX
XX (CORV-) CORVAS INT INC.
XX
XX Lim-wilby M, Levy OE, Brunck TK;
XX WPI; 2002-361643/39.
XX
XX Novel peptide compound having hepatitis C virus protease inhibitory
FT activity useful for treating disorders associated with hepatitis C
FT virus protease
XX
XX Claim 17; Page 65; 69pp; English.
XX
XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
XX Sequence 11 AA;
SQ
Query Match 92.0%; Score 46; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.013; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EEVVPXGXDYS 11
DB 1 EEVVPXGQDYS 11
RESULT 14
ABB80561
ID ABB80561 standard; peptide; 11 AA.
XX
XX ABB80561;
XX
XX 08-OCT-2002 (first entry)
XX
XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
XX
XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT residue 7"
FT Misc-difference 8 /note= "D-form residue"
FT Modified-site 8 /note= "Oxymethionine"
FT Modified-site 11 /note= "C-terminal amide"
XX
XX WO200208251-A2.
XX
XX 31-JAN-2002.
XX

PF 19-JUL-2001; 2001WO-US23169.
 XX 21-JUL-2000; 2000US-220101P.
 XX (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease -
 XX Claim 17; Page 65; 69pp; English.
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX Sequence 11 AA;
 SQ Query Match 92.0%; Score 46; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. NO. 0.013;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDXYS 11
 DB ||||| |||
 1 EEVVPXGMDXS 11

RESULT 15
 ABB80562
 ID ABB80562 standard; peptide; 11 AA.
 AC ABB80562;
 DT 08-OCT-2002 (first entry)
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42.
 XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 8 /note= "D-form residue"
 FT Modified-site 8 /note= "Oxymethionine"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 XX WO200208251-A2.
 PN 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 XX 21-JUL-2000; 2000US-220101P.

PA (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease -
 XX Claim 17; Page 65; 69pp; English.
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX Sequence 11 AA;
 SQ Query Match 92.0%; Score 46; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. NO. 0.013;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDXYS 11
 DB ||||| |||
 1 EEVVPXGMDXS 11

RESULT 16
 ABB80544
 ID ABB80544 standard; peptide; 11 AA.
 XX ABB80544;
 AC ABB80544;
 DT 08-OCT-2002 (first entry)
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #24.
 XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX Synthetic.
 OS Key Location/Qualifiers
 FH Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Modified-site 11 /note= "C-terminal amide"
 XX WO200208251-A2.
 PN 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 XX 21-JUL-2000; 2000US-220101P.
 XX (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease -
 XX

PS Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having

CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the

CC invention are alpha-ketoamide peptide analogues. The peptides have

CC virucide activity, and are useful for treating and in the manufacture of

CC a medicament to treat disorders associated with HCV protease. A

CC pharmaceutical composition comprising the peptide as an active ingredient

CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 82.0%; Score 41; DB 23; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.13;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EEVVPXGXNYS 11

Db 1 EEVVPXGXNYS 11

RESULT 17

ABB80545

ID ABB80545 standard; peptide; 11 AA.

XX AC ABB80545;

XX 08-OCT-2002 (first entry)

DT Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #25.

DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;

KW virucide.

KW Synthetic.

OS Key Location/Qualifiers

XX Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with

FT residue 7"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

FT WO200208251-A2.

PN 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory

XX activity useful for treating disorders associated with hepatitis C

XX virus protease

XX Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having

CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the

CC invention are alpha-ketoamide peptide analogues. The peptides have

CC virucide activity, and are useful for treating and in the manufacture of

CC a medicament to treat disorders associated with HCV protease. A

CC pharmaceutical composition comprising the peptide as an active ingredient

CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 82.0%; Score 41; DB 23; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.13;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EEVVPXGXNYS 11

Db 1 EEVVPXGXNYS 11

RESULT 18

ABB80549

ID ABB80549 standard; peptide; 11 AA.

XX AC ABB80549;

XX 08-OCT-2002 (first entry)

DT Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #29.

DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;

KW virucide.

KW Synthetic.

OS Key Location/Qualifiers

XX Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with

FT residue 7"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

FT WO200208251-A2.

PN 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory

XX activity useful for treating disorders associated with hepatitis C

XX virus protease

XX Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having

CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the

CC invention are alpha-ketoamide peptide analogues. The peptides have

CC virucide activity, and are useful for treating and in the manufacture of

CC a medicament to treat disorders associated with HCV protease. A

CC pharmaceutical composition comprising the peptide as an active ingredient

CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 82.0%; Score 41; DB 23; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.13;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EEVVPXGXDSYS 11
 IIIIII II
 Db 1 EEVVPXGSSYS 11

RESULT 19

ABB80552
 ID ABB80552 standard; peptide; 11 AA.

XX AC ABB80552;
 XX 08-OCT-2002 (first entry)
 XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #32.
 XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX Synthetic.

Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 residue 7"
 FT Misc-difference 8
 FT Modified-site 11 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"

WO200208251-A2.

31-JAN-2002.

19-JUL-2001; 2001WO-US23169.

21-JUL-2000; 2000US-220101P.

(CORV-) CORVAS INT INC.

Lim-wilby M, Levy OE, Brunck TK;

WPI; 2002-361643/39.

Novel peptide compound having hepatitis C virus protease inhibitory
 activity useful for treating disorders associated with hepatitis C
 virus protease

Claim 17; Page 65; 69pp; English.

The sequence represents a peptide compound of the invention having
 hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 invention are alpha-ketoamide peptide analogues. The peptides have
 virucide activity, and are useful for treating and in the manufacture of
 a medicament to treat disorders associated with HCV protease. A
 pharmaceutical composition comprising the peptide as an active ingredient
 is useful for treating disorders associated with hepatitis C virus.

Sequence 11 AA;

Query Match 82.0%; Score 41; DB 23; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.13;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EEVVPXGXDSYS 11
 IIIIII II
 Db 1 EEVVPXGSSYS 11

RESULT 20

ABB80553

ID ABB80553 standard; peptide; 11 AA.

XX ABB80553;
 XX 08-OCT-2002 (first entry)
 XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #33.
 XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX Synthetic.

Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 residue 7"
 FT Misc-difference 8
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"

WO200208251-A2.

31-JAN-2002.

19-JUL-2001; 2001WO-US23169.

21-JUL-2000; 2000US-220101P.

(CORV-) CORVAS INT INC.

Lim-wilby M, Levy OE, Brunck TK;

WPI; 2002-361643/39.

Novel peptide compound having hepatitis C virus protease inhibitory
 activity useful for treating disorders associated with hepatitis C
 virus protease

Claim 17; Page 65; 69pp; English.

The sequence represents a peptide compound of the invention having
 hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 invention are alpha-ketoamide peptide analogues. The peptides have
 virucide activity, and are useful for treating and in the manufacture of
 a medicament to treat disorders associated with HCV protease. A
 pharmaceutical composition comprising the peptide as an active ingredient
 is useful for treating disorders associated with hepatitis C virus.

Sequence 11 AA;

Query Match 82.0%; Score 41; DB 23; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.13;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 EEVVPXGXDSYS 11
 IIIIII II
 Db 1 EEVVPXGSSYS 11

RESULT 21

ABB80521

ID ABB80521 standard; peptide; 11 AA.

XX ABB80521;

08-OCT-2002 (first entry)

Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1.

XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX Synthetic.
OS
FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 6 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT Modified-site 11 residue 7"
FT Modified-site 11 /note= "C-terminal amide"
XX WO200208251-A2.
XX 31-JAN-2002.
XX 19-JUL-2001; 2001WO-US23169.
XX 21-JUL-2000; 2000US-220101P.
XX (CORV-) CORVAS INT INC.
XX Lim-wilby M, Levy OE, Brunck TK;
PI WPI; 2002-361643/39.
XX Novel peptide compound having hepatitis C virus protease inhibitory
FT activity useful for treating disorders associated with hepatitis C
FT virus protease
XX Claim 17; Page 64; 69pp; English.
XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX Sequence 11 AA;
SQ
Query Match 80.0%; Score 40; DB 23; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 EEVVPXGXDXYS 11
DB 1 EEVVPXGMSYS 11
RESULT 22
ABB80522
ID ABB80522 standard; peptide; 11 AA.
XX
AC ABB80522;
XX
DT 08-OCT-2002 (first entry)
XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX virucide.
KW Synthetic.
OS
FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 6 /note= "N-terminal acetyl"
XX WO200208251-A2.

XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX Synthetic.
OS
FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 6 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT Modified-site 11 residue 7"
FT Modified-site 11 /note= "C-terminal amide"
XX WO200208251-A2.
XX 31-JAN-2002.
XX 19-JUL-2001; 2001WO-US23169.
XX 21-JUL-2000; 2000US-220101P.
XX (CORV-) CORVAS INT INC.
XX Lim-wilby M, Levy OE, Brunck TK;
PI WPI; 2002-361643/39.
XX Novel peptide compound having hepatitis C virus protease inhibitory
FT activity useful for treating disorders associated with hepatitis C
FT virus protease
XX Claim 17; Page 64; 69pp; English.
XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX Sequence 11 AA;
SQ
Query Match 80.0%; Score 40; DB 23; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 EEVVPXGXDXYS 11
DB 1 EEVVPXGMSYS 11
RESULT 22
ABB80522
ID ABB80522 standard; peptide; 11 AA.
XX
AC ABB80522;
XX
DT 08-OCT-2002 (first entry)
XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX virucide.
KW Synthetic.
OS
FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 6 /note= "N-terminal acetyl"

FT /note= "Norvalyl carbonyl forming keto-amide linkage with
FT residue 7"
FT /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
FT WO200208251-A2.
PN 31-JAN-2002.
XX 19-JUL-2001; 2001WO-US23169.
XX 21-JUL-2000; 2000US-220101P.
XX (CORV-) CORVAS INT INC.
XX Lim-wilby M, Levy OE, Brunck TK;
PI WPI; 2002-361643/39.
XX Novel peptide compound having hepatitis C virus protease inhibitory
FT activity useful for treating disorders associated with hepatitis C
FT virus protease
XX Claim 17; Page 64; 69pp; English.
XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX Sequence 11 AA;
SQ
Query Match 80.0%; Score 40; DB 23; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 EEVVPXGXDXYS 11
DB 1 EEVVPXGMSYS 11
RESULT 23
ABB80525
ID ABB80525 standard; peptide; 11 AA.
XX
AC ABB80525;
XX
DT 08-OCT-2002 (first entry)
XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5.
DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX virucide.
KW Synthetic.
OS
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT Modified-site 8 residue 7"
FT Misc-difference 8 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
XX WO200208251-A2.
PN

XX PD 31-JAN-2002.
 XX
 XX PF 19-JUL-2001; 2001WO-US23169.
 XX
 XX PR 21-JUL-2000; 2000US-220101P.
 XX
 XX PA (CORV-) CORVAS INT INC.
 XX PI Lim-wilby M, Levy OE, Brunck TK;
 XX DR WPI; 2002-361643/39.
 XX
 XX PT Novel peptide compound having hepatitis C virus protease inhibitory
 XX PT activity useful for treating disorders associated with hepatitis C
 XX PT virus protease -
 XX PS Claim 17; Page 64; 69pp; English.
 XX
 XX CC The sequence represents a peptide compound of the invention having
 XX CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 XX CC invention are alpha-ketoamide peptide analogues. The peptides have
 XX CC virucide activity, and are useful for treating and in the manufacture of
 XX CC a medicament to treat disorders associated with HCV protease. A
 XX CC pharmaceutical composition comprising the peptide as an active ingredient
 XX CC is useful for treating disorders associated with hepatitis C virus.
 XX SQ Sequence 11 AA;
 Query Match 80.0%; Score 40; DB 23; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDYS 11
 Db 1 EEVVPXGMSYS 11
 RESULT 24
 ABB80526
 ID ABB80526 standard; peptide; 11 AA.
 AC ABB80526;
 DT 08-OCT-2002 (first entry)
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6.
 XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Misc-difference 8 /note= "D-form residue"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT WO200208251-A2.
 PN 31-JAN-2002.
 PD
 XX
 XX PF 19-JUL-2001; 2001WO-US23169.
 XX
 XX PR 21-JUL-2000; 2000US-220101P.

XX PA (CORV-) CORVAS INT INC.
 XX PI Lim-wilby M, Levy OE, Brunck TK;
 XX DR WPI; 2002-361643/39.
 XX
 XX PT Novel peptide compound having hepatitis C virus protease inhibitory
 XX PT activity useful for treating disorders associated with hepatitis C
 XX PT virus protease -
 XX PS Claim 17; Page 64; 69pp; English.
 XX
 XX CC The sequence represents a peptide compound of the invention having
 XX CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 XX CC invention are alpha-ketoamide peptide analogues. The peptides have
 XX CC virucide activity, and are useful for treating and in the manufacture of
 XX CC a medicament to treat disorders associated with HCV protease. A
 XX CC pharmaceutical composition comprising the peptide as an active ingredient
 XX CC is useful for treating disorders associated with hepatitis C virus.
 XX SQ Sequence 11 AA;
 Query Match 80.0%; Score 40; DB 23; Length 11;
 Best Local Similarity 81.8%; Pred. No. 0.2;
 Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDYS 11
 Db 1 EEVVPXGMSYS 11
 RESULT 25
 ABB80530
 ID ABB80530 standard; peptide; 11 AA.
 AC ABB80530;
 DT 08-OCT-2002 (first entry)
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #10.
 XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Modified-site 11 /note= "C-terminal amide"
 FT WO200208251-A2.
 PN 31-JAN-2002.
 PD
 XX
 XX PF 19-JUL-2001; 2001WO-US23169.
 XX
 XX PR 21-JUL-2000; 2000US-220101P.
 XX
 XX PA (CORV-) CORVAS INT INC.
 XX PI Lim-wilby M, Levy OE, Brunck TK;
 XX DR WPI; 2002-361643/39.
 XX
 XX PT Novel peptide compound having hepatitis C virus protease inhibitory
 XX PT activity useful for treating disorders associated with hepatitis C
 XX PT virus protease -

XX
PS
XX
XX

Claim 17; Page 64; 69pp; English.

The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.

XX

SQ Sequence 11 AA;

Query Match 80.0%; Score 40; DB 23; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.2;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY

1 EEVVPXGXSYS 11

|||||

Db

1 EEVVPXGXSYS 11

Search completed: June 10, 2003, 13:39:11

Job time : 31.3571 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:31:45 ; Search time 9.64286 Seconds
(without alignments)
33.564 Million cell updates/sec

Title: US-09-909-164-45
Perfect score: 50
Sequence: 1 BEVVPXGXDYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents.AA.*
1: /cgn2_6/ptodata/1/1aa/5A-COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B-COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A-COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B-COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PCUS-COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	33	66.0	140	4	US-08-569-147-76
2	33	66.0	140	4	US-08-569-147-82
3	32	64.0	139	4	US-09-134-001C-5124
4	31	62.0	622	2	US-08-459-146-2
5	31	62.0	622	2	US-08-459-065-2
6	31	62.0	739	4	US-09-413-814-86
7	30	60.0	59	4	US-08-963-851-14
8	30	60.0	121	4	US-09-152-060-68
9	30	60.0	121	4	US-09-152-060-85
10	30	60.0	122	4	US-08-879-995A-1
11	30	60.0	122	3	US-09-215-096-1
12	30	60.0	231	3	US-08-926-842B-20
13	30	60.0	240	3	US-08-926-842B-21
14	30	60.0	241	3	US-08-834-776A-2
15	30	60.0	341	4	US-08-853-948B-4
16	30	60.0	348	4	US-08-853-948B-5
17	30	60.0	368	4	US-09-697-367-24
18	30	60.0	421	4	US-09-093-448-4
19	30	60.0	478	2	US-09-040-799-3
20	30	60.0	478	4	US-09-093-448-1
21	30	60.0	478	4	US-09-093-448-2
22	30	60.0	478	4	US-09-093-448-3
23	30	60.0	1068	2	US-08-429-054A-11
24	30	60.0	1068	2	US-08-718-777-7
25	30	60.0	1068	3	US-09-051-341-7
26	29	58.0	100	2	US-09-047-125-27
27	29	58.0	100	3	US-07-736-335B-27

28	29	58.0	381	4	US-09-134-001C-3003	Sequence 3003, Ap
29	29	58.0	493	4	US-09-411-628-10	Sequence 10, Appl
30	29	58.0	543	4	US-09-739-455-4	Sequence 4, Appl
31	29	58.0	543	4	US-09-739-455-14	Sequence 14, Appl
32	29	58.0	544	4	US-09-732-025-4	Sequence 4, Appl
33	29	58.0	756	4	US-09-085-199B-9	Sequence 9, Appl
34	29	58.0	914	4	US-09-085-199B-4	Sequence 4, Appl
35	29	58.0	1090	4	US-09-085-199B-5	Sequence 5, Appl
36	28	56.0	45	2	US-08-637-759B-236	Sequence 236, App
37	28	56.0	45	2	US-08-871-355A-236	Sequence 236, App
38	28	56.0	45	4	US-09-201-945-236	Sequence 236, App
39	28	56.0	68	2	US-08-637-759B-62	Sequence 62, Appl
40	28	56.0	68	3	US-08-871-355A-62	Sequence 62, Appl
41	28	56.0	68	4	US-09-201-945-62	Sequence 62, Appl
42	28	56.0	181	4	US-09-134-001C-3897	Sequence 3897, Ap
43	28	56.0	216	4	US-09-198-119C-13	Sequence 13, Appl
44	28	56.0	364	4	US-09-338-671-2	Sequence 2, Appl
45	28	56.0	396	1	US-08-769-309A-15	Sequence 15, Appl
46	28	56.0	396	3	US-08-994-570-15	Sequence 15, Appl
47	28	56.0	453	1	US-08-769-309A-14	Sequence 14, Appl
48	28	56.0	453	3	US-08-994-570-14	Sequence 14, Appl
49	28	56.0	463	4	US-09-134-001C-3973	Sequence 3973, Ap
50	28	56.0	529	4	US-09-240-639-4	Sequence 4, Appl
51	28	56.0	534	2	US-08-878-563A-1	Sequence 1, Appl
52	28	56.0	534	4	US-09-270-117-1	Sequence 1, Appl
53	28	56.0	651	1	US-08-769-309A-17	Sequence 17, Appl
54	28	56.0	651	3	US-08-994-570-17	Sequence 17, Appl
55	28	56.0	746	4	US-09-149-934-4	Sequence 4, Appl
56	28	56.0	787	1	US-08-574-763-2	Sequence 2, Appl
57	28	56.0	873	3	US-08-990-140-2	Sequence 2, Appl
58	28	56.0	873	4	US-09-546-238-2	Sequence 2, Appl
59	28	56.0	947	4	US-09-228-986-73	Sequence 73, Appl
60	28	56.0	1167	1	US-08-100-709-2	Sequence 2, Appl
61	28	56.0	1167	1	US-08-176-865-2	Sequence 2, Appl
62	28	56.0	1167	1	US-08-474-038-2	Sequence 2, Appl
63	28	56.0	1167	2	US-08-779-046-2	Sequence 2, Appl
64	28	56.0	1167	2	US-08-881-340-2	Sequence 2, Appl
65	28	56.0	1722	4	US-09-194-612A-1	Sequence 1, Appl
66	28	56.0	1780	1	US-08-769-309A-5	Sequence 5, Appl
67	28	56.0	1780	3	US-08-994-570-5	Sequence 5, Appl
68	27	54.0	24	4	US-09-227-357-403	Sequence 403, App
69	27	54.0	126	2	US-08-879-995A-3	Sequence 3, Appl
70	27	54.0	126	3	US-09-215-096-3	Sequence 3, Appl
71	27	54.0	159	2	US-08-844-086-4	Sequence 4, Appl
72	27	54.0	159	3	US-09-018-211-4	Sequence 4, Appl
73	27	54.0	168	3	US-08-483-534A-2	Sequence 2, Appl
74	27	54.0	179	2	US-08-934-959-3	Sequence 3, Appl
75	27	54.0	195	2	US-08-960-022-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-569-147-76
; Sequence 76, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESS: No. 6180377ris, LLP
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/569,147
;; FILING DATE: 25-March-1996
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Trujillo, Doreen Yatkoo
;; REGISTRATION NUMBER: 35,719
;; REFERENCE/DOCKET NUMBER: CARP-0047
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 76:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 140 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-569-147-76

Query Match 66.0%; Score 33; DB 4; Length 140;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXDY 10
Db 122 VVPTGFDY 129

RESULT 2
US-08-569-147-82
; Sequence 82, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT: HUMANISED ANTIBODIES
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6180377ris, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatkoo
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-569-147-82

Query Match 66.0%; Score 33; DB 4; Length 140;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXDY 10
Db 122 VVPTGFDY 129

RESULT 3
US-09-134-001C-5124
; Sequence 5124, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5124
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5124

Query Match 64.0%; Score 32; DB 4; Length 139;
Best Local Similarity 55.6%; Pred. No. 25;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXDYS 11
Db 32 IVPFGHDYN 40

RESULT 4
US-08-459-146-2
; Sequence 2, Application US/08459146
; Patent No. 5866405
; GENERAL INFORMATION:
; APPLICANT: Choi, Gil Ho
; APPLICANT: Nuss, Donald Lee
; TITLE OF INVENTION: Genetically Engineered Transmissible
; TITLE OF INVENTION: Hypovirulence
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,146
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/832,117
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Roseman, Catherine R
; REGISTRATION NUMBER: 34,240
; REFERENCE/DOCKET NUMBER: 8589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-6208
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 622 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Endothia parasitica (Cryptophnectria
STRAIN: EP713
US-08-459-146-2

Query Match 62.0%; Score 31; DB 2; Length 622;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
| | | | |
DB 31 EEVVPAG 37

RESULT 5

US-08-459-065-2
Sequence 2, Application US/08459065
Patent No. 5882642
GENERAL INFORMATION:
APPLICANT: Choi, Gil Ho
TITLE OF INVENTION: Genetically Engineered Transmissible
TITLE OF INVENTION: Hypovirulence
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,065
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/832,117
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Roseman, Catherine R
REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8589
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Endothia parasitica (Cryptophnectria
ORGANISM: parasitica)
STRAIN: EP713
US-08-459-065-2

Query Match 62.0%; Score 31; DB 2; Length 622;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
| | | | |
DB 31 EEVVPAG 37

RESULT 6

US-09-413-814-86
Sequence 86, Application US/09413814
Patent No. 6225064
GENERAL INFORMATION:
APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
APPLICANT: Bloecker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413.814
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 86
LENGTH: 739
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-413-814-86

Query Match 62.0%; Score 31; DB 4; Length 739;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 VPXGXGYS 11
| | | | |
DB 663 IPLGXDYS 670

RESULT 7

US-08-963-851-14
Sequence 14, Application US/08963851
Patent No. 6300116
GENERAL INFORMATION:
APPLICANT: VAN DER OSTEN, CLAUS
APPLICANT: HALKIER, TORDEN
APPLICANT: ANDERSEN, CARSTEN
APPLICANT: BAUDITZ, PETER
APPLICANT: HANSEN, PETER KAMP
TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
FILE REFERENCE: 4946,200-US
CURRENT APPLICATION NUMBER: US/08/963,851
CURRENT FILING DATE: 1997-11-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 14
LENGTH: 59
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-08-963-851-14

Query Match 60.0%; Score 30; DB 4; Length 59;
Best Local Similarity 45.5%; Pred. No. 24;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXGYS 11

Db 38 EXHIPGGLYS 48

RESULT 8

US-09-152-060-68
 ; Sequence 68, Application US/09152060
 ; Patent No. 6448230
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 28 Human Secreted Proteins
 ; FILE REFERENCE: P2003P1 US
 ; CURRENT APPLICATION NUMBER: US/09/152,060
 ; CURRENT FILING DATE: 1998-09-11
 ; EARLIER APPLICATION NUMBER: PCT/US98/04858
 ; EARLIER FILING DATE: 1998-03-12
 ; EARLIER APPLICATION NUMBER: 60/040,762
 ; EARLIER FILING DATE: 1997-03-14
 ; EARLIER APPLICATION NUMBER: 60/040,710
 ; EARLIER FILING DATE: 1997-03-14
 ; EARLIER APPLICATION NUMBER: 60/050,934
 ; EARLIER FILING DATE: 1997-05-30
 ; EARLIER APPLICATION NUMBER: 60/048,100
 ; EARLIER FILING DATE: 1997-05-30
 ; EARLIER APPLICATION NUMBER: 60/048,357
 ; EARLIER FILING DATE: 1997-05-30
 ; EARLIER APPLICATION NUMBER: 60/048,189
 ; EARLIER FILING DATE: 1997-05-30
 ; EARLIER APPLICATION NUMBER: 60/057,765
 ; EARLIER FILING DATE: 1997-09-05
 ; EARLIER APPLICATION NUMBER: 60/048,970
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/068,368
 ; EARLIER FILING DATE: 1997-12-19
 ; NUMBER OF SEQ ID NOS: 118
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 68
 ; LENGTH: 121
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-152-060-68

Query Match 60.0%; Score 30; DB 4; Length 121;
 Best Local Similarity 85.7%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 EEVVPXG 7
 |||||
 Db 28 EEVVPXG 34

RESULT 9

US-09-152-060-85
 ; Sequence 85, Application US/09152060
 ; Patent No. 6448230
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 28 Human Secreted Proteins
 ; FILE REFERENCE: P2003P1 US
 ; CURRENT APPLICATION NUMBER: US/09/152,060
 ; CURRENT FILING DATE: 1998-09-11
 ; EARLIER APPLICATION NUMBER: PCT/US98/04858
 ; EARLIER FILING DATE: 1998-03-12
 ; EARLIER APPLICATION NUMBER: 60/040,762
 ; EARLIER FILING DATE: 1997-03-14
 ; EARLIER APPLICATION NUMBER: 60/040,710
 ; EARLIER FILING DATE: 1997-03-14
 ; EARLIER APPLICATION NUMBER: 60/050,934
 ; EARLIER FILING DATE: 1997-05-30
 ; EARLIER APPLICATION NUMBER: 60/048,100
 ; EARLIER FILING DATE: 1997-05-30
 ; EARLIER APPLICATION NUMBER: 60/048,357
 ; EARLIER FILING DATE: 1997-05-30

; EARLIER APPLICATION NUMBER: 60/048,189
 ; EARLIER FILING DATE: 1997-05-30
 ; EARLIER APPLICATION NUMBER: 60/057,765
 ; EARLIER FILING DATE: 1997-09-05
 ; EARLIER APPLICATION NUMBER: 60/048,970
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 60/068,368
 ; EARLIER FILING DATE: 1997-12-19
 ; NUMBER OF SEQ ID NOS: 118
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 85
 ; LENGTH: 121
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (67)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (89)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-152-060-85

Query Match 60.0%; Score 30; DB 4; Length 121;
 Best Local Similarity 85.7%; Pred. No. 54;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
 |||||
 Db 28 EEVVPXG 34

RESULT 10

US-08-879-995A-1
 ; Sequence 1, Application US/08879995A
 ; Patent No. 5985606
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Kaser, Matthew R.
 ; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/879,995A
 ; FILING DATE: Herewith
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0326 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-0555
 ; TELEFAX: 415-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 122 amino acids

;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; IMMEDIATE SOURCE:
;; LIBRARY: BRAITUT03
;; CLONE: 2109906
US-08-879-995A-1

Query Match 60.0%; Score 30; DB 2; Length 122;
Best Local Similarity 85.7%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
| | | | |
Db 28 EEVPPGG 34

RESULT 11
US-09-215-096-1
; Sequence 1, Application US/09215096
; Patent No. 6008194
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
FILING DATE:
APPLICATION NUMBER: US/09/215,096
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/879,995
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0326 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BRAITUT03
CLONE: 2109906
US-09-215-096-1

Query Match 60.0%; Score 30; DB 3; Length 122;
Best Local Similarity 85.7%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
| | | | |
Db 28 EEVPPGG 34

RESULT 12

US-08-926-842B-20
; Sequence 20, Application US/08926842B
; Patent No. 6030807
; GENERAL INFORMATION:
; APPLICANT: Sa-No. 6030807ueira, Isabel
; APPLICANT: de Lencastre, Herminia
; TITLE OF INVENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,842B
FILING DATE: 10-SEP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-089 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 231 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
US-08-926-842B-20

Query Match 60.0%; Score 30; DB 3; Length 231;
Best Local Similarity 55.6%; Pred. No. 11e-02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 VVPXGXDYS 11
| | | | |
Db 41 IKPSGVDYS 49

RESULT 13

US-08-926-842B-21
; Sequence 21, Application US/08926842B
; Patent No. 6030807
; GENERAL INFORMATION:
; APPLICANT: Sa-No. 6030807ueira, Isabel
; APPLICANT: de Lencastre, Herminia
; TITLE OF INVENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926,842B
; FILING DATE: 10-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-089 N
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 240 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Salmonella typhimurium
; US-09-926-842B-21

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Query Match          60.0%; Score 30; DB 3; Length 240;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      3 VVPXGXDXYS 11
        :| | | |
DB      41 IKPSGVDXYS 49

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RESULT 14

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US-08-834-776A-2
; Sequence 2, Application US/08834776A
; Patent No. 6060241
; GENERAL INFORMATION:
; APPLICANT: Corteshey-Theulaz, Irene
; TITLE OF INVENTION: Compositions and Methods Relating to
; TITLE OF INVENTION: Drug Discovery and Detection and Treatment of
; TITLE OF INVENTION: Gastrointestinal Diseases
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: Five Palo Alto Square, 3000 El Camino Real
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306-2155
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,776A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ashton, Nina M.
; REGISTRATION NUMBER: 37,273
; REFERENCE/DOCKET NUMBER: GAST-001/01US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-843-5000
; TELEFAX: 415-857-0663
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 241 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-834-776A-2

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Query Match          60.0%; Score 30; DB 3; Length 241;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 EEVVPXG 7
        ||:| | |
DB      199 EEIVPAG 205

```

RESULT 15

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US-08-853-948B-4
; Sequence 4, Application US/08853948B
; Patent No. 6210943
; GENERAL INFORMATION:
; APPLICANT: AKIHAMA, Toyota
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE FROM CITRUS AND DNA ENCODING
; FILE REFERENCE: THE SAME
; FILE REFERENCE: 0049-0235-0
; CURRENT APPLICATION NUMBER: US/08/853,948B
; CURRENT FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Citrus unshiu
; FEATURE:
; OTHER INFORMATION: Xaa at position 109 is one of Ala, Arg, Asn, Asp,
; OTHER INFORMATION: Cys, Gln, Gly, His, Ile, Leu, Lys, Met, Phe,
; OTHER INFORMATION: Pro, Ser, Thr, Trp, Tyr, or Val
; US-08-853-948B-4

```

```

Query Match          60.0%; Score 30; DB 4; Length 341;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      3 VVPXGXDXYS 11
        |:| | | |
DB      228 VIPPGMDFS 236

```

RESULT 16

```

US-08-853-948B-5
; Sequence 5, Application US/08853948B
; Patent No. 6210943
; GENERAL INFORMATION:
; APPLICANT: AKIHAMA, Toyota
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE FROM CITRUS AND DNA ENCODING
; FILE REFERENCE: THE SAME
; FILE REFERENCE: 0049-0235-0
; CURRENT APPLICATION NUMBER: US/08/853,948B
; CURRENT FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Citrus unshiu
; US-08-853-948B-5

```

```

Query Match          60.0%; Score 30; DB 4; Length 348;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      3 VVPXGXDXYS 11
        |:| | | |

```

Db 234 VIPPGMDFS 242

RESULT 17

US-09-697-367-24
; Sequence 24, Application US/09697367
; Patent No. 6323015
; GENERAL INFORMATION:
; APPLICANT: Orozco Jr., Emil M.
; APPLICANT: Calimi, Perry G.
; APPLICANT: Weng, Zude
; APPLICANT: Tarczynski, Mitchell
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE
; FILE REFERENCE: B81166 US NA
; CURRENT APPLICATION NUMBER: US/09/697,367
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 60/084,529
; PRIOR FILING DATE: 1998-MAY-07
; PRIOR APPLICATION NUMBER: PCT/US99/09865
; PRIOR FILING DATE: 1999-MAY-06
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Zea mays
US-09-697-367-24

Query Match 60.0%; Score 30; DB 4; Length 368;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 VVPXGXDXS 11.
|:|:|:|:
Db 217 VIPPGMDFS 225

RESULT 18

US-09-93-448-4
; Sequence 4, Application US/09093448A
; Patent No. 6207704
; GENERAL INFORMATION:
; APPLICANT: Liu, Jun O.
; APPLICANT: Griffith, Eric C.
; APPLICANT: Su, Zhuang
; TITLE OF INVENTION: Type 2 Methionine Aminopeptidase (MetAP2) Inhibitors
; FILE REFERENCE: 0492611-0346
; CURRENT APPLICATION NUMBER: US/09/093,448A
; CURRENT FILING DATE: 1998-06-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 421
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-93-448-4

Query Match 60.0%; Score 30; DB 4; Length 421;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 BEVVPXGXDX 10
|:|:|:|:
Db 412 KEVVSXGDDY 421

RESULT 19

US-09-040-799-3
; Sequence 3, Application US/09040799
; Patent No. 5885820
; GENERAL INFORMATION:
; APPLICANT: CHANG, YIE-HWA

; TITLE OF INVENTION: CLONE OF A NUCLEOTIDE SEQUENCE ENCODING
; TITLE OF INVENTION: A PROTEIN HAVING TWO FUNCTIONS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOWELL & HAFERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS
; STATE: MO
; COUNTRY: USA
; ZIP: 63105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/040,799
; APPLICATION NUMBER: US/09/040,799
; FILING DATE: 18-MAR-1998
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: HOLLAND, DONALD R.
; REGISTRATION NUMBER: 35,197
; REFERENCE/DOCKET NUMBER: 16153-4639
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-040-799-3

Query Match 60.0%; Score 30; DB 2; Length 478;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 BEVVPXGXDX 10
|:|:|:|:
Db 469 KEVVSXGDDY 478

RESULT 20

US-09-093-448-1
; Sequence 1, Application US/09093448A
; Patent No. 6207704
; GENERAL INFORMATION:
; APPLICANT: Liu, Jun O.
; APPLICANT: Griffith, Eric C.
; APPLICANT: Su, Zhuang
; TITLE OF INVENTION: Type 2 Methionine Aminopeptidase (MetAP2) Inhibitors
; FILE REFERENCE: 0492611-0346
; CURRENT APPLICATION NUMBER: US/09/093,448A
; CURRENT FILING DATE: 1998-06-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-093-448-1

Query Match 60.0%; Score 30; DB 4; Length 478;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 BEVVPXGXDX 10
|:|:|:|:
Db 469 KEVVSXGDDY 478

```

RESULT 21
US-09-093-448-2
; Sequence 2, Application US/09093448A
; Patent No. 6207704
; GENERAL INFORMATION:
; APPLICANT: Liu, Jun O.
; APPLICANT: Griffith, Eric C.
; APPLICANT: Su, Zhuang
; TITLE OF INVENTION: Type 2 Methionine Aminopeptidase (MetAP2) Inhibitors
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 0492611-0346
; CURRENT APPLICATION NUMBER: US/09/093,448A
; CURRENT FILING DATE: 1998-06-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-093-448-2

Query Match          60.0%; Score 30; DB 4; Length 478;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 BEVVPXGXDY 10
Db 469 KEVVRGDDY 478

RESULT 22
US-09-093-448-3
; Sequence 3, Application US/09093448A
; Patent No. 6207704
; GENERAL INFORMATION:
; APPLICANT: Liu, Jun O.
; APPLICANT: Griffith, Eric C.
; APPLICANT: Su, Zhuang
; TITLE OF INVENTION: Type 2 Methionine Aminopeptidase (MetAP2) Inhibitors
; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 0492611-0346
; CURRENT APPLICATION NUMBER: US/09/093,448A
; CURRENT FILING DATE: 1998-06-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-093-448-3

Query Match          60.0%; Score 30; DB 4; Length 478;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 BEVVPXGXDY 10
Db 469 KEVVRGDDY 478

RESULT 23
US-08-429-054A-11
; Sequence 11, Application US/08429054A
; Patent No. 5917126
; GENERAL INFORMATION:
; APPLICANT: VAN ASSCHE, CHARLES; LANDO, DANIELLE; BRUNEAU,
; APPLICANT: JEAN; VOELKER, TONI; GERVAIS, MONICA
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHETASE (SPS),
; TITLE OF INVENTION: A PREPARATION METHOD AND CDNA THEREFOR, AND USE OF THE
; TITLE OF INVENTION: CDNA FOR MODIFYING SPS EXPRESSION IN PLANT CELLS
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: BIERMAN AND MUSERLIAN
; STREET: 600 THIRD AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10016
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/429,054A
; FILING DATE: 26-APR-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 842,337
; FILING DATE: 20-March-1992
; APPLICATION NUMBER: PCT/FR 91/00593
; FILING DATE: 18-July-1991
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: French 90402094.9
; FILING DATE: 20-July-1990
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles A. Musierlian
; REGISTRATION NUMBER: 19,683
; REFERENCE/DOCKET NUMBER: 146.1137
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 661-8000
; TELEFAX: (212) 661-8002
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1068
; TYPE: Amino acid
; STRANDEDNESS: Single
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-429-054A-11

Query Match          60.0%; Score 30; DB 2; Length 1068;
Best Local Similarity 55.6%; Pred. No. 6.3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 VVPXGXDYS 11
Db 435 VIPPGMDFS 443

RESULT 24
US-08-718-777-7
; Sequence 7, Application US/08718777
; Patent No. 5981852
; GENERAL INFORMATION:
; APPLICANT: Van Assche, C.
; APPLICANT: Lando, D.
; APPLICANT: Bruneau, J. M.
; APPLICANT: Voelker, T.
; APPLICANT: Gervais, M.
; TITLE OF INVENTION: MODIFICATION OF SUCROSE
; TITLE OF INVENTION: PHOSPHATE
; TITLE OF INVENTION: SYNTHASE IN PLANTS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Barbara Rae-Venter
; STREET: 260 Sheridan Avenue, Suite 440
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/718,777
FILING DATE: NOT YET ASSIGNED
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,471
FILING DATE: 27-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Barbara Rae-Venter
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.072.02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)328-4400
TELEFAX: (415)328-4477
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-718-777-7

Query Match 60.0%; Score 30; DB 2; Length 1068;

Best Local Similarity 55.6%; Pred. No. 6.3e+02; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 2;

QY 3 VVPXGXDYS 11
|:| | |:
Db 435 VIPPGMDFS 443

RESULT 25

US-09-051-341-7
Sequence 7, Application US/09051341
Patent No. 6124528
GENERAL INFORMATION:
APPLICANT: Shewmaker, C. K.
TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rae-Venter Law Group, P.C.
STREET: 260 Sheridan Avenue, Suite 440
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/051,341
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/17351
FILING DATE: 25-OCT-1996
APPLICATION NUMBER: US 08/549,016
FILING DATE: 27-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/372,200
FILING DATE: 12-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barbara Rae-Venter, Ph.D.,
REGISTRATION NUMBER: 32,750
REFERENCE/DOCKET NUMBER: CGNE.110.02US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)328-4400

TELEFAX: (415)328-4477
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1068 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-051-341-7

Query Match 60.0%; Score 30; DB 3; Length 1068;
Best Local Similarity 55.6%; Pred. No. 6.3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXDYS 11
|:| | |:
Db 435 VIPPGMDFS 443

Search completed: June 10, 2003, 13:51:38
Job time : 11.6429 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2003, 13:46:50 ; Search time 15 Seconds
(without alignments)
75.710 Million cell updates/sec

Title: US-09-909-164-45
Perfect score: 50
Sequence: 1 EEVVPXGXDYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published_Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	34	68.0	283	9 US-09-738-626-4881	Sequence 4881, Ap
2	33	66.0	440	9 US-09-813-408-27	Sequence 27, Appl
3	32	64.0	3472	9 US-10-027-805-4	Sequence 4, Appl
4	32	64.0	3472	9 US-10-034-623-4	Sequence 4, Appl
5	32	64.0	3472	9 US-10-027-801-4	Sequence 4, Appl
6	31	62.0	299	10 US-09-815-242-10697	Sequence 10697, A
7	31	62.0	653	9 US-09-820-843A-26	Sequence 26, Appl
8	31	62.0	846	10 US-09-815-242-13904	Sequence 13904, A
9	30	60.0	7	9 US-09-909-062-9	Sequence 1, Appl
10	30	60.0	7	9 US-09-909-062-9	Sequence 9, Appl
11	30	60.0	7	9 US-09-909-062-130	Sequence 130, Appl
12	30	60.0	11	9 US-09-943-123-22	Sequence 22, Appl
13	30	60.0	59	10 US-09-948-080-14	Sequence 14, Appl
14	30	60.0	79	9 US-09-764-891-4601	Sequence 4601, Ap
15	30	60.0	121	9 US-09-852-797-68	Sequence 68, Appl
16	30	60.0	121	9 US-09-852-797-85	Sequence 85, Appl
17	30	60.0	121	10 US-09-853-161-68	Sequence 68, Appl
18	30	60.0	121	10 US-09-853-161-85	Sequence 85, Appl
19	30	60.0	121	10 US-09-852-659A-68	Sequence 68, Appl

20	30	60.0	121	10	US-09-852-659A-85	Sequence 85, Appl
21	30	60.0	135	9	US-09-992-598-359	Sequence 359, App
22	30	60.0	135	9	US-09-989-293A-359	Sequence 359, App
23	30	60.0	135	9	US-09-989-735-359	Sequence 359, App
24	30	60.0	135	9	US-09-990-444-359	Sequence 359, App
25	30	60.0	135	9	US-09-989-730-359	Sequence 359, App
26	30	60.0	135	9	US-09-990-436-359	Sequence 359, App
27	30	60.0	135	9	US-09-991-181-359	Sequence 359, App
28	30	60.0	135	9	US-09-993-687-359	Sequence 359, App
29	30	60.0	135	9	US-09-989-734-359	Sequence 359, App
30	30	60.0	135	9	US-09-997-653-359	Sequence 359, App
31	30	60.0	135	9	US-10-174-590-444	Sequence 444, App
32	30	60.0	135	9	US-10-176-758-444	Sequence 444, App
33	30	60.0	135	9	US-10-175-737-444	Sequence 444, App
34	30	60.0	135	9	US-09-993-667-359	Sequence 359, App
35	30	60.0	135	9	US-10-173-706-444	Sequence 444, App
36	30	60.0	135	9	US-10-175-738-444	Sequence 444, App
37	30	60.0	135	9	US-10-175-752-444	Sequence 444, App
38	30	60.0	135	9	US-10-176-482-444	Sequence 444, App
39	30	60.0	135	9	US-10-176-757-444	Sequence 444, App
40	30	60.0	135	9	US-10-176-913-444	Sequence 444, App
41	30	60.0	135	9	US-10-180-552-444	Sequence 444, App
42	30	60.0	135	9	US-10-180-557-444	Sequence 444, App
43	30	60.0	135	9	US-09-990-438-359	Sequence 359, App
44	30	60.0	135	9	US-09-997-428-359	Sequence 359, App
45	30	60.0	135	9	US-09-997-666-359	Sequence 359, App
46	30	60.0	135	9	US-10-173-700-444	Sequence 444, App
47	30	60.0	135	9	US-10-174-572-444	Sequence 444, App
48	30	60.0	135	9	US-10-174-579-444	Sequence 444, App
49	30	60.0	135	9	US-10-174-582-444	Sequence 444, App
50	30	60.0	135	9	US-10-174-588-444	Sequence 444, App
51	30	60.0	135	9	US-10-175-739-444	Sequence 444, App
52	30	60.0	135	9	US-10-175-740-444	Sequence 444, App
53	30	60.0	135	9	US-10-176-488-444	Sequence 444, App
54	30	60.0	135	9	US-10-176-492-444	Sequence 444, App
55	30	60.0	135	9	US-10-176-747-444	Sequence 444, App
56	30	60.0	135	9	US-10-176-750-444	Sequence 444, App
57	30	60.0	135	9	US-10-176-750-444	Sequence 444, App
58	30	60.0	135	9	US-10-176-985-444	Sequence 444, App
59	30	60.0	135	9	US-10-176-987-444	Sequence 444, App
60	30	60.0	135	9	US-10-176-991-444	Sequence 444, App
61	30	60.0	135	9	US-10-176-993-444	Sequence 444, App
62	30	60.0	135	9	US-10-176-993-444	Sequence 444, App
63	30	60.0	135	9	US-10-184-658-444	Sequence 444, App
64	30	60.0	135	9	US-10-227-884-108	Sequence 108, App
65	30	60.0	135	9	US-09-990-711-359	Sequence 359, App
66	30	60.0	135	9	US-10-173-695-444	Sequence 444, App
67	30	60.0	135	9	US-10-173-697-444	Sequence 444, App
68	30	60.0	135	9	US-10-173-705-444	Sequence 444, App
69	30	60.0	135	9	US-10-174-576-444	Sequence 444, App
70	30	60.0	135	9	US-10-174-585-444	Sequence 444, App
71	30	60.0	135	9	US-10-174-586-444	Sequence 444, App
72	30	60.0	135	9	US-10-175-747-444	Sequence 444, App
73	30	60.0	135	9	US-10-176-481-444	Sequence 444, App
74	30	60.0	135	9	US-10-176-485-444	Sequence 444, App
75	30	60.0	135	9	US-10-176-485-444	Sequence 444, App

ALIGNMENTS

RESULT 1
US-09-738-626-4881
; Sequence 4881, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO

; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4881
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4881

Query Match 68.0%; Score 34; DB 9; Length 283;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 VPXGXDYS 11
||| |||
Db 56 VPAGADYS 63

RESULT 2

US-09-813-408-27
; Sequence 27, Application US/09813408
; Publication No. US20030049619A1
; GENERAL INFORMATION:
; APPLICANT: Delagrave, Simon
; APPLICANT: Maris, Barry
; TITLE OF INVENTION: Methods For The Synthesis Of Polynucleotides And Combinatorial Li
; TITLE OF INVENTION: Of Polynucleotides
; FILE REFERENCE: HER0041
; CURRENT APPLICATION NUMBER: US/09/813,408
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Aeropyrum pernix
US-09-813-408-27

Query Match 66.0%; Score 33; DB 9; Length 440;
Best Local Similarity 66.7%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 EVVPXGXDY 10
||| |||
Db 120 EVLPWGVY 128

RESULT 3

US-10-027-806-4
; Sequence 4, Application US/10027806
; Patent No. US20020160476A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; APPLICANT: Schleper, Christa
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCP0.002A
; CURRENT APPLICATION NUMBER: US/10/027,806
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29

; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3472
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-806-4

Query Match 64.0%; Score 32; DB 9; Length 3472;
Best Local Similarity 45.5%; Pred. No. 11e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 BEVPXGXSDYS 11
|:|:| |:
Db 2294 EDVIPRGISFS 2304

RESULT 4

US-10-034-623-4
; Sequence 4, Application US/10034623
; Publication No. US20020198365A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; APPLICANT: Schleper, Christa
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCP0.002A
; CURRENT APPLICATION NUMBER: US/10/034,623
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/408,020
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/102,294
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3472
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-034-623-4

Query Match 64.0%; Score 32; DB 9; Length 3472;
Best Local Similarity 45.5%; Pred. No. 11e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 BEVPXGXSDYS 11
|:|:| |:
Db 2294 EDVIPRGISFS 2304

RESULT 5

US-10-027-801-4
; Sequence 4, Application US/10027801
; Publication No. US20030054364A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; APPLICANT: Schleper, Christa
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCP0.002A
; CURRENT APPLICATION NUMBER: US/10/027,801
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3472
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-801-4

Query Match 64.0%; Score 32; DB 9; Length 3472;

Best Local Similarity 45.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGXDS 11
|:|:|:|:|
Db 2294 EDVIPRGISFS 2304

RESULT 6
US-09-815-242-10697
; Sequence 10697, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10697
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10697

Query Match 62.0%; Score 31; DB 10; Length 299;
Best Local Similarity 40.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGXDX 10
|:|:|:|:|
Db 218 EQITPTGIEY 227

RESULT 7
US-09-820-843A-26
; Sequence 26, Application US/09820843A
; Publication No. US20030039963A1
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN
; FILE REFERENCE: Q63915
; CURRENT APPLICATION NUMBER: US/09/820,843A
; CURRENT FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 653
; TYPE: PRT

; ORGANISM: Vibrio cholerae
; FEATURE:
; NAME/KEY: misc-feature
; OTHER INFORMATION: iron(III) ABC transporter, permease protein
; NAME/KEY: misc-feature
; OTHER INFORMATION: gi|9654609
US-09-820-843A-26

Query Match 62.0%; Score 31; DB 9; Length 653;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXG 7
|:|:|:|:|
Db 300 EEVVPXG 306

RESULT 8
US-09-815-242-13904
; Sequence 13904, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13904
; LENGTH: 846
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-09-815-242-13904

Query Match 62.0%; Score 31; DB 10; Length 846;
Best Local Similarity 60.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGXDX 10
|:|:|:|:|
Db 762 EDVVDGVDY 771

RESULT 9
US-09-909-062-1
; Sequence 1, Application US/09909062
; Publication No. US20030036501A1
; GENERAL INFORMATION:
; APPLICANT: Saksena, Anil K
; APPLICANT: Girijavallabhan, Vijay M

```

; APPLICANT: Lovey, Raymond G
; APPLICANT: Jao, Edwin
; APPLICANT: Bennett, Frank
; APPLICANT: McCormick, Jinping L
; APPLICANT: Pike, Russell E
; APPLICANT: Bogen, Stephane L
; APPLICANT: Liu, Yi-Tsung
; APPLICANT: Arasappan, Ashok
; APPLICANT: Pinto, Patrick A
; APPLICANT: Njoroge, F George
; APPLICANT: Ganguly, Ashit
; TITLE OF INVENTION: NOVEL PEPTIDES AS NS3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
; FILE REFERENCE: IN01157K-US
; CURRENT APPLICATION NUMBER: US/09/909,062
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/220,109
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: norvaline-C(=O)
; US-09-909-062-1

```

```

Query Match          60.0%; Score 30; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 EEVVPXG 7
    |||||
DB 1 EEVVPXG 7

```

```

RESULT 10
US-09-909-062-9
; Sequence 9, Application US/09909062
; Publication No. US20030036501A1
; GENERAL INFORMATION:
; APPLICANT: Saksena, Anil K
; APPLICANT: Girijavaliabhan, Viyyor M
; APPLICANT: Lovey, Raymond G
; APPLICANT: Jao, Edwin
; APPLICANT: Bennett, Frank
; APPLICANT: McCormick, Jinping L
; APPLICANT: Pike, Russell E
; APPLICANT: Bogen, Stephane L
; APPLICANT: Liu, Yi-Tsung
; APPLICANT: Arasappan, Ashok
; APPLICANT: Pinto, Patrick A
; APPLICANT: Njoroge, F George
; APPLICANT: Ganguly, Ashit
; TITLE OF INVENTION: NOVEL PEPTIDES AS NS3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
; FILE REFERENCE: IN01157K-US
; CURRENT APPLICATION NUMBER: US/09/909,062
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/220,109
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 7
; TYPE: PRT

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: norvaline-C(=O)
; US-09-909-062-9

```

```

Query Match          60.0%; Score 30; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 1 EEVVPXG 7
    |||||
DB 1 EEVVPXG 7

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RESULT 11
US-09-909-062-130
; Sequence 130, Application US/09909062
; Publication No. US20030036501A1
; GENERAL INFORMATION:
; APPLICANT: Saksena, Anil K
; APPLICANT: Girijavaliabhan, Viyyor M
; APPLICANT: Lovey, Raymond G
; APPLICANT: Jao, Edwin
; APPLICANT: Bennett, Frank
; APPLICANT: McCormick, Jinping L
; APPLICANT: Pike, Russell E
; APPLICANT: Bogen, Stephane L
; APPLICANT: Liu, Yi-Tsung
; APPLICANT: Arasappan, Ashok
; APPLICANT: Pinto, Patrick A
; APPLICANT: Njoroge, F George
; APPLICANT: Ganguly, Ashit
; TITLE OF INVENTION: NOVEL PEPTIDES AS NS3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
; FILE REFERENCE: IN01157K-US
; CURRENT APPLICATION NUMBER: US/09/909,062
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/220,109
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 130
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: ACETYLTATION
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (7)..(7)
; OTHER INFORMATION: AMIDATION
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (6)..(6)
; OTHER INFORMATION: norvaline-C(=O)
; US-09-909-062-130

```

```

Query Match          60.0%; Score 30; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 EEVVPXG 7

```

Db 1 EEVVPXG 7
|||||

RESULT 12

US-09-943-123-22
; Sequence 22, Application US/09943123
; Publication No. US20020182701A1
; GENERAL INFORMATION:
; APPLICANT: CHANG, Y-H
; APPLICANT: VETRO, J.A.
; APPLICANT: MICKA, W.S.
; TITLE OF INVENTION: Dominant Negative Variants of Methionine Aminopeptidase
; FILE REFERENCE: 16153-8007
; CURRENT APPLICATION NUMBER: US/09/943,123
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-943-123-22

Query Match 60.0%; Score 30; DB 9; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.4;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGXDY 10
: ||| | ||
Db 2 KEVSKGDDY 11

RESULT 13

US-09-948-080-14
; Sequence 14, Application US/09948080
; Patent No. US20020102702A1
; GENERAL INFORMATION:
; APPLICANT: VAN DER OSTEN, CLAUD
; APPLICANT: HALKIER, TORDEN
; APPLICANT: ANDERSEN, CARSTEN
; APPLICANT: BAUDITZ, PETER
; APPLICANT: HANSEN, PETER KAMP
; TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
; FILE REFERENCE: 4946,200-US
; CURRENT APPLICATION NUMBER: US/09/948,080
; PRIOR FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US/08/963,851
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-948-080-14

Query Match 60.0%; Score 30; DB 10; Length 59;
Best Local Similarity 45.5%; Pred. No. 38;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGXDYS 11
: : | | : ||
Db 38 EKHIFGLEYS 48

RESULT 14

US-09-764-891-4601
; Sequence 4601, Application US/09764891

; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4601
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-891-4601

Query Match 60.0%; Score 30; DB 9; Length 79;
Best Local Similarity 50.0%; Pred. No. 52;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EEVVPXGXDYS 11
: : | | : ||
Db 41 EIIPIGIDYS 50

RESULT 15

US-09-852-797-68
; Sequence 68, Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-68

Query Match 60.0%; Score 30; DB 9; Length 121;
Best Local Similarity 85.7%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXG 7
|||||

Db 28 EEWVPG 34

RESULT 16

US-09-852-797-85

; Sequence 85, Application US/09852797

; Patent No. US20020172994A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 28 Human Secreted Proteins

; FILE REFERENCE: P2003P2

; CURRENT APPLICATION NUMBER: US/09/852,797

; CURRENT FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: 60/265,583

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 09/152,060

; PRIOR FILING DATE: 1998-09-11

; PRIOR APPLICATION NUMBER: PCT/US98/04858

; PRIOR FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: 60/040,762

; PRIOR FILING DATE: 1997-03-14

; PRIOR APPLICATION NUMBER: 60/040,710

; PRIOR FILING DATE: 1997-03-14

; PRIOR APPLICATION NUMBER: 60/050,934

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,100

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,357

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,189

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/057,765

; PRIOR FILING DATE: 1997-09-05

; PRIOR APPLICATION NUMBER: 60/048,970

; PRIOR FILING DATE: 1997-06-06

; PRIOR APPLICATION NUMBER: 60/068,368

; PRIOR FILING DATE: 1997-12-19

; NUMBER OF SEQ ID NOS: 118

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 85

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SITE

; LOCATION: (67)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

; NAME/KEY: SITE

; LOCATION: (89)

; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-852-797-85

Query Match

Best Local Similarity

60.0%; Score 30; DB 9; Length 121;

85.7%; Pred. No. 82;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEWVPG 7

Db 28 EEWVPG 34

RESULT 17

US-09-853-161-68

; Sequence 68, Application US/09853161

; Patent No. US20020076756A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 28 Human Secreted Proteins

; FILE REFERENCE: P2003P3

; CURRENT APPLICATION NUMBER: US/09/853,161

; CURRENT FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: 60/265,583

; PRIOR FILING DATE: 2001-02-02

; PRIOR FILING DATE: 2001-02-02

; PRIOR FILING DATE: 2001-02-02

; PRIOR FILING DATE: 2001-02-02

; PRIOR FILING DATE: 2001-02-02

; PRIOR FILING DATE: 2001-02-02

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 09/152,060

; PRIOR FILING DATE: 1998-09-11

; PRIOR APPLICATION NUMBER: PCT/US98/04858

; PRIOR FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: 60/040,762

; PRIOR FILING DATE: 1997-03-14

; PRIOR APPLICATION NUMBER: 60/040,710

; PRIOR FILING DATE: 1997-03-14

; PRIOR APPLICATION NUMBER: 60/050,934

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,100

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,357

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,189

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/057,765

; PRIOR FILING DATE: 1997-09-05

; PRIOR APPLICATION NUMBER: 60/048,970

; PRIOR FILING DATE: 1997-06-06

; PRIOR APPLICATION NUMBER: 60/068,368

; PRIOR FILING DATE: 1997-12-19

; NUMBER OF SEQ ID NOS: 118

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 68

; LENGTH: 121

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-853-161-68

Query Match

Best Local Similarity

60.0%; Score 30; DB 10; Length 121;

85.7%; Pred. No. 82;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEWVPG 7

Db 28 EEWVPG 34

RESULT 18

US-09-853-161-85

; Sequence 85, Application US/09853161

; Patent No. US20020076756A1

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.

; TITLE OF INVENTION: 28 Human Secreted Proteins

; FILE REFERENCE: P2003P3

; CURRENT APPLICATION NUMBER: US/09/853,161

; CURRENT FILING DATE: 2001-05-11

; PRIOR APPLICATION NUMBER: 60/265,583

; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 09/152,060

; PRIOR FILING DATE: 1998-09-11

; PRIOR APPLICATION NUMBER: PCT/US98/04858

; PRIOR FILING DATE: 1998-03-12

; PRIOR APPLICATION NUMBER: 60/040,762

; PRIOR FILING DATE: 1997-03-14

; PRIOR APPLICATION NUMBER: 60/040,710

; PRIOR FILING DATE: 1997-03-14

; PRIOR APPLICATION NUMBER: 60/050,934

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,100

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,357

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/048,189

; PRIOR FILING DATE: 1997-05-30

; PRIOR APPLICATION NUMBER: 60/057,765

; PRIOR FILING DATE: 1997-09-05

; PRIOR APPLICATION NUMBER: 60/048,970

; PRIOR FILING DATE: 1997-06-06

; PRIOR APPLICATION NUMBER: 60/068,368

; PRIOR FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 85
LENGTH: 121
TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (67)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (89)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-853-161-85

Query Match

Best Local Similarity 60.0%; Score 30; DB 10; Length 121;

Mismatches 0; Conservative 0; Indels 1; Gaps 0;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7

Db 28 EEVPPGG 34

RESULT 19

US-09-852-659A-68

Sequence 68, Application US/09852659A

Patent No. US20020077287A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 28 Human Secreted Proteins

FILE REFERENCE: P2003P4

CURRENT APPLICATION NUMBER: US/09/852,659A

CURRENT FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: 60/265,583

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 09/152,060

PRIOR FILING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: PCT/US98/04858

PRIOR FILING DATE: 1998-03-12

PRIOR APPLICATION NUMBER: 60/040,762

PRIOR FILING DATE: 1997-03-14

PRIOR APPLICATION NUMBER: 60/040,710

PRIOR FILING DATE: 1997-03-14

PRIOR APPLICATION NUMBER: 60/050,934

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,100

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,357

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,189

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/057,765

PRIOR FILING DATE: 1997-09-05

PRIOR APPLICATION NUMBER: 60/048,970

PRIOR FILING DATE: 1997-06-06

PRIOR APPLICATION NUMBER: 60/068,368

PRIOR FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 121

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 68

LENGTH: 121

TYPE: PRT

ORGANISM: Homo sapiens

US-09-852-659A-68

Query Match

Best Local Similarity 60.0%; Score 30; DB 10; Length 121;

Mismatches 0; Conservative 0; Indels 1; Gaps 0;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7

Db 28 EEVPPGG 34

RESULT 20

US-09-852-659A-85

Sequence 85, Application US/09852659A

Patent No. US20020077287A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: 28 Human Secreted Proteins

FILE REFERENCE: P2003P4

CURRENT APPLICATION NUMBER: US/09/852,659A

CURRENT FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: 60/265,583

PRIOR FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: 09/152,060

PRIOR FILING DATE: 1998-09-11

PRIOR APPLICATION NUMBER: PCT/US98/04858

PRIOR FILING DATE: 1998-03-12

PRIOR APPLICATION NUMBER: 60/040,762

PRIOR FILING DATE: 1997-03-14

PRIOR APPLICATION NUMBER: 60/040,710

PRIOR FILING DATE: 1997-03-14

PRIOR APPLICATION NUMBER: 60/050,934

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,100

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,357

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/048,189

PRIOR FILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: 60/057,765

PRIOR FILING DATE: 1997-09-05

PRIOR APPLICATION NUMBER: 60/048,970

PRIOR FILING DATE: 1997-06-06

PRIOR APPLICATION NUMBER: 60/068,368

PRIOR FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 121

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 85

LENGTH: 121

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (67)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE

LOCATION: (89)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-852-659A-85

Query Match 60.0%; Score 30; DB 10; Length 121;

Best Local Similarity 85.7%; Pred. No. 82;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7

Db 28 EEVPPGG 34

RESULT 21

US-09-992-598-359

Sequence 359, Application US/09992598

Patent No. US20020160384A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC20
CURRENT APPLICATION NUMBER: US/09/992,598
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/045787
PRIOR FILING DATE: 1997-06-15
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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;; PRIOR FILING DATE: 1998-07-01
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;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 60.0%; Score 30; DB 9; Length 135;
Best Local Similarity 85.7%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
DB 28 EEVPPGG 34

RESULT 22

US-09-989-293A-359
Sequence 359 Application US/09989293A
Patent No. US20020177164A1

GENERAL INFORMATION:

;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerritsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Godowski, Paul J.
;; APPLICANT: Grimaldi, J. Christopher
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kljavin, Ivar J.

;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.
;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE OF INVENTION: Acids Encoding the Same
;; FILE REFERENCE: P2730FIC66
;; CURRENT APPLICATION NUMBER: US/09/989,293A
;; CURRENT FILING DATE: 2001-11-20
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/065186
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;; PRIOR FILING DATE: 1997-11-24
;; PRIOR APPLICATION NUMBER: 60/075945
;; PRIOR FILING DATE: 1998-02-25
;; PRIOR APPLICATION NUMBER: 60/078910
;; PRIOR FILING DATE: 1998-03-20
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;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 60.0%; Score 30; DB 9; Length 135;
Best Local Similarity 85.7%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVXPXG 7
| | | | |
Db 28 EEVPEGG 34

RESULT 23

US-09-989-735-359
; Sequence 359, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P27301C61
CURRENT APPLICATION NUMBER: US/09/989,735
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
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PRIOR APPLICATION NUMBER: 60/088021
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PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
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PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
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PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
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PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
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PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-24
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 ; PRIOR FILING DATE: 1998-06-25
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 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091544
 ; PRIOR FILING DATE: 1998-07-01
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 ; PRIOR APPLICATION NUMBER: 60/091626
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091633
 ; PRIOR FILING DATE: 1998-07-02
 ; PRIOR APPLICATION NUMBER: 60/091978
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/091982
 ; PRIOR FILING DATE: 1998-07-07
 ; PRIOR APPLICATION NUMBER: 60/092182
 ; PRIOR FILING DATE: 1998-07-09

Query Match 60.0%; Score 30; DB 9; Length 135;

Best Local Similarity 85.7%; Pred. No. 93;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7

Db 28 EEVPPGG 34

RESULT 24

US-09-990-444-359

; Sequence 359, Application US/09990444

; Publication No. US20020193300A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Napier, Mary A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2730P1C19

; CURRENT APPLICATION NUMBER: US/09/990,444

; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
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 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
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 ; PRIOR APPLICATION NUMBER: 60/075945
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 ; PRIOR APPLICATION NUMBER: 60/078910
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 ; PRIOR FILING DATE: 1998-06-11
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;; PRIOR APPLICATION NUMBER: 60/089105
;; PRIOR FILING DATE: 1998-06-12
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;; PRIOR FILING DATE: 1998-06-16
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;; PRIOR FILING DATE: 1998-06-25
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;; PRIOR FILING DATE: 1998-06-25
;; PRIOR APPLICATION NUMBER: 60/090696

;; PRIOR FILING DATE: 1998-06-25
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;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091544
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
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;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 60.0%; Score 30; DB 9; Length 135;
Best Local Similarity 85.7%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 BEVVPXG 7
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Db 28 BEVVPXG 34

RESULT 25

US-09-989-730-359
; Sequence 359, Application US/09989730
; Publication No. US20020197674A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC69
; CURRENT APPLICATION NUMBER: US/09989,730
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1997-10-17
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;	PRIOR APPLICATION NUMBER:	60/090862
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;	PRIOR APPLICATION NUMBER:	60/090863
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;	PRIOR APPLICATION NUMBER:	60/091360
;	PRIOR FILING DATE:	1998-07-01

; PRIOR APPLICATION NUMBER: 60/091478
; PRIOR FILING DATE: 1998-07-02
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091626
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 60.0%; Score 30; DB 9; Length 135;
Best Local Similarity 85.7%; Pred. NO. 93;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
| | | | |
Db 28 EEVVPXG 34

Search completed: June 10, 2003, 14:35:46
Job time : 16.0714 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:31:15 ; Search time 11.2143 Seconds

(without alignments)
94.297 Million cell updates/sec

Title: US-09-909-164-45

Perfect score: 50

Sequence: 1 EEVVPXGXDYS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	72.0	363	2 D69551	conserved hypothet
2	35	70.0	290	2 D98182	6-O-methylguanine-D
3	35	70.0	290	2 AG3104	succinate dehydrog
4	35	70.0	587	2 F81138	disease resistance
5	35	70.0	906	2 T48898	disease resistance
6	35	70.0	908	2 T48899	disease resistance
7	34	68.0	102	2 A42452	V1 protein - tobac
8	34	68.0	156	2 S54619	hypothetical prote
9	34	68.0	247	2 A96001	conserved hypothet
10	34	68.0	257	2 A96546	unknown protein [i
11	34	68.0	394	2 F82491	ferri siderophore r
12	34	68.0	433	2 H87660	peptidoglycan-bind
13	34	68.0	2747	2 B49132	fat facets (faf) s
14	33	66.0	124	1 VKLJ51	trans-regulatory s
15	33	66.0	165	2 AG1272	thiol peroxidases
16	33	66.0	165	2 AH1635	thiol peroxidases
17	33	66.0	196	2 AD0454	conserved hypothet
18	33	66.0	225	2 S57810	hypothetical prote
19	33	66.0	327	2 S40753	hypothetical prote
20	33	66.0	421	1 DERTCM	acyl-coa dehydrog
21	33	66.0	440	2 H72784	probable alkaline
22	33	66.0	1028	2 AF3286	ATP-dependent DNA
23	33	66.0	1088	2 D82246	probable chitinase
24	33	66.0	1150	2 T20173	hypothetical prote
25	32	64.0	99	2 S00210	plastocyanin b - L
26	32	64.0	155	2 S38255	plastocyanin b pre
27	32	64.0	168	2 S58208	conserved hypothet
28	32	64.0	196	2 AI0931	hypothetical prote
29	32	64.0	301	2 F89957	hypothetical prote

ALIGNMENTS

RESULT 1

D69551 conserved hypothetical protein AF2411 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C:Accession: D69551

R:Klenk, H.F.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.;

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiaich, P.; Kaine, B.P.; Syk

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing a

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: D69551

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-363 <KLE>

A:Cross-references: GB:AE001109; GB:AE000782; NID:g2689432; PIDN:AB91255.1; PID:g

Query Match 72.0%; Score 36; DB 2; Length 363;

Best Local Similarity 54.5%; Pred. No. 9;

30	64.0	307	2	F84330
31	64.0	314	2	AH1912
32	64.0	357	1	G69290
33	64.0	366	2	G89350
34	64.0	425	2	T24111
35	64.0	427	2	F64064
36	64.0	565	2	H86665
37	64.0	632	2	H84350
38	64.0	672	2	G88651
39	64.0	1474	2	F69009
40	64.0	3472	2	T31308
41	64.0	6658	2	T13931
42	62.0	117	2	A69487
43	62.0	202	2	H97247
44	62.0	233	2	E72330
45	62.0	296	2	F72745
46	62.0	319	2	S03833
47	62.0	395	2	H84113
48	62.0	421	1	DEHUCM
49	62.0	496	2	S76296
50	62.0	587	2	D81881
51	62.0	622	2	S15009
52	62.0	630	2	F85074
53	62.0	653	2	D82352
54	62.0	840	2	AG0526
55	62.0	846	2	S57580
56	62.0	1741	2	S74910
57	62.0	13055	2	T16580
58	61.0	668	2	JQ2356
59	60.0	21	2	B49042
60	60.0	97	2	JW0011
61	60.0	97	2	A99427
62	60.0	128	2	A90471
63	60.0	165	2	D89493
64	60.0	175	2	S36749
65	60.0	180	2	AG0504
66	60.0	184	2	B86192
67	60.0	184	2	E90335
68	60.0	204	2	S66082
69	60.0	231	1	ISBCP4
70	60.0	231	2	A90637
71	60.0	231	2	A85488
72	60.0	232	2	AB0515
73	60.0	232	2	C71908
74	60.0	232	2	C64606
75	60.0	248	1	ISEB4T

hypothetical prote
hypothetical prote
probable hexosyltr
L-lactate dehydrog
hypothetical prote
toIB protein - Hae
ABC transporter AT
oligopeptidase [im
protein B0212.3 [i
probable membrane
hypothetical 367K
projectin - fruit
response regulator
S-adenosylmethioni
conserved hypothet
hypothetical prote
hypothetical prote
hypothetical prote
acyl-CoA dehydrog
hypothetical prote
probable succinate
hypothetical prote
hypothetical prote
iron(III) ABC tran
penicillin-binding
penicillin-binding
hemolysin - Synecch
hypothetical prote
capsid protein - f
Ig heavy chain V r
plastocyanin - car
partial transposas
hypothetical prote
hypothetical prote
transcription fact
fimbrial chain [im
hypothetical prote
hypothetical prote
general stress pro
L-ribulose-phospha
L-ribulose-5-phosp
L-ribulose-5-phosp
3-oxoacid CoA-tran
3-oxoadipate coA-t
L-ribulose-phospha

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDXS 11
| : | | | : |
Db 120 ENIVPGIDFS 130

RESULT 2
D98182
O6-methylguanine-DNA methyltransferase PA2118 [imported] - Agrobacterium tumefaciens (strain C)
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C:Accession: D98182
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A:Reference number: A97359; PMID:11743194
A:Accession: D98182
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-290 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK88982.1; PID:g15158766; GSPDB:GNO0170
C:Genetics:
A:Gene: AGR_L_818
A:Map position: linear chromosome

Query Match 70.0%; Score 35; DB 2; Length 290;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDXD 10
| : | | | : |
Db 9 EDITPIGSDY 18

RESULT 3
AG3104
6-O-methylguanine-DNA methyltransferase [imported] - Agrobacterium tumefaciens (strain C)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AG3104
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.; Karp, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, S.; E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AG3104
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-290 <KUR>
A:Cross-references: GB:AE008689; PIDN:AA45253.1; PID:g17742937; GSPDB:GNO0187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: ada
A:Map position: linear chromosome

Query Match 70.0%; Score 35; DB 2; Length 290;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDXD 10
| : | | | : |
Db 9 EDITPIGSDY 18

RESULT 4
F81138
succinate dehydrogenase, flavoprotein chain NMB0950 [imported] - Neisseria meningitidis
C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: F81138
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eise
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty,
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignan, V.; Fizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli,
A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC5
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: F81138
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-587 <VET>
A:Cross-references: GB:AE002446; GB:AE002098; NID:g7226185; PIDN:AAF41356.1; PID:g
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0950
C:Superfamily: fumarate reductase flavoprotein; 3-oxosteroid 1-dehydrogenase homol

Query Match 70.0%; Score 35; DB 2; Length 587;
Best Local Similarity 70.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDXD 10
| : | | | : |
Db 366 EVVVPQGEDY 375

RESULT 5
T48898
disease resistance protein RPP8 [validated] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000
C:Accession: T48898
R:McDowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.;
Plant Cell 10, 1861-1874, 1998
A:Title: Intragenic recombination and diversifying selection contribute to the evol
A:Reference number: Z24999; MUID:99030193; PMID:9811794
A:Accession: T48898
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-906 <MCD>
A:Cross-references: EMBL:AF089710; NID:g3928861; PIDN:AAC83165.1; PID:g3928862
A:Experimental source: Landsberg erecta
C:Genetics:
A:Gene: RPP8
A:Introns: 293/1; 342/1
C:Function:
A:Description: promotes resistance to Peronospora parasitica

Query Match 70.0%; Score 35; DB 2; Length 906;
Best Local Similarity 60.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXDXD 10
| : | | | : |
Db 881 EKLVPQGEDY 890

RESULT 6
T48899
disease resistance protein rpp8 [similarity] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000
C:Accession: T48899
R:McDowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.;
Plant Cell 10, 1861-1874, 1998
A:Title: Intragenic recombination and diversifying selection contribute to the evol
A:Reference number: Z24999; MUID:99030193; PMID:9811794
A:Accession: T48899
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-908 <MCD>

A:Cross-references: EMBL:AF089711; NID:g3901293; PIDN:AAC78631.1; PID:g3901294
 A:Experimental source: Columbia

C:Genetics:
 A:Gene: rpp8

A:Introns: 293/1; 342/1

C:Function:

A:Description: susceptible allele of a gene that promotes resistance to Peronospora para

Query Match 70.0%; Score 35; DB 2; Length 908;

Best Local Similarity 60.0%; Pred. No. 40;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXDY 10

|||||

Db 883 EKLVPGGDY 892

RESULT 7

A42452

V1 protein - tobacco yellow dwarf virus (strain Australia)

C:Species: tobacco yellow dwarf virus

C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999

C:Accession: A42452

R:Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.

Virolgy 187, 633-642, 1992

A:Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yellow

A:Reference number: A42452; MUID:92188538; PMID:1546458

A:Accession: A42452

A:Molecule type: DNA

A:Residues: 1-102 <MOR>

A:Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284

Query Match

Best Local Similarity 68.0%; Score 34; DB 2; Length 102;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGXGDXS 11

|||||

Db 7 QVVPXGDXS 16

RESULT 8

S54619

hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae).

N:Alternate names: hypothetical protein O2612; hypothetical protein YOL303.3

C:Species: Saccharomyces cerevisiae

C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002

C:Accession: S54619; S66879

R:de Haan, M.; Maarse, A.C.; Grivell, L.A.

submitted to the EMBL Data Library, May 1995

A:Reference number: S54617

A:Accession: S54619

A:Molecule type: DNA

A:Residues: 1-156 <DEH>

A:Cross-references: EMBL:X87331; NID:gl041652; PIDN:CAA60762.1; PID:g829123

R:de Haan, M.; Grivell, L.A.; Maarse, A.C.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S66877

A:Accession: S66879

A:Molecule type: DNA

A:Residues: 1-156 <DEW>

A:Cross-references: EMBL:Z74920; NID:gl420109; PIDN:CAA99201.1; PID:gl420111; MIPS:YOR01

A:Experimental source: strain S288C

C:Genetics:

A:Cross-references: SGD:S0005539

A:Map position: 13R

C:Superfamily: hypothetical protein YOR013w

Query Match

Best Local Similarity 68.0%; Score 34; DB 2; Length 156;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGXGDXS 10

|||||

Db 50 EVMPLGMDY 58

RESULT 9

A96001

conserved hypothetical protein, homolog to osmotically inducible sensory protein SM

C:Species: Sinorhizobium meliloti

C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001

C:Accession: A96001

R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Barloy-Hu

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A:Title: The complete sequence of the 1.683-kb pSymB megaplasmid from the N2-fixing

A:Reference number: A95842; MUID:21396508; PMID:11481431

A:Accession: A96001

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-247 <KUR>

A:Cross-references: GB:AL591985; PIDN:CAC49673.1; PID:gl5141160; GSPDB:GN00167

A:Experimental source: strain 1021, megaplasmid pSymB

R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hu

pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher,

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Le

hebaull, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Y

A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A:Reference number: A96039; MUID:21368234; PMID:11474104

A:Contents: annotation

C:Genetics:

A:Gene: SMB21444

A:Genome: plasmid

Query Match

Best Local Similarity 68.0%; Score 34; DB 2; Length 247;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDY 10

|||||

Db 48 EDVEPRGADY 57

RESULT 10

A96546

unknown protein [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: A96546

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; A

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewa

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; K

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Mar

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Ta

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: A96546

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-257 <STO>

A:Cross-references: GB:AE005173; NID:gl1094688; PIDN:AAG29624.1; GSPDB:GN00141

C:Genetics:

A:Gene: FBA12.12

A:Map position: 1

Query Match

Best Local Similarity 68.0%; Score 34; DB 2; Length 257;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXGDXS 11

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Db      217 EELKAGADYS 227

RESULT 11
F82491
ferrisiderophore reductase VCA0183 [imported] - Vibrio cholerae (strain N16961 serogroup
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000.#sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: F82491
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: F82491
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-394 <HEI>
A:Cross-references: GB:AE004358; GB:AE003853; NID:g9657566; PIDN:AAF96096.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VCA0183
A:Map position: 2
C:Superfamily: flavohemoglobin; cytochrome-b5 reductase homology; globin homology

Query Match      68.0%; Score 34; DB 2; Length 394;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 EVVPXGXDY 10
Db      194 EVTPEGSDY 202

RESULT 12
H87660
peptidoglycan-binding protein, probable [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
C:Accession: H87660
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
n, J.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
B.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Accession: H87660
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-433 <STO>
A:Cross-references: GB:AE005673; NID:g13425020; PIDN:AAK25284.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC3322

Query Match      68.0%; Score 34; DB 2; Length 433;
Best Local Similarity 54.5%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 EVVPXGXDYS 11
Db      266 EVILPFGDYS 276

RESULT 13
B49132
fat facets (faf) splice form 1 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 19-Dec-1993 #sequence_revision 25-Apr-1997 #text_change 01-Dec-2000
C:Accession: B49132; A49132
R:Fischer-Vize, J.A.; Rubin, G.M.; Lehmann, R.
Development 116, 985-1000, 1992

```

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A:Title: The fat facets gene is required for Drosophila eye and embryo development
A:Reference number: A49132; MUID:93202020; PMID:1295747
A:Contents: isogenic st
A:Accession: B49132
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-2747 <FIS>
A:Cross-references: GB:I04959; NID:gl57411; PIDN:AAF01345.1; PID:g6013474
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBIN:127836, NCBIN:129008, NCBIP:12
A:Accession: A49132
A>Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-2704 'VT', 2707 'ANNV' <FI2>
A:Cross-references: GB:I04958; NID:gl57410; PIDN:AAF01346.1; PID:g6013475
A>Note: sequence extracted from NCBI backbone (NCBIN:127836, NCBIN:129008, NCBIP:12
C:Keywords: alternative splicing

Query Match      68.0%; Score 34; DB 2; Length 2747;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 EEVVPXGXDXYS 11
Db      1394 EVIVPDGQDFS 1404

RESULT 14
VKLSJ
trans-regulatory splicing protein - simian immunodeficiency virus SIVcpz
N:Alternate names: anti-repression trans-activator; art protein; rev protein; trs
C:Species: simian immunodeficiency virus SIVcpz
A>Note: host Pan troglodytes (chimpanzee)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: S09988
R:Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A:Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A:Reference number: S09983; MUID:90259077; PMID:2188136
A:Accession: S09988
A>Status: nucleic acid sequence, not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-124 <HUE>
A:Cross-references: EMBL:X52154; NID:g58866; PIDN:CAA36405.1; PID:g763085
C:Genetics:
A:Gene: rev; trs; art
A:Introns: 27/1
C:Superfamily: AIDS trans-regulatory splicing protein
C:Keywords: AIDS; immunodeficiency; splicing protein; transcription regulation

Query Match      66.0%; Score 33; DB 1; Length 124;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 EVVPXGXDXYS 11
Db      107 ETVPAGGNYS 116

RESULT 15
AG1272
thiol peroxidases homolog lmo1583 [imported] - Listeria monocytogenes (strain EGD-e
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 17-May-2002
C:Accession: AG1272
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Blo
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsh
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Maqueno, E.; Maitournam, A
ok, C.; Schlueter, T.; Smeets, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Weh
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669

```

A:Accession: AG1272
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-165 <GLA>
A:Cross-references: GB:NC_003210; PTDN:CAC99661.1; PID:g16411012; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1583
C:Superfamily: thioredoxin peroxidase

Query Match 66.0%; Score 33; DB 2; Length 165;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPGXDY 10
|||||
Db 144 EVVPEGSDH 152

RESULT 16
AH1635
thiol peroxidases homolog lin1625 [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 17-May-2002
C:Accession: AH1635
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Meok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1635
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-165 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC96856.1; PID:g16414112; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin1625
C:Superfamily: thioredoxin peroxidase

Query Match 66.0%; Score 33; DB 2; Length 165;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPGXDY 10
|||||
Db 144 EVVPEGSDH 152

RESULT 17
AD0454
conserved hypothetical protein YPO3732 [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AD0454
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AD0454
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-196 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC93200.1; PID:g15981648; GSPDB:GN00175
C:Genetics:
A:Gene: YPO3732

Query Match 66.0%; Score 33; DB 2; Length 196;

Best Local Similarity 45.5%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EEVVPXGDYS 11
|||||
Db 76 EEAIPSSDDYA 86

RESULT 18
S57810
hypothetical protein precursor (clone TP11) - tomato
C:Species: Lycopersicon esculentum (tomato)
C>Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C:Accession: S57810
R:Milligan, S.B.; Gasser, C.S.
Plant Mol. Biol. 28, 691-711, 1995
A:Title: Nature and regulation of pistil-expressed genes in tomato.
A:Reference number: S57808; MUID:95375233; PMID:7647301
A:Accession: S57810
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-225 <MIL>
A:Cross-references: EMBL:U20592; NID:g924625; PIDN:AAA80497.1; PID:g924626
C:Superfamily: plant Kunitz-type proteinase inhibitor

Query Match 66.0%; Score 33; DB 2; Length 225;
Best Local Similarity 54.5%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGDYS 11
|||||
Db 32 DEVVPNGKTYA 42

RESULT 19
S40753
hypothetical protein C15H7.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
C:Accession: S40753
R:Smith, A.
submitted to the EMBL Data Library, February 1993
A:Reference number: S40750
A:Accession: S40753
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <SMI>
A:Cross-references: EMBL:222173; NID:g297944; PID:g297948
C:Genetics:
A:Introns: 14/3; 59/2; 115/2; 188/2; 238/3

Query Match 66.0%; Score 33; DB 2; Length 327;
Best Local Similarity 63.6%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGDYS 11
|||||
Db 175 KEVVPNGDKS 185

RESULT 20
DERTCM
acyl-CoA dehydrogenase (EC 1.3.99.3) precursor, medium-chain-specific, mitochondrial
N:Alcinate names: acyl dehydrogenase, medium-chain-specific
C:Species: Rattus norvegicus (Norway rat)
C>Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 01-Dec-2000
C:Accession: A28436; S15128
R:Matsubara, Y.; Kraus, J.P.; Ozasa, H.; Glassberg, R.; Finocchiaro, G.; Ikeda, Y.
J. Biol. Chem. 262, 10104-10108, 1987
A:Title: Molecular cloning and nucleotide sequence of cDNA encoding the entire pre
A:Reference number: A28436; MUID:87280028; PMID:3611054
A:Accession: A28436
A:Molecule type: mRNA

A:Residues: 1-421 <RF1>
 A:Cross-references: GB:J02791; NID:g202688; PIDN:AAA40670.1; PID:g202689
 R:Inagaki, T.; Ohishi, N.; Tsukagoshi, N.; Udaoka, S.; Yagi, K.
 Biochim. Biophys. Acta 1077, 285-290, 1991
 A:Title: Structurally different rat liver medium-chain acyl CoA dehydrogenases directed
 F:1-25/Domain: transit peptide (mitochondrion) #status predicted <TNP>
 A:Reference number: S15128; MUID:91230137; PMID:2029527
 A:Accession: S15128
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 11-81 <BIO>
 C:Superfamily: acyl-CoA dehydrogenase
 C:Keywords: fatty acid beta-oxidation; fatty acid metabolism; flavoprotein; mitochondrion
 F:1-25/Domain: transit peptide (mitochondrion) #status predicted <TNP>
 F:26-421/Product: acyl-CoA dehydrogenase, medium-chain-specific #status predicted <MAT>

Query Match 66.0%; Score 33; DB 1; Length 421;
 Best Local Similarity 50.0%; Pred. No. 47;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDY 10
 ||:| | |
 Db 58 EEIIPVAPDY 67

RESULT 21
 H72784
 Probable alkaline proteinase APE0263 - Aeropyrum pernix (strain K1)
 C:Species: Aeropyrum pernix
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
 C:Accession: H72784
 R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
 awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
 DNA Res. 6, 83-101, 1999
 A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
 A:Reference number: A72450; MUID:99310339; PMID:10382966
 A:Accession: H72784
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-440 <KAW>
 A:Cross-references: DBJ:AP000058; NID:g5103388; PIDN:BAA79178.1; PID:g5103657
 A:Experimental source: strain K1
 C:Genetics:
 A:Gene: APE0263
 C:Superfamily: subtilisin; subtilisin homology

Query Match 66.0%; Score 33; DB 2; Length 440;
 Best Local Similarity 66.7%; Pred. No. 49;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGXDY 10
 ||:| | |
 Db 120 EVLPWGVY 128

RESULT 22
 AF3286
 ATP-dependent DNA helicase BMEI0275 [imported] - Brucella melitensis (strain 16M)
 C:Species: Brucella melitensis
 C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
 C:Accession: AF3286
 R:BelVecchio, V.G.; Kapatal, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova,
 ; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes
 proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
 A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
 A:Reference number: AD3252; PMID:11756688
 A:Accession: AF3286
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1028 <KUR>
 A:Cross-references: GB:AE008917; PIDN:AAU51457.1; PID:gl7982167; GSPDB:GN00190
 A:Experimental source: strain 16M
 C:Genetics:
 A:Gene: BMEI0275

A:Map position: I

Query Match 66.0%; Score 33; DB 2; Length 1028;
 Best Local Similarity 54.5%; Pred. No. 1.2e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDYS 11
 ||:| | |
 Db 76 EKIVPPGARYS 86

RESULT 23
 DB2246

Probable chitinase VC1073 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
 C:Species: Vibrio cholerae
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: DB2246
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson,
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sell
 l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: DB2246
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1088 <HEI>
 A:Cross-references: GB:AE004188; GB:AE003852; NID:g9655530; PIDN:AAF94232.1; GSPDB
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC1073
 A:Map position: 1

Query Match 66.0%; Score 33; DB 2; Length 1088;
 Best Local Similarity 50.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVPXGXDYS 11
 ||:| | |
 Db 966 ETIPAGGEYS 975

RESULT 24
 T20173

Hypothetical protein C53A5.2 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
 C:Accession: T20173; T23857
 R:Mortimore, B.
 Submitted to the EMBL Data Library, November 1996
 A:Reference number: Z19232
 A:Accession: T20173
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1150 <WIL>
 A:Cross-references: EMBL:Z81486; PIDN:CAB03994.1; GSPDB:GN00023; CESP:C53A5.2
 A:Experimental source: clone C53A5
 A:Matthews, L.
 submitted to the EMBL Data Library, August 1996
 A:Reference number: Z19808
 A:Accession: T23857
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1150 <WIL>
 A:Cross-references: EMBL:Z81486; PIDN:CAB03994.1; GSPDB:GN00023; CESP:C53A5.2
 A:Experimental source: clone R02D5
 C:Genetics:
 A:Gene: CESP:C53A5.2
 A:Map position: 5
 A:Introns: 33/3; 63/3; 132/3; 169/3; 221/3; 299/3; 379/2; 423/2; 438/2; 471/1; 513/

Query Match 66.0%; Score 33; DB 2; Length 1150;
 Best Local Similarity 66.7%; Pred. No. 1.4e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXYS 11
I: I I I I I
Db 562 VLPVGDYS 570

RESULT 25

S00210
plastocyanin b - Lombardy poplar
C;Species: Populus nigra var. italica (Lombardy poplar)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 20-Apr-2000
C;Accession: S00210
R;Dmitrov, M.I.; Egorov, C.A.; Donchev, A.A.; Atanasov, B.P.
FEBS Lett. 226, 17-22, 1987
A;Title: Complete amino acid sequence of poplar plastocyanin b.
A;Reference number: S00210
A;Accession: S00210
A;Molecule type: protein
A;Residues: 1-99 <DIM>
C;Superfamily: plastocyanin
C;Keywords: chloroplast; copper; electron transfer; metalloprotein
F;37,84,87,92/Binding site: copper (His, Cys, His, Met) (type 1) #status predicted

Query Match 64.0%; Score 32; DB 2; Length 99;
Best Local Similarity 54.5%; Pred. NO. 16;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EEVVPXGXYS 11
I: I I I I I
Db 43 EDVPSGVDVS 53

Search completed: June 10, 2003, 13:49:18
Job time : 12.2143 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:25:04 ; Search time 4.5 seconds
(without alignments)
101.387 Million cell updates/sec

Title: US-09-909-164-45
Perfect score: 50
Sequence: 1 EVVVPXGXDYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	35	70.0	1058	1	CARB_FUSNN
2	34	68.0	102	1	Y1LK_TYDVA
3	34	68.0	394	1	HMPA_VIBCH
4	34	68.0	2747	1	EAF_DROME
5	33	66.0	124	1	REV_SIVCZ
6	33	66.0	327	1	YK14_CAEEL
7	33	66.0	421	1	ACDM_RAT
8	32	64.0	154	1	PLAS_ORYSA
9	32	64.0	155	1	PLAS_HORVU
10	32	64.0	168	1	PLAT_POPNI
11	32	64.0	196	1	YUNG_SALTY
12	32	64.0	427	1	TOUB_HAEIN
13	32	64.0	1499	1	A10C_HUMAN
14	32	64.0	3174	1	CHAC_HUMAN
15	31	62.0	233	1	HIS9_THEMEA
16	31	62.0	319	1	YHAI_CRYPA
17	31	62.0	421	1	ACDM_HUMAN
18	31	62.0	421	1	ACDM_PIG
19	31	62.0	562	1	TR2M_ERWHE
20	30	60.0	97	1	PLAS_DAUCA
21	30	60.0	121	1	TKNK_HUMAN
22	30	60.0	175	1	HES3_RAT
23	30	60.0	203	1	CTC_BACSU
24	30	60.0	231	1	ARAD_ECOLI
25	30	60.0	231	1	ARAD_SALTY
26	30	60.0	232	1	SCOA_HELPJ
27	30	60.0	232	1	SCOA_HELPY
28	30	60.0	259	1	OVUH_LYMST
29	30	60.0	421	1	AMP2_YEAST
30	30	60.0	421	1	ECB2_HALEL
31	30	60.0	423	1	ECB1_HALEL
32	30	60.0	430	1	FOLC_BACSU
33	30	60.0	457	1	Z185_HUMAN

34	30	60.0	469	1	LET1_KLULA
35	30	60.0	478	1	AMP2_HUMAN
36	30	60.0	478	1	AMP2_MOUSE
37	30	60.0	478	1	AMP2_RAT
38	30	60.0	478	1	GSR2_HUMAN
39	30	60.0	530	1	AHPF_XANCH
40	30	60.0	556	1	APLY_APLKU
41	30	60.0	583	1	HEMO_BRARE
42	30	60.0	890	1	ECN5_CLOPE
43	30	60.0	1049	1	SPS_ORYSA
44	30	60.0	1068	1	SPS_MAIZE
45	30	60.0	1081	1	SPS2_CRAPL
46	30	60.0	1176	1	NIR_NEUCR
47	30	60.0	1401	1	RPOC_VIBCH
48	30	60.0	1501	1	SNQ2_YEAST
49	30	60.0	1729	1	TABP_HUMAN
50	30	60.0	2717	1	ZEPI_HUMAN
51	30	60.0	3099	1	POLG_PEMVM
52	29.5	59.0	472	1	ET2A_XENLA
53	29	58.0	98	1	PLAS_ENTPR
54	29	58.0	98	1	PLAS_ULVAR
55	29	58.0	98	1	PLAS_ULVPE
56	29	58.0	99	1	PLAS_RUMOB
57	29	58.0	99	1	PLAS_TOBAC
58	29	58.0	113	1	Y011_BPT4
59	29	58.0	175	1	HES3_MOUSE
60	29	58.0	230	1	YCAP_ECOLI
61	29	58.0	242	1	PSB4_XENLA
62	29	58.0	258	1	YK10_METJA
63	29	58.0	261	1	YK10_MOUSE
64	29	58.0	338	1	MTBA_METBA
65	29	58.0	354	1	VGLI_VZVD
66	29	58.0	388	1	FM3_CAEEL
67	29	58.0	389	1	SAT_AERPE
68	29	58.0	412	1	DOK2_HUMAN
69	29	58.0	421	1	ACDM_MOUSE
70	29	58.0	424	1	MS11_ARATH
71	29	58.0	435	1	HEM1_DESYM
72	29	58.0	435	1	HEM1_DESYM
73	29	58.0	471	1	TMLH_NEUCR
74	29	58.0	472	1	ET2B_XENLA
75	29	58.0	477	1	CAP2_RAT

ALIGNMENTS

RESULT 1	CARB_FUSNN	STANDARD	PRT: 1058 AA.
AC	Q8RG86:		
DT	15-JUN-2002 (Rel. 41, Created)		
DT	15-JUN-2002 (Rel. 41, Last sequence update)		
DT	15-JUN-2002 (Rel. 41, Last annotation update)		
DE	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthase ammonia chain).		
DE	Carb OR FN0422.		
GN	Fusobacterium nucleatum (subsp. nucleatum).		
OC	Bacteria; Fusobacteria; Fusobacterium.		
OX	NCBI_TaxID=76856;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=ATCC 25586;		
RC	MEDLINE=21886394; PubMed=11889109;		
RA	Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasileva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyripides N., Overbeek R.;		
RA	"Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586."		
RT	Q9zeu7 halomonas e		
RL	J. Bacteriol. 184:2005-2018(2002).		
CC	-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +		

phosphate + L-glutamate + carbamoyl phosphate.
 -!- COFACTOR: Binds three manganese ions (by similarity).
 -!- PATHWAY: Arginine biosynthesis.
 -!- SUBUNIT: Pyrimidine biosynthesis; first step.
 promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (by similarity).
 -!- SIMILARITY: BELONGS TO THE CARB FAMILY.

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EMBL; AE010554; AAL94625.1; ALT_INIT.
 InterPro; IPR005483; CPase_L.
 InterPro; IPR005479; CPase_L_D2.
 InterPro; IPR005480; CPase_L_D3.
 InterPro; IPR005481; CPase_L_N.
 InterPro; IPR004362; MGS-like.
 Pfam; PF00289; CPase_L_chain; 2.
 Pfam; PF02786; CPase_L_D2; 2.
 Pfam; PF02787; CPase_L_D3; 1.
 Pfam; PF02142; MGS; 1.
 PRINTS; PR00098; CPASE.
 PROSITE; PS00866; CPASE_1; 2.
 PROSITE; PS00867; CPASE_2; 2.
 Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
 ATP-binding; Manganese; Complete proteome.
 FT DOMAIN 1 401
 FT DOMAIN 402 546
 FT DOMAIN 547 929
 FT DOMAIN 930 1058
 FT REPEAT 1 546
 FT REPEAT 547 1058
 FT NP_BIND 153 210
 FT NP_BIND 302 352
 FT METAL 284 284
 FT METAL 298 298
 FT METAL 300 300
 FT METAL 820 820
 FT METAL 832 832
 SQ SEQUENCE 1058 AA; 117451 MW; ED7037AF77C1E39F CRC64;

Query Match 70.0%; Score 35; DB 1; Length 1058;
 Best Local Similarity 60.0%; Pred. No. 17;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPGXGDYS 11
 Db 190 EIVPGLNYS 199

RESULT 2
 Y11K_TYDVA
 ID Y11K_TYDVA STANDARD; PRT; 102 AA.
 AC F31619;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE Hypothetical 11.2 kDa protein.
 GN V1.
 OS Tobacco yellow dwarf virus (strain Australia) (TYDV).
 OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
 OX NCBI_TaxID=31599;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92188538; PubMed=1546458;
 RA Morris B.A.N., Richardson K.A., Haley A., Zhan X., Thomas J.E.;

RT The nucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses
 RT infecting monocotyledonous plants.";
 RL Virology 187:633-642(1992).
 CC -----
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 CC -----
 CC EMBL; M81103; AAA47947.1; -.
 DR PIR; A42452; A42452.
 DR InterPro; IPR002621; Gemini_mov.
 DR Pfam; PF01708; Gemini_mov; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 102 AA; 11178 MW; A40ECF1E0AF5B67 CRC64;

Query Match 68.0%; Score 34; DB 1; Length 102;
 Best Local Similarity 60.0%; Pred. No. 2.3;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPGXGDYS 11
 Db 7 QVVPNGINYS 16

RESULT 3
 HMPA_VIBCH
 ID HMPA_VIBCH STANDARD; PRT; 394 AA.
 AC Q9KMY3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Flavohemoprotein (Hemoglobin-like protein) (Flavohemoglobin).
 GN HMP OR VCA0183.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
 RA "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.";
 RT Nature 406:477-483(2000).
 RL Nature 406:477-483(2000).
 CC -!- DOMAIN: CONSISTS OF TWO DISTINCT DOMAINS; ONE IS A HEME-CONTAINING OXYGEN BINDING DOMAIN IN THE N-TERMINAL REGION AND THE OTHER IS AN FAD-CONTAINING REDUCTASE DOMAIN FOUND IN THE C-TERMINAL REGION.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY. TWO-DOMAIN FLAVOHEMOPROTEIN SUBFAMILY.
 CC -!- SIMILARITY: TO A NUMBER OF FAD/NAD(P) FLAVOPROTEIN OXIDOREDUCTASES.

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 CC -----
 CC EMBL; AE004358; AAF96096.1; -.
 DR HSSP; P39662; 1CQX.

DR TIGR; VCA0183; -
 DR InterPro; IPR001834; Cyt_B5_reductase.
 DR InterPro; IPR001709; FPN_cyt_redtse.
 DR InterPro; IPR000971; Globin.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR InterPro; IPR001221; Phe_hydroxylase.
 DR Pfam; PF00042; globin; 1.
 DR Pfam; PF00175; NAD_binding; 1.
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR PRINTS; PR00371; FPNCR.
 DR PRINTS; PR00410; PHEHYDRXLASE.
 DR PROSITE; PS01033; GLOBIN; 1.
 KW Oxidoreductase; NADP; Heme; Flavoprotein; FAD; Iron transport;
 KW Oxygen transport; Transport; Complete proteome.
 FT METAL 53 53
 FT METAL 85 85
 FT NP_BIND 268 273
 FT SEQUENCE 394 AA; 44191 MW; 4490FAE28823A CRC64;
 Query Match 68.0%; Score 34; DB 1; Length 394;
 Best Local Similarity 66.7%; Pred. No. 9.7;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 EVVPGXDY 10
 ||| |||
 Db 194 EVTPGSDY 202

RESULT 4
 FAF_DROME
 ID FAF_DROME STANDARD; PRT; 2747 AA.
 AC P55824;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable ubiquitin carboxyl-terminal hydrolase FAF (EC 3.1.2.15)
 DE (Ubiquitin thiolesterase FAF) (Ubiquitin-specific processing protease
 DE FAF) (Deubiquitinating enzyme FAF) (Fat facets protein).
 GN FAF.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93202020; PubMed=1295747;
 RA Fischer-Vize J.A., Rubin G.M., Lehmann R.;
 RT The fat facets gene is required for Drosophila eye and embryo
 development.";
 RL Development 116:985-1000(1992).
 CC -!- FUNCTION: REQUIRED FOR EYE AND EMBRYO DEVELOPMENT, AND PLAYS A
 CC ROLE IN COMPOUND EYE ASSEMBLY AND OOGENESIS RESPECTIVELY. IN THE
 CC LARVAL EYE DISKS, CELLS OUTSIDE THE ASSEMBLING FACETS REQUIRE THIS
 CC PROTEIN FOR SHORT-RANGE CELL INTERACTIONS THAT PREVENT THE MYSTERY
 CC CELLS FROM BECOMING PHOTORECEPTORS. IT IS ALSO REQUIRED FOR
 CC NUCLEAR MIGRATION AND CELLULARIZATION IN EARLY EMBRYOGENESIS AND
 CC COULD PLAY A ROLE IN POLE CELL DETERMINATION, DEVELOPMENT OR
 CC FUNCTION.
 CC -!- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
 CC ubiquitin + a thiol.
 CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
 CC SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -!- TISSUE SPECIFICITY: EYE DISKS AND OVARIES.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C19.
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 CC -----
 CC EMBL; L04959; AAF01345.1; -;
 CC EMBL; L04958; AAF01346.1; -;
 CC MEROPS; C19.007; -;
 CC FlyBase; FBgn0005632; faf.
 CC InterPro; IPR001394; UCH-2.
 CC Pfam; PF00442; UCH-1; 1.
 CC Pfam; PF00443; UCH-2; 1.
 CC PROSITE; PS00972; UCH_2_1; 1.
 CC PROSITE; PS00973; UCH_2_2; 1.
 CC PROSITE; PS0235; UCH_2_3; 1.
 KW Ubl conjugation pathway; Hydrolase; Thiol protease;
 KW Developmental protein; Vision; Alternative splicing.
 FT ACT_SITE 1677 1677 BY SIMILARITY.
 FT ACT_SITE 1978 1978 BY SIMILARITY.
 FT ACT_SITE 1986 1986 BY SIMILARITY.
 FT VARSPLIC 2705 2747 KCRVVIKKLVESKDEEDATSATTAATTEVTTSPATAS
 FT VARIANT 2725 2725 ORQOL -> VTRANNV (IN SHORT ISOFORM).
 FT SEQUENCE 2747 AA; 307954 MW; 1D97659F7A7B2ADE CRC64;
 Query Match 68.0%; Score 34; DB 1; Length 2747;
 Best Local Similarity 54.5%; Pred. No. 78;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EEVVPXGXNYS 11
 ||| |||
 Db 1394 EVIPVDGQDFS 1404

RESULT 5
 REV_SIVCZ
 ID REV_SIVCZ STANDARD; PRT; 124 AA.
 AC P17280;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE REV protein (Anti-repression transactivator protein) (ART/TRS).
 DE REV.
 GN REV.
 OS Chimpanzee immunodeficiency virus (SIV(cpz)) (CIV).
 OC Viruses; Retroviruses; Retroviridae; Lentivirus.
 OX NCBI_TaxID=11723;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90259077; PubMed=2188136;
 RA Huet T., Cheynier R., Meyerhans A., Roelants G., Wain-Hobson S.;
 RT "Genetic organization of a chimpanzee lentivirus related to HIV-1.";
 RL Nature 345:356-359(1990).
 CC -!- FUNCTION: REV APPEARS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE
 CC NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.
 CC -!- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.
 CC -!- PTM: PHOSPHOPROTEIN WHOSE STATE OF PHOSPHORYLATION IS MEDIATED
 CC BY A SPECIFIC SERINE KINASE ACTIVITY PRESENT IN THE NUCLEUS.
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 CC -----
 CC EMBL; X52154; CAA36405.1; -;
 CC PIR; S09988; VKLJSI.
 CC HIV; X52154; REVSCPZ.
 CC InterPro; IPR000625; REV_protein.
 CC Pfam; PF00424; REV; 1.
 KW Transcription regulation; AIDS; phosphorylation; Nuclear protein.
 SQ SEQUENCE 124 AA; 13701 MW; F5877D1BDF65A7B2 CRC64;

Query Match 66.0%; Score 33; DB 1; Length 124;
 Best Local Similarity 60.0%; Pred. No. 4.6;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVPXGXDYS 11
 | | | | |
 Db 107 ETVPAGNGYS 116

RESULT 6

ID YK14_CAEEL STANDARD; PRT; 327 AA.
 AC P34338;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein C15H7.4 in chromosome III.
 GN C15H7.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kerhaw J., Kirsten J., Laister N.,
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkneen R.,
 RA Sins M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
 RA Woldman P.;
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).

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 DR EMBL; Z22173; CAA80126.1; -
 DR PIR; S40753; S40753.
 DR WormPep; C15H7.4; CE00082.
 KW Hypothetical protein.
 SQ SEQUENCE 327 AA; 35566 MW; 716BC2BDD2E9607E CRC64;

Query Match 66.0%; Score 33; DB 1; Length 327;
 Best Local Similarity 63.6%; Pred. No. 13;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EVVPXGXDYS 11
 :|:|:|:|:|
 Db 175 KEVVPNGGDKS 185

RESULT 7

ACDM_RAT STANDARD; PRT; 421 AA.
 ID ACDM_RAT
 AC P08503;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acyl-CoA dehydrogenase, medium-chain specific, mitochondrial precursor
 DE (EC 1.3.99.3) (MCAD).

GN ACDM.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=87280028; PubMed=3611054;
 RA Matsubara Y., Kraus J.P., Ozasa H., Glassberg R., Finocchiaro G.,
 RA Ikeda Y., Mole J., Rosenberg L.E., Tanaka K.;
 RT "Molecular cloning and nucleotide sequence of cDNA encoding the
 RT entire precursor of rat liver medium chain acyl coenzyme A
 RT dehydrogenase";
 RL J. Biol. Chem. 262:10104-10108(1987).
 CC -!- FUNCTION: THIS ENZYME IS SPECIFIC FOR ACYL CHAIN LENGTHS OF 4 TO
 CC 16.
 CC -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
 CC ETF.
 CC -!- COFACTOR: FAD.
 CC -!- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
 CC step.
 CC -!- SUBUNIT: HOMOTETRAMER.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -!- MISCELLANEOUS: A NUMBER OF STRAIGHT-CHAIN ACYL-COA DEHYDROGENASES
 CC OF DIFFERENT SUBSTRATE SPECIFICITIES ARE PRESENT IN MAMMALIAN
 CC TISSUES.
 CC -!- SIMILARITY: BELONGS TO THE ACYL-COA DEHYDROGENASE FAMILY.
 CC
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EMBL; J02791; AAA40670.1; -

PIR; A28436; DERTCM.

HSP; P11310; LEGD.

InterPro; IPR001552; Acyl-CoA_dh.

Pfam; PF00441; Acyl-CoA_dh; 1.

Pfam; PF02770; Acyl-CoA_dh_M; 1.

Pfam; PF02771; Acyl-CoA_dh_N; 1.

PROSITE; PS00072; ACYL_COA_DH_1; 1.

PROSITE; PS00073; ACYL_COA_DH_2; 1.

Oxidoreductase; Flavoprotein; FAD; Fatty acid metabolism;

Mitochondrion; Transit peptide.

TRANSIT 1 25 MITOCHONDRION.

CHAIN 26 421 ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN

SPECIFIC.

ACT_SITE 193 193 FORMS A HYDROGEN-BOND WITH THE FLAVIN

ACT_SITE 401 401 N(5) OF THE FAD COFACTOR (BY SIMILARITY).

SEQUENCE 421 AA; 46555 MW; 2CF076F8C919BDE8 CRC64;

Query Match 66.0%; Score 33; DB 1; Length 421;

Best Local Similarity 50.0%; Pred. No. 17;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDY 10

|||:| |

Db 58 EEIIPVADPY 67

RESULT 8

PLAS_ORYSA STANDARD; PRT; 154 AA.
 ID PLAS_ORYSA
 AC P20423; Q5SBB8;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Plastocyanin, chloroplast precursor.

GN PETE.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Ilpoom; TISSUE=Leaf;
RA Lee J.-S.;
RT "Molecular cloning and characterization of plastocyanin precursor in rice."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 58-154.
RC STRAIN=cv. Japonica;
RX MEDLINE=89386623; PubMed=2780337;
RA Yano H., Kamo M., Taugita A., Aso K., Nozu Y.;
RT "The amino acid sequence of plastocyanin from rice (*Oryza sativa*, subspecies japonica)."
RL Protein Seq. Data Anal. 2:385-389(1989).
CC -1- FUNCTION: Participates in electron transfer between P700 and the cytochrome b6-f complex in photosystem I.
CC -1- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID MEMBRANE SURFACE IN CHLOROPLASTS.
CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
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CC
DR EMBL; AF093636; AAC78108.1; -.
DR PIR; S06105; S06105.
DR PIR; JT0352; JT0352.
DR HSP; P00289; 2PCF.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR001235; Copper_blue.
DR Pfam; PF00127; copper-bind; 1.
DR PRINTS; PR00156; COPPERBLUE.
DR PRODOM; PD001235; Copper_blue; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
KW Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
KW Transit peptide.
FT TRANSIT 1 57 CHLOROPLAST.
FT CHAIN 58 154 PLASTOCYANIN.
FT DOMAIN 58 154 PLASTOCYANIN-LIKE.
FT METAL 94 94 COPPER (BY SIMILARITY).
FT METAL 139 139 COPPER (BY SIMILARITY).
FT METAL 142 142 COPPER (BY SIMILARITY).
FT METAL 147 147 COPPER (BY SIMILARITY).
SQ SEQUENCE 154 AA; 15577 MW; E45725D25B5F400D CRC64;
Query Match 64.0%; Score 32; DB 1; Length 154;
Best Local Similarity 54.5%; Pred. No. 9.6;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Oy 1 EEVXPXGXDYS 11
Db 100 EDVPSGVDVS 110
RESULT 9.
PLAS HORVU STANDARD; PRT; 155 AA.
AC P08248;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Plastocyanin, chloroplast precursor.

GN PETE.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Bomi;
RA Nielsen O.S., Gausing K.;
RT "The precursor of barley plastocyanin: sequence of cDNA clones and gene expression in different tissues."
RL FEBS Lett. 225:159-162(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. NK 1558;
RX MEDLINE=94039081; PubMed=8223592;
RA Nielsen P., Gausing K.;
RT "In vitro binding of nuclear proteins to the barley plastocyanin gene promoter region."
RL Eur. J. Biochem. 217:97-104(1993).
CC -1- FUNCTION: Participates in electron transfer between P700 and the cytochrome b6-f complex in photosystem I.
CC -1- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID MEMBRANE SURFACE IN CHLOROPLASTS.
CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
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CC
DR EMBL; Y00704; CAA68696.1; -.
DR PIR; Z28347; CAA82201.1; -.
DR HSP; P00289; 2PCF.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR001235; Copper_blue.
DR Pfam; PF00127; copper-bind; 1.
DR PRINTS; PR00156; COPPERBLUE.
DR PRODOM; PD001235; Copper_blue; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
KW Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
KW Transit peptide.
FT TRANSIT 1 58 CHLOROPLAST.
FT CHAIN 59 155 PLASTOCYANIN.
FT DOMAIN 59 155 PLASTOCYANIN-LIKE.
FT METAL 95 95 COPPER (BY SIMILARITY).
FT METAL 140 140 COPPER (BY SIMILARITY).
FT METAL 143 143 COPPER (BY SIMILARITY).
FT METAL 148 148 COPPER (BY SIMILARITY).
FT VARIANT 120 120 T -> N (IN CV. NK 1558).
SQ SEQUENCE 155 AA; 15709 MW; DAA7EABE5F64F91 CRC64;
Query Match 64.0%; Score 32; DB 1; Length 155;
Best Local Similarity 54.5%; Pred. No. 9.6;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Oy 1 EEVXPXGXDYS 11
Db 101 EDVPSGVDVS 111
RESULT 10
PLAT POPNI STANDARD; PRT; 168 AA.
AC P11970;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Plastocyanin B, chloroplast precursor.
GN PEST.
OS Populus nigra (Lombardy poplar).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Malpighiales; Salicaceae; Populus.
OX NCBI_TaxID=3691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Italica; TISSUE=Leaf;
RA Reichert J., Jenzelewski V., Haehnel W.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 70-168.
RC STRAIN=cv. Italica;
RA Dmitrov M.I., Egorov C.A., Donchev A.A., Atanasov B.P.;
RT "Complete amino acid sequence of poplar plastocyanin b.";
RL FEBS Lett. 226:17-22(1987).
CC -1- FUNCTION: Participates in electron transfer between P700 and the
CC cytochrome b6-f complex in photosystem I.
CC -1- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID
CC MEMBRANE SURFACE IN CHLOROPLASTS.
CC -1- SIMILARITY: THERE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF
CC POPULAR PLASTOCYANINS A AND B.
CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
CC
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CC -----
DR EMBL; Z50186; CAA90565.1; -
DR PIR; S00210; S00210.
DR HSP; P00299; 1PLC.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR001235; Copper_blue.
DR Pfam; PF00127; copper-bind; 1.
DR PRINTS; PR00156; COPPERBLU6.
DR PRODOM; PD001235; Copper_blue; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
KW Transit peptide; Multigene family.
FT TRANSIT 1 69
FT CHAIN 70 168
FT DOMAIN 70 168
FT METAL 106 106 PLASTOCYANIN B.
FT METAL 153 153 PLASTOCYANIN-LIKE.
FT METAL 156 156 COPPER.
FT METAL 161 161 COPPER.
FT METAL 161 161 COPPER.
SQ SEQUENCE 168 AA; 16981 MW; F20DAGEA2038AEA CRC64;
Query Match 64.0%; Score 32; DB 1; Length 168;
Best Local Similarity 54.5%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 EEVVPXGXDS 11
Db 112 EDAPVSGVDVS 122
RESULT 11
YJAG_SALTY STANDARD; PRT; 196 AA.
AC Q9L912;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein yJAG.
GN YJAG OR STM4169 OR STMFI.23 OR STY3716.
OS Salmonella typhimurium, and

OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella
OX NCBI_TaxID=602, 601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2";
RL Nature 413:852-856(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18";
RL Nature 413:848-852(2001).
CC -1- SIMILARITY: STRONG, TO H.INFLUENZAE HI0431.
CC -----
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CC -----
DR EMBL; AF170176; AAF33519.1; -
DR EMBL; AE008894; AAL22997.1; -
DR EMBL; AL627279; CAD09475.1; -
DR StyGene; SG????; yJag.
DR Hypothetical protein; Complete proteome.
KW SEQUENCE 196 AA; 22704 MW; E40049CE5EE564150 CRC64;
SQ
Query Match 64.0%; Score 32; DB 1; Length 196;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 EEVVPXGXDY 10
Db 76 EEATPAADY 85
RESULT 12
TOLB_HAEIN STANDARD; PRT; 427 AA.
AC P44677; P94811;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE TolB protein precursor.
GN TOLB OR HI0382.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;

RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RA "whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd.";
 RL Science 269:496-512(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=1479;
 RC MEDLINE=97080550; PubMed=8921895;
 RA Sen K., Sikkema D.J., Murphy T.F.;
 RA "Isolation and characterization of the Haemophilus influenzae tolQ,
 RT tolR, tolA and tolB genes";
 RL Gene 178:75-81(1996).
 CC -!- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
 CC -!- (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Periplasmic (Potential).
 CC -!- SIMILARITY: BELONGS TO THE TOLB FAMILY.
 CC -----
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 CC -----
 DR EMBL; U32722; AAC22040.1; -;
 DR EMBL; U32470; AAC44597.1; -;
 DR HSSP; P19935; 1CRZ.
 DR TIGR; HT0382; -;
 KW Transport; Protein transport; Periplasmic; Signal; Complete proteome.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 427 TOLB PROTEIN.
 FT VARIANT 6 6 R -> H (IN STRAIN 1479).
 FT VARIANT 14 14 V -> I (IN STRAIN 1479).
 FT VARIANT 17 19 VGS -> ITH (IN STRAIN 1479).
 FT VARIANT 21 21 A -> V (IN STRAIN 1479).
 FT VARIANT 79 79 R -> H (IN STRAIN 1479).
 FT VARIANT 129 129 T -> A (IN STRAIN 1479).
 FT VARIANT 160 160 A -> G (IN STRAIN 1479).
 FT VARIANT 237 237 A -> T (IN STRAIN 1479).
 FT VARIANT 322 322 S -> N (IN STRAIN 1479).
 FT VARIANT 326 326 A -> V (IN STRAIN 1479).
 FT VARIANT 328 328 A -> S (IN STRAIN 1479).
 SQ SEQUENCE 427 AA; 44967 MW; 0882201AEE9254B9 CRC64;
 Query Match 64.0%; Score 32; DB 1; Length 427;
 Best Local Similarity 60.0%; Pred. No. 29;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 EVVPGXNDYS 11
 Db 103 QVVPNGNGYS 112
 RESULT 13
 ALOC_HUMAN STANDARD; PRT; 1499 AA.
 AC 060312; Q96914;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Potential phospholipid-transporting ATPase VC (EC 3.6.3.1) (ATPVC)
 DE (Aminophospholipid translocase VC).
 GN ATP10C OR ATPVC OR KIAA0566.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21225279; PubMed=11326269;
 RA Meguro M., Kashiwagi A., Mitsuwa K., Nakao M., Kondo I., Saitoh S.,
 RA Oshimura M.;
 RA "A novel maternally expressed gene, ATP10C, encodes a putative
 RT aminophospholipid translocase associated with Angelman syndrome.";
 RL Nat. Genet. 28:19-20(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21313119; PubMed=11353404;
 RA Herzog L.B.K., Kim S.-J., Cook E.H. Jr., Ledbetter D.H.;
 RA "The human aminophospholipid-transporting ATPase gene ATP10C maps
 RT adjacent to UBE3A and exhibits similar imprinted expression";
 RL Am. J. Hum. Genet. 68:1501-1509(2001).
 RN [3]
 RP SEQUENCE OF 337-1499 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98290545; PubMed=9628581;
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Ohara O.;
 RA "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:331-39(1998).
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O -> ADP + phosphate.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- TISSUE SPECIFICITY: Wide expression, with highest levels in
 CC kidney, followed by lung, brain, prostate, testis, ovary, and
 CC small intestine.
 CC -!- DISEASE: Defects in ATP10C may be a cause of Angelman syndrome
 CC (AS), also known as 'happy puppet syndrome'.
 CC -!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
 CC ATPASES). SUBFAMILY IV.
 CC -----
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 CC -----
 DR EMBL; AB051358; BAB47392.1; -;
 DR EMBL; AY029504; AAK33100.1; -;
 DR EMBL; AY029487; AAK33100.1; JOINED.
 DR EMBL; AY029488; AAK33100.1; JOINED.
 DR EMBL; AY029489; AAK33100.1; JOINED.
 DR EMBL; AY029490; AAK33100.1; JOINED.
 DR EMBL; AY029491; AAK33100.1; JOINED.
 DR EMBL; AY029492; AAK33100.1; JOINED.
 DR EMBL; AY029493; AAK33100.1; JOINED.
 DR EMBL; AY029494; AAK33100.1; JOINED.
 DR EMBL; AY029495; AAK33100.1; JOINED.
 DR EMBL; AY029496; AAK33100.1; JOINED.
 DR EMBL; AY029497; AAK33100.1; JOINED.
 DR EMBL; AY029498; AAK33100.1; JOINED.
 DR EMBL; AY029499; AAK33100.1; JOINED.
 DR EMBL; AY029500; AAK33100.1; JOINED.
 DR EMBL; AY029501; AAK33100.1; JOINED.
 DR EMBL; AY029502; AAK33100.1; JOINED.
 DR EMBL; AY029503; AAK33100.1; JOINED.
 DR EMBL; AB011138; BAA25492.1; -;
 DR Genbank; HGNC:13547; ATP10C.
 DR MIM; 605855; -;
 DR MIM; 105830; -;
 DR InterPro; IPR001757; ATPase_E1-E2.
 DR InterPro; IPR001454; Hlgase/hydrolase.
 DR Pfam; PF00702; Hydrolase; 1.

DR PRINTS: PR00119; CATAPSE.
 DR PROSITE; PS00154; ATPASE_E1_E2; 1.
 KW Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
 MW Multigene family.
 FT DOMAIN 1 86 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 87 106 POTENTIAL.
 FT DOMAIN 107 110 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 111 128 POTENTIAL.
 FT DOMAIN 129 309 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 310 332 POTENTIAL.
 FT DOMAIN 337 362 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 363 384 POTENTIAL.
 FT DOMAIN 385 1087 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1088 1108 POTENTIAL.
 FT DOMAIN 1109 1119 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1120 1140 POTENTIAL.
 FT DOMAIN 1141 1170 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1171 1192 POTENTIAL.
 FT DOMAIN 1193 1199 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1200 1222 POTENTIAL.
 FT DOMAIN 1223 1228 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1229 1249 POTENTIAL.
 FT DOMAIN 1250 1267 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1268 1292 POTENTIAL.
 FT DOMAIN 1293 1499 CYTOPLASMIC (POTENTIAL).
 FT MOD_RES 427 427 PHOSPHORYLATION (BY SIMILARITY).
 FT METAL 1031 1031 MAGNESIUM (BY SIMILARITY).
 FT METAL 1035 1035 MAGNESIUM (BY SIMILARITY).
 FT DOMAIN 467 470 POLY-GLU.
 FT CONFLICT 388 388 Q -> R (IN REF. 3).
 SQ SEQUENCE 1499 AA; 167687 MW; D4996A4D0635A68D CRC64;
 Query Match 64.0%; Score 32; DB 1; Length 1499;
 Best Local Similarity 63.6%; Pred. No. 1.1e+02;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDS 11
 I I I I I I I
 DB 469 EEVVPXGXDS 479

RESULT 14
 CHAC_HUMAN STANDARD; PRT; 3174 AA.
 AC Q96RL7; Q9Y2J1; Q9H995;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Chorea (Chorea-acanthocytosis protein).
 GN CHAC OR KIAA0986.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.; ALTERNATIVE SPLICING, AND VARIANT CHAC PRO-1452.
 RX MEDLINE=21275959; PubMed=11381253;
 RA Rampoldi L., Dobson-Stone C., Rubio J., Daneke A., Chalmers R.,
 RA Wood N.W., Verellen C., Ferrer X., Malandrini A., Fabrizio G.M.,
 RA Brown R., Vance J., Pericak-Vance M., Rudolf G., Carrie S., Alonso E.,
 RA Manfredi M., Nemeth A.H., Monaco A.P.;
 RT "A conserved sorting-associated protein is mutant in chorea-
 acanthocytosis";
 RL Nat. Genet. 28:119-120(2001).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM B).
 RX MEDLINE=21275960; PubMed=11381254;
 RA Ueno S., Maruki Y., Nakamura M., Tomemori Y., Kamae K., Tanabe H.,
 RA Yamashita Y., Matsuda S., Kaneko S., Sano A.;
 RT "The gene encoding a newly discovered protein, chorein, is mutated in
 chorea-acanthocytosis";
 RL Nat. Genet. 28:121-122(2001).
 RN [3]

RP SEQUENCE OF 1638-3174 FROM N.A. (ISOFORM B).
 RC TISSUE=Brain;
 RX MEDLINE=9946063; PubMed=10231032;
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XIII.
 The complete sequences of 100 new cDNA clones from brain which code
 for large proteins in vitro.";
 RL DNA Res. 6:63-70(1999).
 RN [4]
 RP SEQUENCE OF 1749-2130 FROM N.A.
 RC TISSUE=Placenta;
 RX Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 2200-3174 FROM N.A.
 RA ISOZAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
 RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
 RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
 RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
 RA Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y., Oshima A.;
 RT "NEDO human cDNA sequencing project";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 CC !- FUNCTION: May play a role in the control of protein cycling
 through the trans-Golgi network to early and late endosomes,
 lysosomes and plasma membrane.
 CC !- ALTERNATIVE PRODUCTS: 2 isoforms; A (shown here) and B; are
 produced by alternative splicing.
 CC !- TISSUE SPECIFICITY: Widely expressed. Higher expression is found
 in brain, heart, skeletal muscle and kidney.
 CC !- DISEASE: Defects in CHAC are the cause of chorea-acanthocytosis
 (CHAC), an autosomal recessive neurodegenerative disorder
 characterized by the gradual onset of hyperkinetic movements and
 abnormal erythrocyte morphology. Basal ganglia atrophy in the
 brain is a pathological feature of the disease. Other clinical
 symptoms include psychiatric features, epilepsy, peripheral
 neuropathy, myopathy and oral self-mutilation.
 CC !- SIMILARITY: CONTAINS 10 TPR REPEATS.
 CC
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 CC
 DR EMBL; AF337532; AAK61861.1; -
 DR EMBL; AB054005; BAB59128.1; -
 DR EMBL; AB023203; BAA76830.1; -
 DR EMBL; BC020576; AAH20576.1; -
 DR EMBL; AK022967; BAB14337.1; -
 DR Genew; HGNC:1908; CHAC.
 DR MIM; 605978; -
 DR MIM; 200150; -
 KW Repeat; TPR repeat; Alternative splicing; Disease mutation.
 FT REPEAT 212 245 TPR 1.
 FT REPEAT 373 406 TPR 2.
 FT REPEAT 537 575 TPR 3.
 FT REPEAT 1256 1289 TPR 4.
 FT REPEAT 1291 1320 TPR 5.
 FT REPEAT 2009 2041 TPR 6.
 FT REPEAT 2568 2601 TPR 7.
 FT REPEAT 2717 2751 TPR 8.
 FT REPEAT 2860 2898 TPR 9.
 FT REPEAT 3086 3119 TPR 10.
 FT VARSPLIC 3064 3174
 FT LTCWOYSEDFTEKPEFIVHGRRLRIEAKERKSVFHFAREF
 FT GKNHFKSTPDADWILTKLQEAPEPSL -> KIQFYREW
 FT ITHNKKSSDDDDDDDDDDSLNH (IN ISOFORM B).
 FT S -> P (IN CHAC).
 FT /FTID-VAR.012803.
 FT VARIANT 1452 1452
 FT CONFLICT 1198 1198 R -> K (IN REF. 2 AND 3).


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FT CONFLICT 2127 2129 GIE -> VSA (IN REF. 4).
FT CONFLICT 2281 2281 G -> E (IN REF. 5).
FT CONFLICT 2413 2413 T -> R (IN REF. 5).
FT CONFLICT 2567 2567 K -> E (IN REF. 5).
SQ SEQUENCE 3174 AA; 360299 MW; FD2AB895B4A7149E CRC64;

Query Match
Best Local Similarity 64.0%; Score 32; DB 1; Length 3174;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXNDY 10
| :| | |
Db 242 ENIVPEGYDF 251

RESULT 15
HIS9_THEME STANDARD; PRT; 233 AA.
AC Q9WZL1;
DT 16-OCT-2001 (Rel. 40, Created)
DE 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable histidinol-phosphatase (EC 3.1.3.15) (HolPase).
GN HIS9 OR TM0804.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
OC Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MSB8 / DSM 3109;
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima."
RL Nature 393:323-329(1999).
CC -1- CATALYTIC ACTIVITY: L-histidinol-phosphate + H(2)O = L-histidinol
CC + phosphate.
CC -1- PATHWAY: Histidine biosynthesis; eighth step.
CC -1- SIMILARITY: BELONGS TO THE PHP FAMILY OF HYDROLASE. HISK FAMILY.
CC
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CC
CC EMBL; X14524; CAA32666.1; -
CC DR PIR; S03833; S03833.
CC DR MEROPS; C07.001; -
CC DR InterPro; IPR002704; Peptidase_C7.
CC DR Pfam; PF01830; Peptidase_C7; 1.
CC DR ProDom; PD040949; Peptidase_C7; 1.
CC DR Hypothetical protein; Hydrolase; Thiol protease.
CC KW Hypothetical protein; Hydrolase; Thiol protease.
CC SQ SEQUENCE 319 AA; 35443 MW; ALEF775F9AEE7A CRC64;

Query Match 62.0%; Score 31; DB 1; Length 319;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
| | | | |
Db 31 EEVVPAG 37

RESULT 17
ACDM_HUMAN STANDARD; PRT; 421 AA.
AC P11310; Q9NYF1;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-CoA dehydrogenase, medium-chain specific, mitochondrial precursor
DE (EC 1.3.99.3) (MCAD).
GN ACADM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87231952; PubMed=3035565;
RA Kelly D.P., Kim J.-J.P., Billadello J.J., Hainline B.E., Chu T.W.,

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RESULT 16
YHAL_CRYPA STANDARD; PRT; 319 AA.
ID YHAL_CRYPA
AC P10941;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein 1 in hypovirulence-associated DS-RNA genetic
DE element (Contains: P29 proteinase).
DE Cryphonectria parasitica (Chestnut blight fungus) (Endothia
OS parasitica).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Diaporthales; Valsaceae; Cryphonectria.
OX NCBI_TaxID=5116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EP713;
RX MEDLINE=89251594; PubMed=2721496;
RA Rae B.P., Hillman B.I., Tartaglia J., Nuss D.L.;
RT "Characterization of double-stranded RNA genetic elements associated
RT with biological control of chestnut blight: organization of terminal
RT domains and identification of gene products."
RL EMBL J. 8:657-663(1989).
CC -1- MISCELLANEOUS: DOUBLE-STRANDED RNA GENETIC ELEMENTS ARE ASSOCIATED
CC WITH BIOLOGICAL CONTROL OF THE FUNGAL DISEASE CHESTNUT BLIGHT.
CC THIS DS-RNA ARE ASSOCIATED WITH HYPOVIRULENCE. THEY ARE LOCALIZED
CC IN THE CYTOPLASM.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C7.
CC
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CC
CC EMBL; X14524; CAA32666.1; -
CC DR PIR; S03833; S03833.
CC DR MEROPS; C07.001; -
CC DR InterPro; IPR002704; Peptidase_C7.
CC DR Pfam; PF01830; Peptidase_C7; 1.
CC DR ProDom; PD040949; Peptidase_C7; 1.
CC DR Hypothetical protein; Hydrolase; Thiol protease.
CC KW Hypothetical protein; Hydrolase; Thiol protease.
CC SQ SEQUENCE 319 AA; 35443 MW; ALEF775F9AEE7A CRC64;

Query Match 62.0%; Score 31; DB 1; Length 319;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
| | | | |
Db 31 EEVVPAG 37

RESULT 17
ACDM_HUMAN STANDARD; PRT; 421 AA.
AC P11310; Q9NYF1;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Acyl-CoA dehydrogenase, medium-chain specific, mitochondrial precursor
DE (EC 1.3.99.3) (MCAD).
GN ACADM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87231952; PubMed=3035565;
RA Kelly D.P., Kim J.-J.P., Billadello J.J., Hainline B.E., Chu T.W.,

```

- RT Strauss A.W.: "Nucleotide sequence of medium-chain acyl-CoA dehydrogenase mRNA and its expression in enzyme-deficient human tissue.";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:4068-4072(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA TISSUE-Colon;
 RC TISSUE-Liver;
 RL Sun F., Wang Y., Block G.D.:
 RT "Medium-chain acyl-CoA dehydrogenase.";
 RN Submitted (Mar-2000) to the EMBL/GenBank/DDBJ databases.
 RP [3]
 RA SEQUENCE FROM N.A.
 RC TISSUE-Liver;
 RL Strausberg R.;
 RT Submitted (Mar-2001) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RA SEQUENCE OF 314-342 FROM N.A., AND VARIANT MCAD GLU-329.
 RX MEDLINE-90365752; PubMed-2393404;
 RA Matsubara Y., Narisawa K., Miyabayashi S., Tada K., Coates P.M.,
 Bachmann C., Elsas L.J. II, Pollitt R.J., Rhead W.J., Roe C.R.;
 RT "Identification of a common mutation in patients with medium-chain
 acyl-CoA dehydrogenase deficiency.";
 RL Biochem. Biophys. Res. Commun. 171:498-505(1990).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
 RX MEDLINE-96420477; PubMed-8823176;
 RA Lee H.J., Wang M., Paschke R., Nandy A., Ghisla S., Kim J.J.;
 RT "Crystal structures of the wild type and the Glu376Gly/Thr255Glu
 mutant of human medium-chain acyl-CoA dehydrogenase: Influence of the
 location of the catalytic base on substrate specificity.";
 RL Biochemistry 35:12412-12420(1996).
 RN [6]
 RP REVIEW ON VARIANTS MCAD.
 RX MEDLINE-93250819; PubMed-1363805;
 RA Tanaka K., Yokota I., Coates P.M., Strauss A.W., Kelly D.P.,
 Zhang Z.F., Gregersen N., Andresen B.S., Matsubara Y., Curtis D.,
 Chen Y.-T.;
 RT "Mutations in the medium chain acyl-CoA dehydrogenase (MCAD) gene.";
 RL Hum. Mutat. 1:271-279(1992).
 RN [7]
 RP VARIANT MCAD GLU-329.
 RX MEDLINE-90368980; PubMed-2394825;
 RA Yokota I., Indo Y., Coates P.M., Tanaka K.;
 RT "Molecular basis of medium chain acyl-coenzyme A dehydrogenase
 deficiency. An A to G transition at position 985 that causes a
 lysine-304 to glutamate substitution in the mature protein is the
 single prevalent mutation.";
 RL J. Clin. Invest. 86:1000-1003(1990).
 RN [8]
 RP VARIANT MCAD GLU-329.
 RX MEDLINE-91067682; PubMed-2251268;
 RA Kelly D.P., Whelan A.J., Ogden M.L., Alpers R., Zhang Z.F., Bellus G.,
 Gregersen N., Dorland L., Strauss A.W.;
 RT "Molecular characterization of inherited medium-chain acyl-CoA
 dehydrogenase deficiency.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9236-9240(1990).
 RN [9]
 RP VARIANTS MCAD ILE-149; ARG-244; ARG-267 AND THR-375.
 RX MEDLINE-92081773; PubMed-1684086;
 RA Yokota I., Coates P.M., Hale D.E., Rinaldo P., Tanaka K.;
 RT "Molecular survey of a prevalent mutation, 985A-to-G transition, and
 identification of five infrequent mutations in the medium-chain acyl-
 CoA dehydrogenase (MCAD) gene in 55 patients with MCAD deficiency.";
 RL Am. J. Hum. Genet. 49:1280-1291(1991).
 RN [10]
 RP VARIANT MCAD GLU-329.
 RX MEDLINE-91224627; PubMed-1902818;
 RA Gregersen N., Andresen B.S., Bross P., Winter V., Ruediger N.,
 Engst S., Christensen E., Kelly D., Strauss A.W., Koelvræ S.,
 Bolund L., Ghisla S.;
 RT "Molecular characterization of medium-chain acyl-CoA dehydrogenase
 (MCAD) deficiency: identification of a lys329 to glu mutation in the
 MCAD gene, and expression of inactive mutant enzyme protein in E.
 coli.";
 RL Hum. Genet. 86:545-551(1991).
 RN [11]
 RP VARIANT MCAD GLU-329 FREQUENCY.
 RX MEDLINE-91109464; PubMed-1671131;
 RA Blakemore A.I., Singleton H., Pollitt R.J., Engel P.C., Kolvræ S.,
 Gregersen N., Curtis D.;
 RT "Frequency of the G985 MCAD mutation in the general population.";
 RL Lancet 337:298-299(1991).
 RN [12]
 RP VARIANTS MCAD THR-326 AND ARG-336.
 RX MEDLINE-94256509; PubMed-8198141;
 RA Andresen B.S., Jensen T.G., Bross P., Knudsen I., Winter V.,
 Koelvræ S., Bolund L., Ding J.-H., Chen Y.-T., van Hove J.L.K.,
 Curtis D., Yokota I., Tanaka K., Kim J.-J.P., Gregersen N.;
 RT "Disease-causing mutations in exon 11 of the medium-chain acyl-CoA
 dehydrogenase gene.";
 RL Am. J. Hum. Genet. 54:975-988(1994).
 RN [13]
 RP VARIANT MCAD 115-GLY-CYS-116 DEL.
 RX MEDLINE-95327425; PubMed-7603790;
 RA Ziadeh R., Hoffman E.P., Finegold D.N., Hoop R.C., Brackett J.C.,
 Strauss A.W., Naylor E.W.;
 RT "Medium chain acyl-CoA dehydrogenase deficiency in Pennsylvania:
 neonatal screening shows high incidence and unexpected mutation
 frequencies.";
 RL Pediatr. Res. 37:675-678(1995).
 RN [14]
 RP VARIANT MCAD ARG-195.
 RX MEDLINE-95015014; PubMed-7929823;
 RA Brackett J.C., Sims H.F., Steiner R.D., Nunge M., Zimmerman E.M.,
 Demartini B., Rinaldo P., Slaugh R., Strauss A.W.;
 RT "A novel mutation in medium chain acyl-CoA dehydrogenase causes sudden
 neonatal death.";
 RL J. Clin. Invest. 94:1477-1483(1994).
 RN [15]
 RP VARIANT MCAD ALA-193.
 RX MEDLINE-97301766; PubMed-9158144;
 RA Andresen B.S., Bross P., Udvari S., Kirk J., Gray G., Knöch S.,
 Chamoles N., Knudsen I., Winter V., Wilcken B., Yokota I., Hart K.,
 Packman S., Harper J.P., Saudubray J.M., Hale D.E., Bolund L.,
 Koelvræ S., Gregersen N.;
 RT "The molecular basis of medium-chain acyl-CoA dehydrogenase (MCAD)
 deficiency in compound heterozygous patients: is there correlation
 between genotype and phenotype?";
 RL Hum. Mol. Genet. 6:695-707(1997).
 RN [16]
 RP CHARACTERIZATION OF VARIANT MCAD ALA-193.
 RX MEDLINE-99102080; PubMed-9882619;
 RA Kuchler B., Abdel-Ghany A.G., Bross P., Nandy A., Rasched I.,
 Ghisla S.;
 RT "Biochemical characterization of a variant human medium-chain acyl-CoA
 dehydrogenase with a disease-associated mutation localized in the
 active site.";
 RL Biochem. J. 337:225-230(1999).
 RN [17]
 RP VARIANT HIS-67.
 RX PubMed-11349232;
 RA Andresen B.S., Dobrowolski S.F., O'Reilly L., Muenzer J.,
 McCandless S.E., Frazier D.W., Udvari S., Bross P., Knudsen I.,
 Banas R., Chace D.H., Engel P.C., Naylor E.W., Gregersen N.;
 RT "Medium-chain acyl-CoA dehydrogenase (MCAD) mutations identified by
 MS/MS-based prospective screening of newborns differ from those
 observed in patients with clinical symptoms: identification and
 characterization of a new, prevalent mutation that results in mild
 MCAD deficiency.";
 RL Am. J. Hum. Genet. 68:1408-1418(2001).
 RN [18]
 RP VARIANT MCAD LEU-245.
 RX PubMed-11409868;
 RA Zschocke J., Schulze A., Lindner M., Fiesel S., Olgemöller K.,
 Hoffmann G.F., Penzien J., Rüter J.P.N., Wanders R.J.A.,
 Mayatepek E.;

CC -1- CATALYTIC ACTIVITY: L-tryptophan + O(2) = indole-3-acetamide +
 CC CO(2) + H(2)O.
 CC -1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF AUXINS FROM TRYPTOPHAN.
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 CC -----
 CC EMBL: L33867; AAC17187.1; -
 CC InterPro: IPR002937; Amino_Oxidase.
 CC InterPro: IPR00205; NAD_binding.
 CC Pfam: PF01593; Amino_Oxidase; 1.
 CC Oxidoreductase; Monooxygenase; Auxin biosynthesis.
 CC SEQUENCE 562 AA; 62513 MW; 621E7AA389DF886 CRC64;
 CC
 CC Query Match 62.0%; Score 31; DB 1; Length 562;
 CC Best Local Similarity 62.5%; Pred. No. 63;
 CC Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 CC
 CC QY 3 VVPXGXDY 10
 CC :|||
 CC 456 LVPAGADY 463
 CC
 CC RESULT 20
 CC PLAS_DAUCA STANDARD; PRT; 97 AA.
 CC AC P20422;
 CC DT 01-FEB-1991 (Rel. 17, Created)
 CC DT 01-FEB-1991 (Rel. 17, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE Plastocyanin.
 CC GN PETE.
 CC OS Daucus carota (Carrot).
 CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 CC OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
 CC ON NCBI_TaxID=4039;
 CC RN [1]
 CC RP SEQUENCE.
 CC RA Shoji A., Yoshizaki F., Karahashi A., Sugimura Y., Shimokoriyama M.;
 CC RT "Complete amino acid sequence of plastocyanin from Daucus carota.";
 CC RL Selkagaku 57:1036-1036(1985).
 CC -1- FUNCTION: Participates in electron transfer between P700 and the
 CC cytochrome b6-f complex in photosystem I.
 CC -1- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID
 CC MEMBRANE SURFACE IN CHLOROPLASTS.
 CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
 CC PTR: JWO011; JWO011.
 CC DR HSSP: P17341; IPLB.
 CC DR InterPro: IPR000923; BlueCu1.
 CC DR Pfam: PF001235; Copper_blue.
 CC DR PRINTS: PR00127; copper-bind; 1.
 CC DR PROSITE: PS001235; COPPERBLUE.
 CC DR PROSITE: PS00196; COPPER_BLUE; 1.
 CC DR Chloroplast; Electron transport; Copper; Thylakoid; Membrane.
 CC FT DOMAIN 1 97 PLASTOCYANIN-LIKE.
 CC FT METAL 37 37 COPPER (BY SIMILARITY).
 CC FT METAL 82 82 COPPER (BY SIMILARITY).
 CC FT METAL 85 85 COPPER (BY SIMILARITY).
 CC FT METAL 90 90 COPPER (BY SIMILARITY).
 CC SEQUENCE 97 AA; 10181 MW; B15DE6B8428F72D4 CRC64;
 CC
 CC Query Match 60.0%; Score 30; DB 1; Length 97;
 CC Best Local Similarity 54.5%; Pred. No. 16;
 CC Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC QY 1 EEVVPXGXDS 11

Db 43 EDEVPGVDVS 53

:|:|:|:|

RESULT 21

TRNK_HUMAN STANDARD; PRT; 121 AA.
 AC Q9UHF0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neurokinin B precursor (NKB) (Neuromedin K) (ZNEUROK1).
 GN TAC3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sheppard P., Jelinek L., Whitmore T., Blumberg H., Lehner J.,
 RL O'Hara P.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=20322570; PubMed=10866201;
 RA Page N.M., Woods R.J., Gardiner S.M., Lomthiasong K., Gladwell R.T.,
 RA Butlin D.J., Manyonda I.T., Lowry P.J.;
 RT "Excessive placental neurokinin B secretion during the third trimester
 causes pre-eclampsia.";
 RL Nature 405:797-800(2000).
 CC -1- FUNCTION: TACHIKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
 CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
 CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
 CC MUSCLES (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DEVELOPMENTAL STAGE: In pregnancy, the expression of NKB is
 CC confined to the outer syncytiotrophoblast of the placenta,
 CC significant concentrations of NKB can be detected in plasma as
 CC early as week 9, and plasma concentrations of NKB are grossly
 CC elevated in pregnancy-induced hypertension and pre-eclampsia.
 CC -1- SIMILARITY: BELONGS TO THE TACHIKININ FAMILY.
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 CC -----
 CC EMBL: AF186112; AAF01430.1; -
 CC EMBL: AF216586; AAF76980.1; -
 CC Genew: HGNC:11521; TAC3.
 CC MIM: 162330;
 CC InterPro: IPR003635; Neurokinin.
 CC InterPro: IPR002040; Tachykinin.
 CC ProDom: PD020370; Neurokinin; 1.
 CC PROSITE: PS00267; TACHYKININ; 1.
 CC Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
 CC Amidation; Signal.
 CC FT SIGNAL 1 16 POTENTIAL.
 CC FT PROPEP 17 78 BY SIMILARITY.
 CC FT PEPTIDE 81 90 NEUROKININ B.
 CC FT PROPEP 94 121 BY SIMILARITY.
 CC FT MOD_RES 90 90 AMIDATION (G-91 PROVIDE AMIDE GROUP) (BY
 CC SIMILARITY).
 CC SEQUENCE 121 AA; 13438 MW; 14C9AF2EE9DECA CRC64;
 CC
 CC Query Match 60.0%; Score 30; DB 1; Length 121;
 CC Best Local Similarity 85.7%; Pred. No. 20;
 CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
Db 28 EEVPPGG 34

RESULT 22
HES3_RAT
ID HES3_RAT STANDARD; PRT; 175 AA.
AC Q04667; 1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Transcription factor HES-3 (Hairy and enhancer of split 3).
GN HES3 OR HES-3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=94040724; PubMed=1340473;
RA Sasai Y., Kageyama R., Tagawa Y., Shigemoto R., Nakanishi S.;
RT "Two mammalian helix-loop-helix factors structurally related to
Drosophila hairy and enhancer of split.";
RL Genes Dev. 6:2620-2634(1992).
CC -!- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE A BHLH
CC PROTEIN FOR THEIR TRANSCRIPTION.
CC -!- SUBUNIT: TRANSCRIPTION REPRESSION REQUIRES FORMATION OF A COMPLEX
CC WITH A CO-REPRESSOR PROTEIN (GROUCHO).
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN PURKINJE CELLS.
CC -!- DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A
CC HELIX-INTERRUPTING PROLINE) THAT BINDS TO THE N-BOX (CACNAG),
CC RATHER THAN THE CANONICAL E-BOX (CANNTG).
CC -!- DOMAIN: THE CARBOXY-TERMINAL WRPW MOTIF IS A TRANSCRIPTIONAL
CC REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GROUCHO, A
CC TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA BY
CC HAIRY-RELATED PROTEINS
CC -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.

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DR EMBL; D13418; BAA02683.1; -
DR PIR; S36749; S36749.
DR TRANSFAC; T01651; -
DR InterPro; IPR001092; HLB_basic.
DR Pfam; PF00010; HLB; 1.
DR SMART; SM00353; HLB; 1.
DR PROSITE; PS00038; HLB_1; 1.
DR PROSITE; PS00888; HLB_2; 1.
KW Transcription regulation; DNA-binding; Nuclear protein; Repressor.
FT DNA_BIND 1 6
FT DOMAIN 7 50 BASIC DOMAIN.
FT DOMAIN 108 167 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
FT DOMAIN 172 175 PRO-RICH.
FT WRPW MOTIF (REQUIRED FOR ACTIVITY)
FT (BY SIMILARITY)
SQ SEQUENCE 175 AA; 19137 MW; D490663869155CB3 CRC64;
Query Match 60.0%; Score 30; DB 1; Length 175;
Best Local Similarity 62.5%; Pred. No. 30;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 3 VVPXGXDY 10
Db 58 LVPSGVGY 65

RESULT 23
CTC_BACSU
ID CTC_BACSU STANDARD; PRT; 203 AA.
AC P14194;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE General stress protein etc.
GN CTC.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96051385; PubMed=7584024;
RA Ogasawara N., Nakai S., Yoshikawa H.;
RT "Systematic sequencing of the 180 kilobase region of the Bacillus
subtilis chromosome containing the replication origin.";
RL DNA Res. 1:1-14(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Broussier R., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Etian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaer-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Puigc P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis.";
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE OF 1-185 FROM N.A.
RX MEDLINE=90066361; PubMed=2555671;
RA Nilsson D., Hove-Jensen B., Arnvig K.;
RT "Primary structure of the tms and prs genes of Bacillus subtilis.";
RL Mol. Gen. Genet. 218:565-571(1989).
RN [4]
RP SEQUENCE OF 1-13.
RC STRAIN=168 / IS58;
RX MEDLINE=94282319; PubMed=8012595;
RA Voelker U., Engelmann S., Maul B., Riethdorf S., Voelker A.,
RA Schmid R., Mach H., Hecker M.;
RT "Analysis of the induction of general stress proteins of Bacillus
subtilis.";
RL Microbiology 140:741-752(1994).
CC -!- FUNCTION: NOT KNOWN.

-|- DEVELOPMENTAL STAGE: EXPRESSED AT THE END OF EXPONENTIAL GROWTH UNDER CONDITIONS IN WHICH THE ENZYMES OF THE TCA CYCLE ARE REPRESSED.
 -|- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, GLUCOSE LIMITATION AND OXYGEN LIMITATION.
 -|- SIMILARITY: BELONGS TO THE L25P FAMILY OF RIBOSOMAL PROTEINS.

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EMBL; D26185; BAA05287.1; -
 EMBL; Z99104; CAB11828.1; -
 EMBL; X16518; CAA34524.1; -
 PIR; S05373; S05373.
 Subtilist; BG10115; etc.
 InterPro; IPR001021; Ribosomal_L25.
 Pfam; PF01386; Ribosomal_L25p; 1.
 ProDom; PD012503; Ribosomal_L25; 1.
 TIGRFAMs; TIGR00731; ctc.TL5; 1.
 Heat shock; Complete proteome.
 INIT_MET 0
 VARIANT 1 1 A -> R (IN STRAIN IS58).
 VARIANT 9 9 T -> Q (IN STRAIN IS58).
 VARIANT 12 12 T -> I (IN STRAIN IS58).
 SEQUENCE 203 AA; 21924 MW; 5130A04D0E86247 CRC64;

Query Match 60.0%; Score 30; DB 1; Length 203;
 Best Local Similarity 62.5%; Pred. No. 35;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 VPXGXDS 11
 : | | | | |
 Db 157 LPAGSDYS 164

RESULT 24

ARAD_ECOLI STANDARD; PRT; 231 AA.
 AC P08203;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4) (Phosphoribulose isomerase).
 DE ARAD OR B0061.
 GN Escherichia coli.
 OS Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OC NCBI_TaxID=562;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B;
 RX MEDLINE=87163495; PubMed=3549454;
 RA Lee N., Gielow W., Martin R., Hamilton E., Fowler A.;
 RT "The organization of the arabad operon of Escherichia coli.";
 RL Gene 47:231-244(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=91083835; PubMed=2261080;
 RA Chen H., Sun Y., Stark T., Beattie W., Moses R.E.;
 RT "Nucleotide sequence and deletion analysis of the polB gene of Escherichia coli.";
 RL DNA Cell Biol. 9:631-635(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=91067495; PubMed=2251150;

RA Mineno J., Fukui H., Ishino Y., Kato I., Shinagawa H.;
 RT "Nucleotide sequence of the arad gene of Escherichia coli K12 encoding the L-ribulose 5-phosphate 4-epimerase.";
 RL Nucleic Acids Res. 18:6722-6722(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=92334977; PubMed=1630901;
 RA Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N., Isono K., Mizobuchi K., Nakata A.;
 RT "Systematic sequencing of the Escherichia coli genome: analysis of the 0-2.4 min region.";
 RL Nucleic Acids Res. 20:3305-3308(1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [6]
 RP SEQUENCE OF 222-231 FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=91017565; PubMed=2217198;
 RA Bonner C.A., Hays S., McEntee K., Goodman M.F.;
 RT "DNA polymerase II is encoded by the DNA damage-inducible dna gene of Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7663-7667(1990).
 RN [7]
 RP SEQUENCE OF 158-231 FROM N.A.
 RC STRAIN=K12 / W3110;
 RX MEDLINE=91238699; PubMed=2034216;
 RA Iwasaki H., Ishino Y., Itoh H., Nakata A., Shinagawa H.;
 RT "Escherichia coli DNA polymerase II is homologous to alpha-like DNA polymerases.";
 RL Mol. Gen. Genet. 226:24-33(1991).
 CC -|- CATALYTIC ACTIVITY: L-ribulose 5-phosphate = D-xylulose 5-phosphate.
 CC -|- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
 CC -|- PATHWAY: L-arabinose catabolism; third step.
 CC -|- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY. ARAD/FUCA SUBFAMILY.

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 EMBL; M15263; AAA23464.1; -
 EMBL; M35371; -; NOT_ANNOTATED_CDS.
 EMBL; M62646; AAA24405.1; -
 EMBL; D10483; BAA01332.1; -
 EMBL; AE000116; AAC73172.1; -
 EMBL; M37727; AAA23683.1; -
 EMBL; M38283; AAA63763.1; -
 EMBL; X56048; CAA39519.1; -
 PIR; D29022; ISECP4.
 PIR; S13593; ISECK4.
 PIR; A36236; A36236.
 PIR; S40577; S40577.
 ECO2DBASE; G028.1; 6TH EDITION.
 Ecogene; EGI0055; arad.
 InterPro; IPR001303; Aldolase_II_N.
 InterPro; IPR004661; Arad.
 Pfam; PF00596; Aldolase_II; 1.
 TIGRFAMs; TIGR00760; arad; 1.
 KW Arabinose catabolism; Isomerase; Zinc; Complete proteome.

FT METAL 76 76 ZINC (BY SIMILARITY).
FT METAL 95 95 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT METAL 171 171 ZINC (BY SIMILARITY).
FT VARIANT 50 50 V -> I.
FT VARIANT 70 70 T -> A.
FT VARIANT 216 216 D -> N.
SQ SEQUENCE 231 AA; 25519 MW; 1753F75958332163 CRC64;
Query Match 60.0%; Score 30; DB 1; Length 231;
Best Local Similarity 55.6%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 3 VVPXGXDYS 11
Db 41 IKPSGVDYS 49
RESULT 25
ARAD_SALTY STANDARD; PRT; 231 AA.
ID ARAD_SALTY STANDARD; PRT; 231 AA.
AC P06190;
DT 01-JAN-1988 (Rel. 06, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4) (Phosphoribulose isomerase).
DE ARAD OR STM0101.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=85232046; PubMed=3891514;
RA Lin H.-C., Lei S.-P., Studnicka G., Wilcox G.;
RT "The arabid operon of Salmonella typhimurium LT2. III. Nucleotide sequence of arab and its flanking regions, and primary structure of its product, L-ribulose-5-phosphate 4-epimerase.";
RL Gene 34:129-134(1985).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium LT2.";
RL Nature 413:852-856(2001).
CC -!- CATALYTIC ACTIVITY: L-ribulose 5-phosphate = D-xylulose 5-phosphate.
CC -!- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
CC -!- PATHWAY: L-arabinose catabolism: third step.
CC -!- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY. ARAD/FUCA SUBFAMILY.
CC -!- CAUTION: Ref.1 sequence differs from that shown due to a frameshift in position 202.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M11047; AAA27025.1; ALT_FRAME.
CC DR EMBL: AEO08698; AAL19065.1; -.
CC DR PIR: A24986; ISEB4T.

DR StyGene; SG10015; arad.
DR InterPro: IPR001303; Aldolase_II_N.
DR InterPro: IPR004661; Arad.
DR Pfam: PF00596; Aldolase_II; 1.
DR TIGRFAMS: TIGR00760; arad; 1.
KW Arabinose catabolism; isomerase; zinc; Complete proteome.
FT METAL 76 76 ZINC (BY SIMILARITY).
FT METAL 95 95 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT METAL 171 171 ZINC (BY SIMILARITY).
SQ SEQUENCE 231 AA; 25531 MW; DA473505739284F9 CRC64;
Query Match 60.0%; Score 30; DB 1; Length 231;
Best Local Similarity 55.6%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 3 VVPXGXDYS 11
Db 41 IKPSGVDYS 49

Search completed: June 10, 2003, 13:40:24
Job time : 4.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:30:25 ; Search time 25.7857 Seconds
(without alignments)
87.898 Million cell updates/sec

Title: US-09-909-164-45
Sequence: 1 EFVVPXGXDYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

- Database :
- 1: SP_ARCHAEA:*
 - 2: SP_BACTERIA:*
 - 3: SP_FUNGI:*
 - 4: SP_HUMAN:*
 - 5: SP_INVERTEBRATE:*
 - 6: SP_MAMMAL:*
 - 7: SP_MHC:*
 - 8: SP_ORGANELLE:*
 - 9: SP_PHAGE:*
 - 10: SP_PLANT:*
 - 11: SP_RODENT:*
 - 12: SP_VIRUS:*
 - 13: SP_VERTEBRATE:*
 - 14: SP_UNCLASSIFIED:*
 - 15: SP_VIRUS:*
 - 16: SP_BACTERIAP:*
 - 17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	36	72.0	298	2	052367		052367 rhizobium t
2	36	72.0	363	17	030260		030260 archaeoglob
3	35	70.0	78	6	Q9XST4		Q9XST4 canis famil
4	35	70.0	143	5	Q9VSY8		Q9VSY8 drosophila
5	35	70.0	217	4	O00404		O00404 homo sapien
6	35	70.0	290	16	Q8U7J0		Q8U7J0 agrobacteri
7	35	70.0	299	4	Q9UEE9		Q9UEE9 homo sapien
8	35	70.0	587	16	Q9JZP8		Q9JZP8 neisseria m
9	35	70.0	692	5	Q9VIR0		Q9VIR0 drosophila
10	35	70.0	906	10	Q9ZSY4		Q9ZSY4 arabidopsis
11	35	70.0	908	10	Q9FJK8		Q9FJK8 arabidopsis
12	35	70.0	908	10	Q8W4J9		Q8W4J9 arabidopsis
13	35	70.0	908	10	Q9ZSY3		Q9ZSY3 arabidopsis
14	35	70.0	909	10	Q9W5A1		Q9W5A1 arabidopsis
15	35	70.0	1063	16	Q8RG86		Q8RG86 fusobacteri
16	34	68.0	156	3	Q12479		Q12479 saccharomyc

17	34	68.0	175	10	Q8VX88	08VY88 arabidopsis
18	34	68.0	247	16	Q92U66	Q92U66 rhizobium m
19	34	68.0	257	10	Q9C6J0	Q9C6J0 arabidopsis
20	34	68.0	433	16	Q9A382	Q9A382 caulobacter
21	34	68.0	1442	17	Q96VH5	Q96VH5 sulfolobus
22	34	68.0	2778	5	Q9V9T6	Q9V9T6 drosophila
23	33	66.0	143	17	Q8TX62	Q8TX62 methanopyru
24	33	66.0	165	16	Q92BC5	Q92BC5 listeria in
25	33	66.0	165	16	Q8Y6U8	Q8Y6U8 listeria mo
26	33	66.0	196	16	Q8ZAO9	Q8ZAO9 yersinia pe
27	33	66.0	210	10	Q6S890	Q6S890 cycloclolla
28	33	66.0	225	10	Q40129	Q40129 lycopersico
29	33	66.0	253	16	Q8XPA8	Q8XPA8 clostridium
30	33	66.0	312	11	Q9D876	Q9D876 mus musculu
31	33	66.0	440	17	Q9DFI3	Q9DFI3 aeropyrum p
32	33	66.0	471	11	Q8RI26	Q8RI26 mus musculu
33	33	66.0	484	11	Q8VDI8	Q8VDI8 mus musculu
34	33	66.0	517	16	Q8XZL5	Q8XZL5 raistonia s
35	33	66.0	563	13	Q9DJJ4	Q9DJJ4 halichoeres
36	33	66.0	563	16	Q99XL5	Q99XL5 streptococc
37	33	66.0	678	12	Q9ELX6	Q9ELX6 cercopitheci
38	33	66.0	1028	16	Q8YJL1	Q8YJL1 brucella me
39	33	66.0	1088	16	Q9KT32	Q9KT32 vibrio chol
40	33	66.0	1150	5	O17704	O17704 caenorhabdi
41	33	66.0	1828	16	Q98K29	Q98K29 rhizobium l
42	32	64.0	105	11	Q9CRG3	Q9CRG3 mus musculu
43	32	64.0	140	17	Q8TNG3	Q8TNG3 methanosarc
44	32	64.0	154	10	Q9SBB8	Q9SBB8 oryza sativ
45	32	64.0	219	5	Q9GQ04	Q9GQ04 eriocheir s
46	32	64.0	253	15	P88362	P88362 human immun
47	32	64.0	266	11	Q9JMA5	Q9JMA5 mus musculu
48	32	64.0	275	5	Q9VJX6	Q9VJX6 drosophila
49	32	64.0	280	5	Q9VMN9	Q9VMN9 drosophila
50	32	64.0	295	11	O70565	O70565 mus musculu
51	32	64.0	295	11	O88271	O88271 mus musculu
52	32	64.0	301	16	Q99TD4	Q99TD4 staphylococ
53	32	64.0	307	17	Q9HP60	Q9HP60 halobacteri
54	32	64.0	314	16	Q8YJX8	Q8YJX8 anabaena sp
55	32	64.0	336	11	Q9D8M6	Q9D8M6 mus musculu
56	32	64.0	336	11	Q9CX34	Q9CX34 mus musculu
57	32	64.0	354	11	Q9CRE7	Q9CRE7 mus musculu
58	32	64.0	357	17	O29920	O29920 archaeoglob
59	32	64.0	365	17	O29451	O29451 archaeoglob
60	32	64.0	406	17	Q8TY23	Q8TY23 methanopyru
61	32	64.0	423	16	Q92M00	Q92M00 rhizobium m
62	32	64.0	425	5	Q9XVK4	Q9XVK4 caenorhabdi
63	32	64.0	511	2	O52680	O52680 escherichia
64	32	64.0	543	3	Q8TFF4	Q8TFF4 trichoderma
65	32	64.0	564	17	Q8U2A4	Q8U2A4 pyrococcus
66	32	64.0	565	16	Q9CIN1	Q9CIN1 lactococcus
67	32	64.0	632	17	Q9HNP8	Q9HNP8 halobacteri
68	32	64.0	672	5	O45063	O45063 caenorhabdi
69	32	64.0	745	5	Q95P45	Q95P45 carcinus ma
70	32	64.0	873	10	Q9LKL4	Q9LKL4 zea mays (m
71	32	64.0	884	10	Q94F60	Q94F60 dichantheli
72	32	64.0	1031	5	Q906A3	Q906A3 callinectes
73	32	64.0	1082	10	Q94D25	Q94D25 oryza sativ
74	32	64.0	1410	2	O52673	O52673 escherichia
75	32	64.0	1420	2	O52666	O52666 escherichia

ALIGNMENTS

RESULT 1
O52367 PRELIMINARY: PRT; 298 AA.
ID O52367
AC O52367
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Aryl-alcohol dehydrogenase homolog (Fragment).
GN XYLBI.

OS Rhizobium tropici.
 OG Plasmid pRtrCFN299a.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=398;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CFN299;
 RA Rosenblueth M., Hynes M.F., Martinez-Romero E.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -|- COFACTOR: ZINC (BY SIMILARITY).
 CC -|- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
 CC FAMILY.
 DR EMBL; AF036920; AAC04779.1; -.
 DR HSP; P07846; 1SDG.
 DR InterPro; IPR002328; ADH_zinc.
 DR InterPro; IPR002085; Adh_zn_family.
 DR Pfam; PF00107; adh_zinc; 1.
 DR PROSITE; PS00059; ADH_ZINC; 1.
 KW Oxidoreductase; Plasmid; Zinc.
 FT NON_TER 298
 SQ SEQUENCE 298 AA; 31092 MW; 49B2F8117C33AE87 CRC64;
 Query Match 72.0%; Score 36; DB 2; Length 298;
 Best Local Similarity 50.0%; Pred. No. 12;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 EVVPGXDYS 11
 I:| | | |
 Db 250 EIIPEGADFS 259
 RESULT 2
 O30260 PRELIMINARY; PRT; 363 AA.
 ID O30260;
 AC O30260;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Hypothetical protein AF2411.
 GN AF2411.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Richardson D.L., Kerlavage A.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 DR EMBL; AE001109; AAB91255.1; -.
 DR TIGR; AF2411; -.
 DR InterPro; IPR002103; Bac_luciferase.
 DR Pfam; PF00296; bac_luciferase; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 363 AA; 41736 MW; 0B976AE788F4803 CRC64;
 Query Match 72.08; Score 36; DB 17; Length 363;
 Best Local Similarity 54.58; Pred. No. 15;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EEVVPXGDYS 11
 I:| | | |
 Db 120 ENIVPYGIDFS 130
 RESULT 3
 Q9XST4 PRELIMINARY; PRT; 78 AA.
 ID Q9XST4;
 AC Q9XST4;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE P97 homologous protein (Fragment).
 GN P97.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=THYROID.
 RX MEDLINE=20422104; PubMed=10964405;
 RA Pichon B., Mercan D., Pouillon V., Christophe-Hobertus C.,
 RA Christophe D.;
 RT "A method for the large-scale cloning of nuclear proteins and nuclear
 RT targeting sequences on a functional basis.";
 RL Anal. Biochem. 284:231-239(2000).
 DR EMBL; AJ388531; CAB46833.1; -.
 FT NON_TER 78
 SQ SEQUENCE 78 AA; 8895 MW; B62486313555FBA1 CRC64;
 Query Match 70.0%; Score 35; DB 6; Length 78;
 Best Local Similarity 54.5%; Pred. No. 4.4;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EEVVPXGDYS 11
 I:| | | |
 Db 16 EDVVPSSGEYS 26
 RESULT 4
 Q9VSY8 PRELIMINARY; PRT; 143 AA.
 ID Q9VSY8;
 AC Q9VSY8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE CG3911 protein.
 GN CG3911.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=107311132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
 RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glaesser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclele J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT The genome sequence of *Brosophila melanogaster*.;
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003552; AAF50270.1; -;
 DR FLYBase: FBgn0035992; CG3911.
 SQ SEQUENCE 143 AA; 16471 MW; 1DC346DC22C02AA2 CRC64;

Query Match 70.0%; Score 35; DB 5; Length 143;
 Best Local Similarity 66.7%; Pred. No. 8.7;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXD 9
 |||||
 Db 135 EEVVPAGED 143

RESULT 5
 000404 PRELIMINARY; PRT; 217 AA.
 AC 000404;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE P97 homologous protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RX MEDLINE=97160586; PubMed=9006920;

RA Nobukuni T., Kobayashi M., Oomori A., Ichinose S., Iwanaga T.,
 RA Takahashi I., Hashimoto K., Hattori S., Kaibuchi K., Miyata Y.,
 RT "An Alu-linked repetitive sequence corresponding to 280 amino acids is
 expressed in a novel bovine protein, but not in its human homologue.";
 RL J. Biol. Chem. 272:2801-2807(1997).
 DR EMBL: D85939; BAA20069.1; -;
 SQ SEQUENCE 217 AA; 24061 MW; B404BA2E35497828 CRC64;

Query Match 70.0%; Score 35; DB 4; Length 217;
 Best Local Similarity 54.5%; Pred. No. 14;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDYS 11
 |::|::|
 Db 16 EDVVPSSGEYS 26

RESULT 6
 Q8U7J0

ID Q8U7J0 PRELIMINARY; PRT; 290 AA.
 AC Q8U7J0;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 6-O-methylguanine-DNA methyltransferase.
 GN ADA OR ATU4459 OR AGR.L.818.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kutayavin T., Levy R., Li M.-J., McLelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saenphimmachak-C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Ramm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nestor E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 C58.";
 RL Science 294:2317-2323(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmiel K., Gordon J., Vaudin M., Hartchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Dougherty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 Agrobacterium tumefaciens C58.";
 RL Science 294:2323-2328(2001).
 DR EMBL: AE003374; AAL45253.1; -;
 DR EMBL: AE008240; AAK8982.1; -;
 KW Methyltransferase; Transferase; Complete proteome.
 SQ SEQUENCE 290 AA; 31587 MW; B626592EF519977F CRC64;

Query Match 70.0%; Score 35; DB 16; Length 290;
 Best Local Similarity 50.0%; Pred. No. 19;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDY 10
 |::|::|
 Db 9 EDITPGSDY 18

RESULT 7
 Q9UEE9 PRELIMINARY; PRT; 299 AA.
 ID Q9UEE9
 AC Q9UEE9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE BCNT protein (CRANIOFACIAL development protein 1).
 GN BCNT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98267221; PubMed=9602175;
 RA Takahashi I., Nobukuni T., Oomori H., Kobayashi M., Tanaka S.,
 RA Ohshima K., Okada N., Masui T., Hashimoto K., Iwashita S.;
 RT "Existence of a bovine LINE repetitive insert that appears in the cDNA
 of bovine protein BCNT in ruminant, but not in human, genomes.";

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RL Gene 211:387-394(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB009285; BAA31867.1; -
DR EMBL; BC000991; AAH00991.1; -
SQ SEQUENCE 299 AA; 33593 MW; F4A9E928B669451A CRC64;

Query Match          70.0%; Score 35; DB 4; Length 299;
Best Local Similarity 70.0%; Pred. No. 20;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGXDS 11
Db 16 EDYVPSGGEYS 26

RESULT 8
RQ9ZP8 PRELIMINARY; PRT; 587 AA.
ID Q9ZP8
AC Q9ZP8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Succinate dehydrogenase, flavoprotein subunit.
GN NM00950.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tetelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwin M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58";
RL Science 287:1809-1815(2000).
CC -1-COFACITOR: FAD (BY SIMILARITY).
DR EMBL; AE002446; AAF41356.1; -
DR TIGR; NMB0950; -
DR InterPro; IPR003953; FAD_bind2.
DR InterPro; IPR001327; FAD_pyr_redox.
DR InterPro; IPR003952; FRD/SDH_FAD.
DR InterPro; IPR001100; Pyr_redox.
DR InterPro; IPR004112; Succ_DH_flav_C.
DR Pfam; PF00890; FAD_binding_2; 1.
DR Pfam; PF02910; succ_DH_flav_C; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNRDRTASE1.
DR PROSITE; PS00504; FRD_SDH_FAD_BINDING; 1.
DR FAD; Flavoprotein; Oxidoreductase; Complete proteome.
SQ SEQUENCE 587 AA; 64502 MW; 9581701B08069003 CRC64;

Query Match          70.0%; Score 35; DB 16; Length 587;
Best Local Similarity 70.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGXDX 10
Db 366 EVVVPQGEDY 375

RESULT 9

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Q9VI90 PRELIMINARY; PRT; 692 AA.
ID Q9VI90
AC Q9VI90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CG10040 protein (Roughened eye).
GN RN CG10040 OR CG14600 OR CG14601.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Flosier C., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laslo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC St Pierre S.E., Galindo M.I., Couso J.P., Thor S.;
RT "Control of Drosophila imaginal disc development by rotund and
RT roughened eye: differentially expressed transcripts of the same gene
RT encoding distinct zinc finger proteins.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003672; AAF54035.1; -
DR EMBL; AF395904; AAL59598.1; -
DR HSSP; P08153; 1ZFD.
DR FlyBase; FBgn0037494; rn.
DR InterPro; IPR000822; znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 5.
DR ProDom; PD000003; znf_C2H2; 1.
DR SMART; SM00355; znf_C2H2; 5.
DR PROSITE; PS00028; ZINC_FINGER_C2H2.1; 5.
DR PROSITE; PS0157; ZINC_FINGER_C2H2.2; 5.
DR DNA-binding; Metal-binding; Zinc-binding; Zinc-finger.

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SQ SEQUENCE 692 AA; 75774 MW; BD010502BB65042E CRC64;

Query Match 70.0%; Score 35; DB 5; Length 692;
 Best Local Similarity 60.0%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVFXGXDS 11
 I::|||
 Db 26 EIPAGGDYS 35

RESULT 10

Q9ZSY4 PRELIMINARY; PRT; 906 AA.

AC Q9ZSY4
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Disease resistance protein RPP8.
 GN RPP8.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LA-ER;
 RA McDowell J.M., Dhandaydham M., Long T.A., Aarts M.G., Goff S.,
 RA Holub E.B., Dangl J.L.;
 RT "Intragenetic recombination and diversifying selection contribute to the
 RT evolution of downy mildew resistance at the RPP8 locus of
 RT Arabidopsis.";
 RL Plant Cell 10:1861-1874(1998).
 DR EMBL; AF089710; AAC83165.1; -;
 DR InterPro; IPR000767; Disease_resist.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR002182; NB-ARC.
 DR Pfam; PF00560; LRR; 1.
 DR Pfam; PF00931; NB-ARC; 1.
 DR PRINTS; PR00364; DISEASERSIST.
 SQ SEQUENCE 906 AA; 104201 MW; 52905EB143676F8F CRC64;

Query Match 70.0%; Score 35; DB 10; Length 906;
 Best Local Similarity 60.0%; Pred. No. 70;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVVFXGXDS 10
 I::|||
 Db 881 EKLVPGGEDY 890

RESULT 11

Q9FJK8 PRELIMINARY; PRT; 908 AA.

AC Q9FJK8
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Disease resistance protein.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=99087489; PubMed=9872454;
 RA Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VII.

RT Sequence features of the regions of 1,013,767 bp covered by sixteen
 RT physically assigned pl and TAC clones.";
 RL DNA Res. 5:297-308(1998).
 DR EMBL; AB015468; BAB10695.1; -;
 DR InterPro; IPR000767; Disease_resist.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR002182; NB-ARC.
 DR Pfam; PF00560; LRR; 2.
 DR Pfam; PF00931; NB-ARC; 1.
 DR PRINTS; PR00364; DISEASERSIST.
 SQ SEQUENCE 908 AA; 104448 MW; 3111991B17239693 CRC64;

Query Match 70.0%; Score 35; DB 10; Length 908;
 Best Local Similarity 60.0%; Pred. No. 70;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVVFXGXDS 10
 I::|||
 Db 883 EKLVPGGEDY 892

RESULT 12

Q8W4J9 PRELIMINARY; PRT; 908 AA.

AC Q8W4J9
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Disease resistance protein RPP8.
 GN AT5G43470, MW20.19.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OC NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Yamada K.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY062514; AAL32592.1; -;
 DR InterPro; IPR000767; Disease_resist.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR002182; NB-ARC.
 DR Pfam; PF00560; LRR; 2.
 DR Pfam; PF00931; NB-ARC; 1.
 DR PRINTS; PR00364; DISEASERSIST.
 SQ SEQUENCE 908 AA; 104649 MW; 4461F553128F3A15 CRC64;

Query Match 70.0%; Score 35; DB 10; Length 908;
 Best Local Similarity 60.0%; Pred. No. 70;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVVFXGXDS 10
 I::|||
 Db 883 EKLVPGGEDY 892

RESULT 13

Q9ZSY3 PRELIMINARY; PRT; 908 AA.

AC Q9ZSY3
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE RPP8 (disease resistance protein RPP8).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eukaryotes II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COL;
 RX MEDLINE=99030193; PubMed=9811794;
 RA McDowell J.M., Dhondydam M., Long T.A., Aarts M.G.M., Goff S.,
 RA Holub E.B., Dangl J.L.;
 RT "Intragenic recombination and diversifying selection contribute to the
 RT evolution of downy mildew resistance at the RPP8 locus of
 RT Arabidopsis.";
 RL Plant Cell 10:1861-1874(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
 RT clones.";
 RL DNA Res. 7:31-63(2000).
 DR EMBL; AF089711; AAC78631.1; -;
 DR EMBL; AB025638; BAA97426.1; -;
 DR InterPro; IPR000767; Disease_resist.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR002182; NB-ARC.
 DR Pfam; PF00560; LRR; 2.
 DR Pfam; PF00931; NB-ARC; 1.
 DR PRINTS; PR00364; DISEASERSIST.
 SQ SEQUENCE 908 AA; 104681 MW; 1BFA35BB6B0CB5CD CRC64;

Query Match 70.0%; Score 35; DB 10; Length 908;
 Best Local Similarity 60.0%; Pred. No. 70;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXDY 10
 Db 883 EKLVPGGEDY 892

RESULT 14

Q9M5A1 ID Q9M5A1 PRELIMINARY; PRT; 909 AA.
 AC Q9M5A1;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Viral resistance protein.
 GN HRT.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DI-17;
 RA Cooley M.B., Pathirana S., Wu H., Kachroo P., Klessig D.F.;
 RT "Members of the Arabidopsis HRT/RPP8 family of resistance genes confer
 RT resistance to both viral and oomycete pathogens.";
 RL Plant Cell 0:0-0(2000).
 DR EMBL; AF234174; AAF36987.1; -;
 DR InterPro; IPR000767; Disease_resist.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR002182; NB-ARC.
 DR Pfam; PF00560; LRR; 2.
 DR Pfam; PF00931; NB-ARC; 1.
 DR PRINTS; PR00364; DISEASERSIST.
 SQ SEQUENCE 909 AA; 105052 MW; 06262B71A2B3037F CRC64;

Query Match 70.0%; Score 35; DB 10; Length 909;
 Best Local Similarity 60.0%; Pred. No. 70;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDY 10
 Db 884 EKLVPGGEDY 893

RESULT 15

Q8RG86 ID Q8RG86 PRELIMINARY; PRT; 1063 AA.
 AC Q8RG86;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Carbamoyl-phosphate synthase large chain (EC 6.3.5.5).
 GN FN0422.
 OS Fusobacterium nucleatum (subsp. nucleatum).
 OC Bacteria; Fusobacteriia; Fusobacterium.
 OX NCBI_TaxID=76856;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 25866;
 RX MEDLINE=21886394; PubMed=11889109;
 RA Kapral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
 RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
 RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
 RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
 RA Fonstein M., Kyripides N., Overbeek R.;
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium
 RT nucleatum strain ATCC 25866.";
 RL J. Bacteriol. 184:2005-2018(2002).
 DR EMBL; AF010554; AAL94625.1; -;
 KW Ligase; Complete proteome.
 SQ SEQUENCE 1063 AA; 118008 MW; 39700E10B7CCE411 CRC64;

Query Match 70.0%; Score 35; DB 16; Length 1063;
 Best Local Similarity 60.0%; Pred. No. 84;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGXDYS 11
 Db 195 EIVPGLNYS 204

RESULT 16

Q12479 ID Q12479 PRELIMINARY; PRT; 156 AA.
 AC Q12479;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE ORF YOR013W.
 GN YOR013W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetaceae; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC De haan M., Grivell L.A., Maarse A.C.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FY1679;
 RA De haan M., Maarse A.C., Grivell L.A.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FY1679;

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RX MEDLINE=94019318; PubMed=8413243;
RA Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlenny G.,
RA Sherman F.;
RT "CYC2 encodes a factor involved in mitochondrial import of yeast
RT cytochrome c.";
RL Mol. Cell. Biol. 13:6442-6451(1993).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RX MEDLINE=94169519; PubMed=7764548;
RA Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
RT "Molecular cloning of a gene, DHS1, which complements a drug-
RT hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
RL Biosci. Biotechnol. Biochem. 58:391-395(1994).
DR EMBL; 274920; CAA99201.1; -
DR EMBL; X87331; CAA60762.1; -
DR SGD; S0005539; YOR013W.
SQ SEQUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;

Query Match 68.0%; Score 34; DB 3; Length 156;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVXPXGXDY 10
II:| | |
DB 50 EVVPLGMDY 58

RESULT 17
Q8VY88 PRELIMINARY; PRT; 175 AA.
AC Q8VY88;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical 19.2 kDa protein.
GN AT1G50910.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY072348; AAL61955.1; -
DR InterPro; IPR002110; ANK.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW Hypothetical protein.
SQ SEQUENCE 175 AA; 19189 MW; 7F72AB1EC82C4190 CRC64;

Query Match 68.0%; Score 34; DB 10; Length 175;
Best Local Similarity 54.5%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDS 11
II::| | |
DB 135 EELLKAGADYS 145

RESULT 18
Q92U66 PRELIMINARY; PRT; 247 AA.
AC Q92U66
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

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DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein RB1273.
GN RB1273 OR SWB2144.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Plasmid pSymb (megaplasmid 2).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396508; PubMed=11481431;
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA Vorholter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA Golding B., Puehler A.;
RT "The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
DR EMBL; AL603646; CAC49673.1; -
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 247 AA; 28930 MW; 2F14F383E66D420 CRC64;

Query Match 68.0%; Score 34; DB 16; Length 247;
Best Local Similarity 60.0%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDY 10
II:| | | |
DB 48 EDVEPRGADY 57

RESULT 19
Q9C670 PRELIMINARY; PRT; 257 AA.
AC Q9C670;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Hypothetical 28.6 kDa protein.
GN F8A12.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Dewar K.,
RA Dunn P., Egtu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
DR EMBL; AC079284; AAG50930.1; -
DR InterPro; IPR002110; ANK.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Hypothetical protein; Repeat.

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SQ SEQUENCE 257 AA; 28578 MW; 714C7A4387F32B5C CRC64;

Query Match 68.0%; Score 34; DB 10; Length 257;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDXS 11
||:| | |||

DB 217 EELLKAGADYS 227

RESULT 20

ID Q9A382 PRELIMINARY; PRT; 433 AA.

AC Q9A382; 2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Peptidoglycan-binding protein, putative.

GN CC3322

OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;

CC Caulobacter.

OX NCBI_TaxID=155892;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 19089 / CB15;

RX MEDLINE=21173698; PubMed=11259647;

RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,

RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,

RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

RA Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,

RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;

RT "Complete genome sequence of Caulobacter crescentus.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

DR EMBL; AE005994; AAK25284.1;

DR HSSP; P41052; 1LTM.

DR TIGR; CC3322;

DR InterPro; IPR002477; PG_binding.

DR Pfam; PF01471; PG_binding_1; 1.

DR Complete proteome.

QY SEQUENCE 433 AA; 46169 MW; F7DD18B9F4CA10A7 CRC64;

Query Match 68.0%; Score 34; DB 16; Length 433;
Best Local Similarity 54.5%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDXS 11
||:| | |||

DB 266 EVILPPGFDYS 276

RESULT 21

ID Q96YH5 PRELIMINARY; PRT; 1442 AA.

AC Q96YH5; 2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE Hypothetical protein S2195.

GN S2195

OS Sulfolobus tokodaii.

OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;

CC Sulfolobus.

OX NCBI_TaxID=111955;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=JCM 10545 / 7;

RX PubMed=11572479;

RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
RL EMBL; AF000989; BAB67302.1;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 1442 AA; 156497 MW; D63EC2C35228121F CRC64;

Query Match 68.0%; Score 34; DB 17; Length 1442;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDX 10
||:| | |||

DB 863 EEITPGANY 872

RESULT 22

Q9V9T6

ID Q9V9T6 PRELIMINARY; PRT; 2778 AA.

AC Q9V9T6; Q9Y0Z7;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE FAF protein (BCDNA:LD22582)

GN FAF OR BCDNA:LD22582 OR CG1945.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celnik S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers J.-H.C., Blazek R.G., Champagne M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Ballif J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegun J.,

RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Moberly C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Shue B.C., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,


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RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster." Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE OF 1090-2778 FROM N.A.
RA Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,
RA Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C.,
RA Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,
RA Galle R., George R.A., Harris N.D., Hoskins R.A., Evans-Holm M.,
RA Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M.,
RA Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T.,
RA Celniker S.E.;
RT "Full length Drosophila melanogaster cDNA sequence."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003779; AAF57198.1; -
DR EMBL; AF145677; AAD38652.1; -
DR FlyBase; FBgn005632; faf.
DR InterPro; IPR001394; UCH-2.
DR Pfam; PF00442; UCH-1; 1.
DR Pfam; PF00443; UCH-2; 1.
DR PROSITE; PS00972; UCH_2_1; 1.
DR PROSITE; PS00973; UCH_2_2; 1.
DR PROSITE; PS0235; UCH_2_3; 1.
SQ SEQUENCE 2778 AA; 311140 MW; FFB90438BA53A02B CRC64;

Query Match 68.0%; Score 34; DB 5; Length 2778;
Best Local Similarity 54.5%; Pred. No. 4.1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEWVPXGXDXS 11
Db 1394 EVIYPDQDFS 1404
I:|||||I:|

RESULT 23
Q8TX62 PRELIMINARY; PRT; 143 AA.
AC Q8TX62;
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE Uncharacterized conserved protein.
GN MK0814.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natale D.A., Rogozin I.B., Tatuzov R.L., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozhavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophyly of archaeal methanogens."
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR EMBL; AE010372; AAM02027.1; -
KW Complete proteome.
SQ SEQUENCE 143 AA; 15734 MW; 4C8B28A1PBEDD0B CRC64;

Query Match 66.0%; Score 33; DB 17; Length 143;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEWVPXGXDX 10
Db 75 EELVPGAGY 84
I:|||||I:|

RESULT 24
Q92BC5 PRELIMINARY; PRT; 165 AA.
AC Q92BC5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein lin1625.
GN LIN1625.
OS Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-GLIP 11262 / SEROVAR 6A;
RX PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Neofari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species."
RL Science 294:849-852(2001).
DR EMBL; AL596169; CAC96856.1; -
DR L1stalist; LIN01625; -
DR InterPro; IPR000866; AhpC-TSA.
DR InterPro; IPR002065; Tpx.
DR Pfam; PF00578; AhpC-TSA; 1.
DR PROSITE; PS01265; tpx; UNKNOWN_1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 165 AA; 18162 MW; 77705B7CD8BC8F4D CRC64;

Query Match 66.0%; Score 33; DB 16; Length 165;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EEWVPXGXDX 10
Db 144 EEWPEGSDH 152
I:|||||I:|

RESULT 25
Q8Y6U8 PRELIMINARY; PRT; 165 AA.
AC Q8Y6U8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein lmo1583.
GN LMO1583.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-EGD-E / SEROVAR 1/2A;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Neofari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,

```

RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of *Listeria species*.";
 RL Science 294:849-852(2001)
 DR EMBL: AL591979; CAC99661.1; -.
 DR Listlist; LMO01583; -.
 DR InterPro; IPR000866; AhpC-TSA.
 DR InterPro; IPR002065; TPX.
 DR Pfam; PF00578; AhpC-TSA; 1.
 DR PROSITE; PS01265; TPX; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 165 AA; 18133 MW; 77705B7CC46D424D CRC64;

Query Match . 66.0%; Score 33; DB 16; Length 165;
 Best Local Similarity 66.7%; Pred. No. 28;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 EVVPXGXDY 10
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 Db 144 EVVPEGSDH 152

Search completed: June 10, 2003, 13:46:38
 Job time : 26.7857 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:24:45 ; Search time 31.3571 Seconds
(without alignments)
46.744 Million cell updates/sec

Title: US-09-909-164-46
Perfect score: 50
Sequence: 1 EFVVPXDXYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	94.0	11	23	Hepatitis C virus
2	47	94.0	11	23	Hepatitis C virus
3	47	94.0	11	23	Hepatitis C virus
4	47	94.0	11	23	Hepatitis C virus
5	47	94.0	11	23	Hepatitis C virus
6	46	92.0	11	23	Hepatitis C virus
7	46	92.0	11	23	Hepatitis C virus
8	46	92.0	11	23	Hepatitis C virus
9	46	92.0	11	23	Hepatitis C virus
10	46	92.0	11	23	Hepatitis C virus

11	46	92.0	11	23	ABB80538	Hepatitis C virus
12	46	92.0	11	23	ABB80542	Hepatitis C virus
13	46	92.0	11	23	ABB80543	Hepatitis C virus
14	46	92.0	11	23	ABB80561	Hepatitis C virus
15	46	92.0	11	23	ABB80562	Hepatitis C virus
16	41	82.0	11	23	ABB80544	Hepatitis C virus
17	41	82.0	11	23	ABB80545	Hepatitis C virus
18	41	82.0	11	23	ABB80549	Hepatitis C virus
19	41	82.0	11	23	ABB80552	Hepatitis C virus
20	41	82.0	11	23	ABB80553	Hepatitis C virus
21	40	80.0	11	23	ABB80522	Hepatitis C virus
22	40	80.0	11	23	ABB80525	Hepatitis C virus
23	40	80.0	11	23	ABB80526	Hepatitis C virus
24	40	80.0	11	23	ABB80530	Hepatitis C virus
25	40	80.0	11	23	ABB80535	Hepatitis C virus
26	40	80.0	11	23	ABB80536	Hepatitis C virus
27	40	80.0	11	23	ABB80539	Hepatitis C virus
28	40	80.0	11	23	ABB80540	Hepatitis C virus
29	40	80.0	11	23	ABB80546	Hepatitis C virus
30	40	80.0	11	23	ABB80550	Hepatitis C virus
31	40	80.0	11	23	ABB80554	Hepatitis C virus
32	40	80.0	11	23	ABB80555	Hepatitis C virus
33	40	80.0	11	23	ABB80559	Hepatitis C virus
34	40	80.0	11	23	ABB80563	Hepatitis C virus
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38	40	80.0	11	23	ABB80567	Hepatitis C virus
39	40	80.0	11	23	ABB80568	Hepatitis C virus
40	40	80.0	11	23	ABB80523	Hepatitis C virus
41	39	78.0	11	23	ABB80527	Hepatitis C virus
42	39	78.0	11	23	ABB80531	Hepatitis C virus
43	39	78.0	11	23	ABB80532	Hepatitis C virus
44	39	78.0	11	23	ABB80537	Hepatitis C virus
45	39	78.0	11	23	ABB80541	Hepatitis C virus
46	39	78.0	11	23	ABB80548	Hepatitis C virus
47	39	78.0	11	23	ABB80558	Hepatitis C virus
48	39	78.0	11	23	ABB80560	Hepatitis C virus
49	35	70.0	143	22	ABB60256	Drosophila melanog
50	35	70.0	150	21	AA828379	Arabidopsis thalia
51	35	70.0	299	22	ABG00168	Novel human diagno
52	35	70.0	587	21	RAY74287	Neisseria meningit
53	35	70.0	692	22	ABB64835	Drosophila melanog
54	34	68.0	150	22	AA87623	Bovine mammary tis
55	34	68.0	175	21	AA810069	Arabidopsis thalia
56	34	68.0	283	22	AA81127	C glutamicum prote
57	34	68.0	576	22	AAU87272	Novel central nerv
58	34	68.0	1022	22	ABG03621	Novel human diagno
59	34	68.0	1022	22	ABG05826	Novel human diagno
60	34	68.0	1022	22	ABG08173	Drosophila melanog
61	34	68.0	2778	22	ABB58683	Eubacterial DNA po
62	33	66.0	25	23	ABG62372	MAB L243 VH region
63	33	66.0	140	16	AA864232	Humanized antibody
64	33	66.0	140	16	AA864235	CDR-grafted L243-g
65	33	66.0	140	16	AA864265	MHC-II MAB L243 he
66	33	66.0	140	16	AA864257	Listeria monocytog
67	33	66.0	165	23	ABB48059	Group B Streptococ
68	33	66.0	222	22	AAU03629	Streptococcus poly
69	33	66.0	222	23	ABP26468	Murine JNK3 bindin
70	33	66.0	244	21	AA812881	Murine JNK3 bindin
71	33	66.0	484	21	AA812882	Streptococcus poly
72	33	66.0	563	23	ABP27069	Staphylococcus epi
73	33	64.0	139	23	ABP40279	Propionibacterium
74	32	64.0	150	22	AAU43140	Drosophila melanog
75	32	64.0	275	22	ABB63063	Drosophila melanog

ALIGNMENTS

RESULT 1
ID ABB80547 standard: peptide; 11 AA.

XX	AC	ABB80547;
XX	DT	08-OCT-2002 (first entry)
XX	DE	Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #27.
XX	KW	Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
XX	OS	Synthetic.
XX	FH	Key Location/Qualifiers
FT	Modified-site	1 /note= "N-terminal acetyl"
FT	Modified-site	6 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
FT	Modified-site	11 /note= "C-terminal amide"
XX	PN	WO200208251-A2.
XX	PD	31-JAN-2002.
XX	PF	19-JUL-2001; 2001WO-US23169.
XX	PR	21-JUL-2000; 2000US-220101P.
XX	PA	(CORV-) CORVAS INT INC.
XX	PI	Lim-wilby M, Levy OE, Brunck TK;
XX	DR	WPI; 2002-361643/39.
XX	PT	Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
XX	PS	Claim 17; Page 65; 69pp; English.
XX	CC	The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
XX	SQ	Sequence 11 AA;
	Query Match	94.0%; Score 47; DB 23; Length 11;
	Best Local Similarity	90.9%; Pred. No. 0.0081;
	Matches 10; Conservative	0; Mismatches . 1; Indels 0; Gaps 0;
QY	1 EEVVPXGDYS 11	
DB	1 EEVVPXGTDYS 11	
RESULT 2		
ABB80548		
ID	ABB80548 standard; peptide; 11 AA.	
XX	AC	ABB80548;
XX	XX	.
DT	08-OCT-2002 (first entry)	
DE	Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #28.	
XX	KW	Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
XX	KW	

FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 11
FT /note= "C-terminal amide"

XX WO200208251-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory
FT activity useful for treating disorders associated with hepatitis C
FT virus protease

XX Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 94.0%; Score 47; DB 23; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.0081;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGXDXS 11

DB 1 EEVVPXGSDYS 11

RESULT 4

ABB80556
ID ABB80556 standard; peptide; 11 AA.

XX ABB80556;

XX 08-OCT-2002 (first entry)

XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #36.

XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with

FT residue 7"

FT Misc-difference 8 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

XX WO200208251-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory
FT activity useful for treating disorders associated with hepatitis C
FT virus protease

XX Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 94.0%; Score 47; DB 23; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.0081;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGXDXS 11

DB 1 EEVVPXGSDYS 11

RESULT 5

ABB80557
ID ABB80557 standard; peptide; 11 AA.

XX ABB80557;

XX 08-OCT-2002 (first entry)

XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #37.

XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with

FT residue 7"

FT Misc-difference 8 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

XX WO200208251-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX PI Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 XX activity useful for treating disorders associated with hepatitis C
 XX virus protease -
 XX Claim 17; Page 65; 69pp; English.
 XX The sequence represents a peptide compound of the invention having
 XX hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 XX invention are alpha-ketoamide peptide analogues. The peptides have
 XX virucide activity, and are useful for treating and in the manufacture of
 XX a medicament to treat disorders associated with HCV protease. A
 XX pharmaceutical composition comprising the peptide as an active ingredient
 XX is useful for treating disorders associated with hepatitis C virus.
 XX Sequence 11 AA;
 XX Query Match 94.0%; Score 47; DB 23; Length 11;
 XX Best Local Similarity 90.9%; Pred. No. 0.0081;
 XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDYS 11
 DB 1 EEVVPXGSDYS 11
 RESULT 6
 ABB80524
 ID ABB80524 standard; peptide; 11 AA.
 XX AC ABB80524;
 XX 08-OCT-2002 (first entry)
 XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
 XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX virucide.
 XX Synthetic.
 XX Key Location/Qualifiers
 XX Modified-site 1 /note= "N-terminal acetyl"
 XX Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 XX Misc-difference 9 /note= "D-form residue"
 XX Modified-site 11 /note= "C-terminal amide"
 XX WO200208251-A2.
 XX 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 XX 21-JUL-2000; 2000US-220101P.
 XX (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 XX activity useful for treating disorders associated with hepatitis C
 XX virus protease -

XX Claim 17; Page 64; 69pp; English.
 XX The sequence represents a peptide compound of the invention having
 XX hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 XX invention are alpha-ketoamide peptide analogues. The peptides have
 XX virucide activity, and are useful for treating and in the manufacture of
 XX a medicament to treat disorders associated with HCV protease. A
 XX pharmaceutical composition comprising the peptide as an active ingredient
 XX is useful for treating disorders associated with hepatitis C virus.
 XX Sequence 11 AA;
 XX Query Match 92.0%; Score 46; DB 23; Length 11;
 XX Best Local Similarity 90.9%; Pred. No. 0.013;
 XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDYS 11
 DB 1 EEVVPXGMDYS 11
 RESULT 7
 ABB80528
 ID ABB80528 standard; peptide; 11 AA.
 XX AC ABB80528;
 XX 08-OCT-2002 (first entry)
 XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
 XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX virucide.
 XX Synthetic.
 XX Key Location/Qualifiers
 XX Modified-site 1 /note= "N-terminal acetyl"
 XX Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 XX Misc-difference 8 /note= "D-form residue"
 XX Modified-site 11 /note= "C-terminal amide"
 XX WO200208251-A2.
 XX 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 XX 21-JUL-2000; 2000US-220101P.
 XX (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 XX activity useful for treating disorders associated with hepatitis C
 XX virus protease -
 XX Claim 17; Page 64; 69pp; English.
 XX The sequence represents a peptide compound of the invention having
 XX hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 XX invention are alpha-ketoamide peptide analogues. The peptides have
 XX virucide activity, and are useful for treating and in the manufacture of
 XX a medicament to treat disorders associated with HCV protease. A

CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.

XX SQ Sequence 11 AA;

Query Match 92.0%; Score 46; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXGXDYS 11
 ||||| |||
 Db 1 EEVVPXGMDYS 11

RESULT 8
 ABB80529
 ID ABB80529 standard; peptide; 11 AA.

XX AC ABB80529;
 XX DT 08-OCT-2002 (first entry)
 XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9.
 XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.

XX OS Synthetic.

XX FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"

FT Misc-difference 8 /note= "D-form residue"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

FT WO200208251-A2.

XX PI 31-JAN-2002.

XX PF 19-JUL-2001; 2001WO-US23169.

XX PR 21-JUL-2000; 2000US-220101P.

XX PA (CORV-) CORVAS INT INC.

XX PI Lim-wilby M, Levy OE, Brunck TK;

XX DR WPI; 2002-361643/39.

XX PT Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease

XX PS Claim 17; Page 64; 69pp; English.

XX CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.

XX SQ Sequence 11 AA;

Query Match 92.0%; Score 46; DB 23; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXGXDYS 11
 ||||| |||

Db 1 EEVVPXGMDYS 11

RESULT 10

ABB80534

Best Local Similarity 90.9%; Pred. No. 0.013;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXGXDYS 11
 ||||| |||
 Db 1 EEVVPXGMDYS 11

RESULT 9
 ABB80533
 ID ABB80533 standard; peptide; 11 AA.

XX AC ABB80533;

XX DT 08-OCT-2002 (first entry)

XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #13.

XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT residue 7"

FT Modified-site 11 /note= "C-terminal amide"

FT WO200208251-A2.

XX PI 31-JAN-2002.

XX PF 19-JUL-2001; 2001WO-US23169.

XX PR 21-JUL-2000; 2000US-220101P.

XX PA (CORV-) CORVAS INT INC.

XX PI Lim-wilby M, Levy OE, Brunck TK;

XX DR WPI; 2002-361643/39.

XX PT Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease

XX PS Claim 17; Page 64; 69pp; English.

XX CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.

XX SQ Sequence 11 AA;

Query Match 92.0%; Score 46; DB 23; Length 11;

Best Local Similarity 90.9%; Pred. No. 0.013;

Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXGXDYS 11
 ||||| |||

Db 1 EEVVPXGMDYS 11

RESULT 10

ABB80534

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT residue 7"
FT
FT Misc-difference 8
FT /note= "D-form residue"
FT Modified-site 11
FT /note= "C-terminal amide"
FT
XX WO200208251-A2.
XX
XX 31-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-US23169.
XX
XX 21-JUL-2000; 2000US-220101P.
XX
XX (CORV-) CORVAS INT INC.
XX
XX Lim-wilby M, Levy OE, Brunck TK;
XX WPI; 2002-361643/39.
XX
XX Novel peptide compound having hepatitis C virus protease inhibitory
FT activity useful for treating disorders associated with hepatitis C
FT virus protease
FT
XX Claim 17; Page 65; 69pp; English.
XX
XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
SQ Sequence 11 AA;
Query Match 92.0%; Score 46; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EEVVPXGXDXS 11
DB 1 EEVVPXGQDYS 11
RESULT 13
ABB80543
ID ABB80543 standard; peptide; 11 AA.
XX
XX ABB80543;
XX
XX 08-OCT-2002 (first entry)
XX
XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #23.
XX
XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX virucide.
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT residue 7"
FT Misc-difference 8 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 11

FT /note= "C-terminal amide"
XX WO200208251-A2.
XX 31-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-US23169.
XX
XX 21-JUL-2000; 2000US-220101P.
XX
XX (CORV-) CORVAS INT INC.
XX
XX Lim-wilby M, Levy OE, Brunck TK;
XX WPI; 2002-361643/39.
XX
XX Novel peptide compound having hepatitis C virus protease inhibitory
FT activity useful for treating disorders associated with hepatitis C
FT virus protease
FT
XX Claim 17; Page 65; 69pp; English.
XX
XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
SQ Sequence 11 AA;
Query Match 92.0%; Score 46; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EEVVPXGXDXS 11
DB 1 EEVVPXGQDYS 11
RESULT 14
ABB80561
ID ABB80561 standard; peptide; 11 AA.
XX
XX ABB80561;
XX
XX 08-OCT-2002 (first entry)
XX
XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
XX
XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX virucide.
XX Synthetic.
XX
XX Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT residue 7"
FT Misc-difference 8 /note= "D-form residue"
FT Modified-site 8 /note= "Oxymethionine"
FT Modified-site 11 /note= "C-terminal amide"
FT
XX WO200208251-A2.
XX 31-JAN-2002.
XX

PF 19-JUL-2001; 2001WO-US23169.
 PR 21-JUL-2000; 2000US-220101P.
 XX (CORV-) CORVAS INT INC.
 XX Llm-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease
 XX Claim 17; Page 65; 69pp; English.
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX Sequence 11 AA;
 SQ Query Match 92.0%; Score 46; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. NO. 0.013;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXGXDYS 11
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 Db 1 EEVVPXGMDYS 11
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RESULT 15
 ABB80562
 ID ABB80562 standard; peptide; 11 AA.
 XX ABB80562;
 AC ABB80562;
 XX 08-OCT-2002 (first entry)
 DT Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42.
 DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX virucide.
 KW Synthetic.
 OS Key Location/Qualifiers
 FH Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT Modified-site 6 residue 7"
 FT Misc-difference 8 /note= "D-form residue"
 FT Modified-site 8 /note= "Oxymethionine"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT WO200208251-A2.
 PN 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 PF 21-JUL-2000; 2000US-220101P.
 PR Novel peptide compound having hepatitis C virus protease inhibitory
 XX activity useful for treating disorders associated with hepatitis C
 XX virus protease

PA (CORV-) CORVAS INT INC.
 XX Llm-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease
 XX Claim 17; Page 65; 69pp; English.
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX Sequence 11 AA;
 SQ Query Match 92.0%; Score 46; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. NO. 0.013;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXGXDYS 11
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 Db 1 EEVVPXGMDYS 11
 ||||| |||

RESULT 16
 ABB80544
 ID ABB80544 standard; peptide; 11 AA.
 XX ABB80544;
 AC ABB80544;
 XX 08-OCT-2002 (first entry)
 DT Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #24.
 DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX virucide.
 KW Synthetic.
 OS Key Location/Qualifiers
 FH Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT Modified-site 6 residue 7"
 FT Modified-site 11 /note= "C-terminal amide"
 FT WO200208251-A2.
 PN 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 PF 21-JUL-2000; 2000US-220101P.
 PR (CORV-) CORVAS INT INC.
 XX Llm-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease
 XX

PS Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 82.0%; Score 41; DB 23; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.13;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXDS 11

Db 1 EEVVPXGTSYS 11

RESULT 17

ABB80545

ID ABB80545 standard; peptide; 11 AA.

XX ABB80545;

DT 08-OCT-2002 (first entry)

DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #25.

XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with

FT residue 7"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

FT WO200208251-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory

XX activity useful for treating disorders associated with hepatitis C

XX virus protease

XX Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having

XX hepatitis C virus (HCV) protease inhibitory activity. The peptides of the

XX invention are alpha-ketoamide peptide analogues. The peptides have

XX virucide activity, and are useful for treating and in the manufacture of

XX a medicament to treat disorders associated with HCV protease. A

XX pharmaceutical composition comprising the peptide as an active ingredient

CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 82.0%; Score 41; DB 23; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.13;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXDS 11

Db 1 EEVVPXGTSYS 11

RESULT 18

ABB80549

ID ABB80549 standard; peptide; 11 AA.

XX ABB80549;

DT 08-OCT-2002 (first entry)

DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #29.

XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;

XX virucide.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with

FT residue 7"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

FT WO200208251-A2.

XX 31-JAN-2002.

XX 19-JUL-2001; 2001WO-US23169.

XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;

XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory

XX activity useful for treating disorders associated with hepatitis C

XX virus protease

XX Claim 17; Page 65; 69pp; English.

XX The sequence represents a peptide compound of the invention having

XX hepatitis C virus (HCV) protease inhibitory activity. The peptides of the

XX invention are alpha-ketoamide peptide analogues. The peptides have

XX virucide activity, and are useful for treating and in the manufacture of

XX a medicament to treat disorders associated with HCV protease. A

XX pharmaceutical composition comprising the peptide as an active ingredient

XX is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

Query Match 82.0%; Score 41; DB 23; Length 11;

Best Local Similarity 81.8%; Pred. No. 0.13;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6
FT Modified-site 6
FT Modified-site 11
FT Modified-site 11 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT residue 7"
FT /note= "C-terminal amide"
XX WO200208251-A2.
PN 31-JAN-2002.
XX 19-JUL-2001; 2001WO-US23169.
XX 21-JUL-2000; 2000US-220101P.
PR (CORV-) CORVAS INT INC.
XX Lim-wilby M, Levy OE, Brunck TK;
XX WPI; 2002-361643/39.
DR Novel peptide compound having hepatitis C virus protease inhibitory
XX activity useful for treating disorders associated with hepatitis C
XX virus protease
XX Claim 17; Page 64; 69pp; English.
XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX SQ Sequence 11 AA;
Query Match 80.0%; Score 40; DB 23; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 EEVVPXGXDYS 11
Db 1 EEVVPXGMSYS 11
RESULT 22
ABB80522
ID ABB80522 standard; peptide; 11 AA.
XX ABB80522;
XX 08-OCT-2002 (first entry)
XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6
FT Modified-site 6
FT Modified-site 11 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT residue 7"
FT /note= "C-terminal amide"
XX WO200208251-A2.

FT /note= "Norvalyl carbonyl forming keto-amide linkage with
FT residue 7"
FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 11
FT /note= "C-terminal amide"
XX WO200208251-A2.
PN 31-JAN-2002.
XX 19-JUL-2001; 2001WO-US23169.
XX 21-JUL-2000; 2000US-220101P.
PR (CORV-) CORVAS INT INC.
XX Lim-wilby M, Levy OE, Brunck TK;
XX WPI; 2002-361643/39.
DR Novel peptide compound having hepatitis C virus protease inhibitory
XX activity useful for treating disorders associated with hepatitis C
XX virus protease
XX Claim 17; Page 64; 69pp; English.
XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX SQ Sequence 11 AA;
Query Match 80.0%; Score 40; DB 23; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 EEVVPXGXDYS 11
Db 1 EEVVPXGMSYS 11
RESULT 23
ABB80525
ID ABB80525 standard; peptide; 11 AA.
XX ABB80525;
XX 08-OCT-2002 (first entry)
XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5.
XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6
FT Modified-site 6
FT Modified-site 11 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT residue 7"
FT /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
XX WO200208251-A2.

XX PS Claim 17; Page 64; 69pp; English.
XX CC The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.

XX SQ Sequence 11 AA;
Query Match 80.0%; Score 40; DB 23; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.2;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 EEVVPXGXDS 11
|||||
Db 1 EEVVPXGGSYS 11

Search completed: June 10, 2003, 13:39:12
Job time : 32.3571 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2003, 13:31:45 ; Search time 9.64286 Seconds

(without alignments)
33.564 Million cell updates/sec

Title: US-09-909-164-46

Perfect score: 50

Sequence: 1 EVVVPXGXDYS 11

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Issued Patents.AA.*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/1aa/PCUS_COMB.pep.*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	66.0	140	4	US-08-569-147-76
2	33	66.0	140	4	US-08-569-147-82
3	32	64.0	139	4	US-09-134-001C-5124
4	31	62.0	622	2	US-08-459-146-2
5	31	62.0	622	2	US-08-459-065-2
6	31	62.0	739	4	US-09-413-814-86
7	30	60.0	59	4	US-08-963-851-14
8	30	60.0	121	4	US-09-152-060-68
9	30	60.0	121	4	US-09-152-060-85
10	30	60.0	122	2	US-08-879-995A-1
11	30	60.0	122	3	US-09-215-096-1
12	30	60.0	231	3	US-08-526-842B-20
13	30	60.0	240	3	US-08-926-842B-21
14	30	60.0	241	3	US-08-834-776A-2
15	30	60.0	341	4	US-08-853-948B-4
16	30	60.0	348	4	US-08-853-948B-5
17	30	60.0	368	4	US-09-697-367-24
18	30	60.0	421	4	US-09-093-448-4
19	30	60.0	478	2	US-09-040-799-3
20	30	60.0	478	4	US-09-093-448-1
21	30	60.0	478	4	US-09-093-448-2
22	30	60.0	478	4	US-09-093-448-3
23	30	60.0	1068	2	US-08-429-054A-11
24	30	60.0	1068	2	US-08-718-777-7
25	30	60.0	1068	3	US-09-051-341-7
26	29	58.0	100	2	US-09-047-125-27
27	29	58.0	100	3	US-07-736-335E-27

28	29	58.0	381	4	US-09-134-001C-3003	Sequence 3003, Ap
29	29	58.0	493	4	US-09-411-628-10	Sequence 10, Appl
30	29	58.0	543	4	US-09-739-455-4	Sequence 4, Appl
31	29	58.0	543	4	US-09-739-455-14	Sequence 14, Appl
32	29	58.0	544	4	US-09-732-025-4	Sequence 4, Appl
33	29	58.0	756	4	US-09-085-199B-9	Sequence 9, Appl
34	29	58.0	914	4	US-09-085-199B-4	Sequence 4, Appl
35	29	58.0	1090	4	US-09-085-199B-5	Sequence 5, Appl
36	28	56.0	45	2	US-08-637-739B-236	Sequence 236, App
37	28	56.0	45	3	US-08-871-355A-236	Sequence 236, App
38	28	56.0	45	4	US-09-201-945-236	Sequence 236, App
39	28	56.0	68	2	US-08-637-759B-62	Sequence 62, Appl
40	28	56.0	68	3	US-08-871-355A-62	Sequence 62, Appl
41	28	56.0	68	4	US-09-201-945-62	Sequence 62, Appl
42	28	56.0	181	4	US-09-134-001C-3897	Sequence 3897, Ap
43	28	56.0	216	4	US-09-198-119C-13	Sequence 13, Appl
44	28	56.0	364	4	US-09-338-671-2	Sequence 2, Appl
45	28	56.0	396	1	US-08-769-309A-15	Sequence 15, Appl
46	28	56.0	396	3	US-08-994-570-15	Sequence 15, Appl
47	28	56.0	453	1	US-08-769-309A-14	Sequence 14, Appl
48	28	56.0	453	3	US-08-994-570-14	Sequence 14, Appl
49	28	56.0	463	4	US-09-134-001C-3973	Sequence 3973, Ap
50	28	56.0	529	4	US-09-240-639-4	Sequence 4, Appl
51	28	56.0	534	2	US-08-878-563A-1	Sequence 1, Appl
52	28	56.0	534	4	US-09-270-117-1	Sequence 1, Appl
53	28	56.0	651	1	US-08-769-309A-17	Sequence 17, Appl
54	28	56.0	651	3	US-08-994-570-17	Sequence 17, Appl
55	28	56.0	746	4	US-09-149-934-4	Sequence 4, Appl
56	28	56.0	787	1	US-08-574-763-2	Sequence 2, Appl
57	28	56.0	873	3	US-08-990-140-2	Sequence 2, Appl
58	28	56.0	873	4	US-09-546-238-2	Sequence 2, Appl
59	28	56.0	947	4	US-09-228-986-73	Sequence 73, Appl
60	28	56.0	1167	1	US-08-100-709-2	Sequence 2, Appl
61	28	56.0	1167	1	US-08-176-865-2	Sequence 2, Appl
62	28	56.0	1167	1	US-08-474-038-2	Sequence 2, Appl
63	28	56.0	1167	2	US-08-779-046-2	Sequence 2, Appl
64	28	56.0	1167	2	US-08-881-340-2	Sequence 2, Appl
65	28	56.0	1722	1	US-09-194-612A-1	Sequence 1, Appl
66	28	56.0	1780	1	US-08-769-309A-5	Sequence 5, Appl
67	28	56.0	1780	3	US-08-994-570-5	Sequence 5, Appl
68	27	54.0	24	4	US-09-227-357-403	Sequence 403, App
69	27	54.0	126	2	US-08-879-995A-3	Sequence 3, Appl
70	27	54.0	126	3	US-09-215-096-3	Sequence 3, Appl
71	27	54.0	159	2	US-08-844-086-4	Sequence 4, Appl
72	27	54.0	159	3	US-09-018-211-4	Sequence 4, Appl
73	27	54.0	168	3	US-08-483-534A-2	Sequence 2, Appl
74	27	54.0	179	2	US-08-934-959-3	Sequence 3, Appl
75	27	54.0	195	2	US-08-960-022-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-08-569-147-76
; Sequence 76, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESS: No. 6180377ris, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/569,147
;; FILING DATE: 25-March-1996
;; CLASSIFICATION: 536
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Trujillo, Doreen Yanko
;; REGISTRATION NUMBER: 35,719
;; REFERENCE/DOCKET NUMBER: CARP-0047
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (215) 568-3100
;; TELEFAX: (215) 568-3439
;; INFORMATION FOR SEQ ID NO: 76:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 140 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-569-147-76

Query Match 66.0%; Score 33; DB 4; Length 140;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXDY 10
||| |
DB 122 VVPTGFDY 129

RESULT 2
US-08-569-147-82
; Sequence 82, Application US/08569147
; Patent No. 6180377
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMANISED ANTIBODIES
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: No. 6180377ris, LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,147
; FILING DATE: 25-March-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0047
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-569-147-82

Query Match 66.0%; Score 33; DB 4; Length 140;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXDY 10
||| |
DB 122 VVPTGFDY 129

RESULT 3
US-09-134-001C-5124
; Sequence 5124, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5124
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-5124

Query Match 64.0%; Score 32; DB 4; Length 139;
Best Local Similarity 55.6%; Pred. No. 25;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXDYS 11
||| |
DB 32 IVPFGHDYN 40

RESULT 4
US-08-459-146-2
; Sequence 2, Application US/08459146
; Patent No. 5866405
; GENERAL INFORMATION:
; APPLICANT: Choi, Gil Ho
; APPLICANT: Nuss, Donald Lee
; TITLE OF INVENTION: Genetically Engineered Transmissible
; TITLE OF INVENTION: Hypovirulence
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,146
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/832,117
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Roseman, Catherine R
; REGISTRATION NUMBER: 34,240
; REFERENCE/DOCKET NUMBER: 8589
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-6208
; TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Endothia parasitica (Cryptophnectria
ORGANISM: parasitica)
STRAIN: EP713
US-08-459-146-2

Query Match 62.0%; Score 31; DB 2; Length 622;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXG 7
Db 31 EEVVPAG 37

RESULT 5
US-08-459-065-2
Sequence 2, Application US/08459065
Patent No. 5882642
GENERAL INFORMATION:
APPLICANT: Choi, Gil Ho
TITLE OF INVENTION: Genetically Engineered Transmissible
TITLE OF INVENTION: Hypovirulence
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,065
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/832,117
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Roseman, Catherine R
REGISTRATION NUMBER: 34,240
REFERENCE/DOCKET NUMBER: 8589
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-6208
TELEFAX: (201) 235-3500
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 622 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Endothia parasitica (Cryptophnectria
ORGANISM: parasitica)
STRAIN: EP713
US-08-459-065-2

Query Match 62.0%; Score 31; DB 2; Length 622;
Best Local Similarity 85.7%; Pred. No. 2.2e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXG 7
Db 31 EEVVPAG 37

RESULT 6
US-09-413-814-86
Sequence 86, Application US/09413814
Patent No. 6225064
GENERAL INFORMATION:

APPLICANT: Gesellschaft fuer Biotechnologische Forschung mbH
APPLICANT: Bristol-Myers Squibb, Co.
APPLICANT: Beyer, Stefan
APPLICANT: Bloescker, Helmut
APPLICANT: Brandt, Petra
APPLICANT: Cino, Paul M
APPLICANT: Dougherty, Brian A
APPLICANT: Goldberg, Steven L
APPLICANT: Hofle, Gerhard
APPLICANT: Mueller, Joachim
APPLICANT: Reichenbach, Hans
TITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or
TITLE OF INVENTION: heteropolyketide compounds
FILE REFERENCE: PCT/US 99/23535
CURRENT APPLICATION NUMBER: US/09/413,814
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
NUMBER OF SEQ ID NOS: 107
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 86
LENGTH: 739
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-413-814-86

Query Match 62.0%; Score 31; DB 4; Length 739;
Best Local Similarity 62.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 VPXGXDXYS 11
Db 663 IPLGGDYS 670

RESULT 7
US-08-963-851-14
Sequence 14, Application US/08963851
Patent No. 6300116
GENERAL INFORMATION:
APPLICANT: VAN DER OSTEN, CLAUS
APPLICANT: HALKIER, TORDEN
APPLICANT: ANDERSEN, CARSTEN
APPLICANT: BAUDITZ, PETER
APPLICANT: HANSEN, PETER KAMP
TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
FILE REFERENCE: 4946,200-US
CURRENT APPLICATION NUMBER: US/08/963,851
CURRENT FILING DATE: 1997-11-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 14
LENGTH: 59
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-08-963-851-14

Query Match 60.0%; Score 30; DB 4; Length 59;
Best Local Similarity 45.5%; Pred. No. 24;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGXDXYS 11

Db 38 EKHIPGLEYS 48

RESULT 8

US-09-152-060-68
; Sequence 68, Application US/09152060
; Patent No. 6448230

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-152-060-68

Query Match 60.0%; Score 30; DB 4; Length 121;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 EEVVPXG 7
Db 28 EEVVPXG 34

RESULT 9

US-09-152-060-85
; Sequence 85, Application US/09152060
; Patent No. 6448230

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30

; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (89)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-152-060-85

Query Match 60.0%; Score 30; DB 4; Length 121;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 EEVVPXG 7
Db 28 EEVVPXG 34

RESULT 10

US-08-879-995A-1
; Sequence 1, Application US/08879995A
; Patent No. 5985606

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/879,995A
FILING DATE: Herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0326 US
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids

; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT03
; CLONE: 2109906
; US-08-879-995A-1

Query Match 60.0%; Score 30; DB 2; Length 122;
Best Local Similarity 85.7%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
| | | | |
DB 28 EEVVPGG 34

RESULT 11
US-09-215-096-1
; Sequence 1, Application US/09215096
; Patent No. 6008194
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: HUMAN PREPROTACHYKININ B
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/215.096
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/879,995
; FILING DATE:

ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0326 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:

INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: BRAITUT03
; CLONE: 2109906
; US-09-215-096-1

Query Match 60.0%; Score 30; DB 3; Length 122;
Best Local Similarity 85.7%; Pred. No. 55;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
| | | | |
DB 28 EEVVPGG 34

US-08-926-842B-20
; Sequence 20, Application US/08926842B
; Patent No. 6030807
; GENERAL INFORMATION:
; APPLICANT: Sa-No. 6030807ueira, Isabel
; APPLICANT: de Lencastre, Herminia
; TITLE OF INVENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/926.842B
; FILING DATE: 10-SEP-1997
; CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-089 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521

INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; US-08-926-842B-20

Query Match 60.0%; Score 30; DB 3; Length 231;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 VVPXGDYS 11
: | | | |
DB 41 IKPSGVDYS 49

RESULT 13
US-08-926-842B-21
; Sequence 21, Application US/08926842B
; Patent No. 6030807
; GENERAL INFORMATION:
; APPLICANT: Sa-No. 6030807ueira, Isabel
; APPLICANT: de Lencastre, Herminia
; TITLE OF INVENTION: HIGHLY REGULABLE PROMOTER FOR HETEROLOGOUS GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,842B
FILING DATE: 10-SEP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-089 N
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 240 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Salmonella typhimurium
US-08-926-842B-21

Query Match 60.0%; Score 30; DB 3; Length 240;
Best Local Similarity 55.6%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 VVPXGXDYS 11
DB 41 IKPSGVDYS 49

RESULT 14
US-08-834-776A-2
Sequence 2, Application US/08834776A
Patent No. 6060241
GENERAL INFORMATION:
APPLICANT: Cortesey-Theulaz, Irene
TITLE OF INVENTION: Compositions and Methods Relating to
TITLE OF INVENTION: Drug Discovery and Detection and Treatment of
TITLE OF INVENTION: Gastrointestinal Diseases
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: Five Palo Alto Square, 3000 El Camino Real
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,776A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ashton, Nina M.
REGISTRATION NUMBER: 37,273
REFERENCE/DOCKET NUMBER: GAST-001/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0663
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 241 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-834-776A-2

Query Match 60.0%; Score 30; DB 3; Length 241;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
DB 199 EEIVPAG 205

RESULT 15
US-08-853-948B-4
Sequence 4, Application US/08853948B
Patent No. 6210943
GENERAL INFORMATION:
APPLICANT: AKIHAMA, Toyota
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE FROM CITRUS AND DNA ENCODING
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 0049-0235-0
CURRENT APPLICATION NUMBER: US/08/853,948B
CURRENT FILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 341
TYPE: PRT
ORGANISM: Citrus unshiu
FEATURE:
OTHER INFORMATION: Xaa at position 109 is one of Ala, Arg, Asn, Asp,
OTHER INFORMATION: Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe,
OTHER INFORMATION: Pro, Ser, Thr, Trp, Tyr, or Val
US-08-853-948B-4

Query Match 60.0%; Score 30; DB 4; Length 341;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXDYS 11
DB 228 VIPPGMDFS 236

RESULT 16
US-08-853-948B-5
Sequence 5, Application US/08853948B
Patent No. 6210943
GENERAL INFORMATION:
APPLICANT: AKIHAMA, Toyota
TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE FROM CITRUS AND DNA ENCODING
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 0049-0235-0
CURRENT APPLICATION NUMBER: US/08/853,948B
CURRENT FILING DATE: 1997-05-09
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 348
TYPE: PRT
ORGANISM: Citrus unshiu
US-08-853-948B-5

Query Match 60.0%; Score 30; DB 4; Length 348;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXDYS 11
DB 11111111

Db 234 VIPGMDFS 242

RESULT 17

US-09-697-367-24
; Sequence 24, Application US/09697367
; Patent No. 6323015
; GENERAL INFORMATION:

; APPLICANT: Orozco Jr., Emil M.
; APPLICANT: Caimi, Perry G.
; APPLICANT: Weng, Zude

; APPLICANT: Tarczynski, Mitchell
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE
; FILE REFERENCE: B1166 US NA

; CURRENT APPLICATION NUMBER: US/09/697,367
; CURRENT FILING DATE: 2000-10-26

; PRIOR APPLICATION NUMBER: 60/084,529
; PRIOR FILING DATE: 1998-MAY-07

; PRIOR APPLICATION NUMBER: PCT/US99/09865
; PRIOR FILING DATE: 1999-MAY-06

; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Microsoft Office 97

; SEQ ID NO 24
; LENGTH: 368
; TYPE: PRT

; ORGANISM: Zea mays
US-09-697-367-24

Query Match 60.0%; Score 30; DB 4; Length 368;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXDXYS 11
:|:|:|:|
Db 217 VIPGMDFS 225

RESULT 18

US-09-093-448-4
; Sequence 4, Application US/09093448A
; Patent No. 6207704
; GENERAL INFORMATION:

; APPLICANT: Liu, Jun O.
; APPLICANT: Griffith, Eric C.

; APPLICANT: Su, Zhuang
; TITLE OF INVENTION: Type 2 Methionine Aminopeptidase (MetAP2) Inhibitors

; TITLE OF INVENTION: and Uses Thereof
; FILE REFERENCE: 0492611-0346

; CURRENT APPLICATION NUMBER: US/09/093,448A
; CURRENT FILING DATE: 1998-06-08

; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 4
; LENGTH: 421
; TYPE: PRT

; ORGANISM: Saccharomyces cerevisiae
US-09-093-448-4

Query Match 60.0%; Score 30; DB 4; Length 421;
Best Local Similarity 60.0%; Pred. No. 2.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDX 10
:|:|:|:|
Db 412 KEVSKGDDY 421

RESULT 19

US-09-040-799-3
; Sequence 3, Application US/09040799
; Patent No. 5885820
; GENERAL INFORMATION:

; APPLICANT: CHANG, YIE-HWA

; TITLE OF INVENTION: CLONE OF A NUCLEOTIDE SEQUENCE ENCODING
; TITLE OF INVENTION: A PROTEIN HAVING TWO FUNCTIONS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: HOWELL & HAERKAMP, L.C.
; STREET: 7733 FORSYTH BLVD., SUITE 1400
; CITY: ST. LOUIS

; STATE: MO
; COUNTRY: USA
; ZIP: 63105

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/040,799
; FILING DATE: 18-MAR-1998

; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:

; NAME: HOLLAND, DONALD R
; REGISTRATION NUMBER: 35,197

; REFERENCE/DOCKET NUMBER: 16153-4639
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 314-727-5188
; TELEFAX: 314-727-6092

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 478 amino acids
; TYPE: amino acid

; STRANDEDNESS:
; TOPOLOGY: linear

; MOLECULE TYPE: protein
US-09-040-799-3

Query Match 60.0%; Score 30; DB 2; Length 478;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDX 10
:|:|:|:|
Db 469 KEVSRGDDY 478

RESULT 20

US-09-093-448-1
; Sequence 1, Application US/09093448A
; Patent No. 6207704

; GENERAL INFORMATION:
; APPLICANT: Liu, Jun O.

; APPLICANT: Griffith, Eric C.
; APPLICANT: Su, Zhuang

; TITLE OF INVENTION: Type 2 Methionine Aminopeptidase (MetAP2) Inhibitors
; TITLE OF INVENTION: and Uses Thereof

; FILE REFERENCE: 0492611-0346
; CURRENT APPLICATION NUMBER: US/09/093,448A

; CURRENT FILING DATE: 1998-06-08
; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1

; LENGTH: 478
; TYPE: PRT

; ORGANISM: Mus musculus
US-09-093-448-1

Query Match 60.0%; Score 30; DB 4; Length 478;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDX 10
:|:|:|:|
Db 469 KEVSRGDDY 478

RESEARCH DESIGN

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/718,777
; FILING DATE: NOT YET ASSIGNED
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/175,471
; FILING DATE: 27-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara Rae-Venter
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.072.02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)328-4400
; TELEFAX: (415)328-4477
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1068 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-718-777-7

Query Match 60.0%; Score 30; DB 2; Length 1068;
Best Local Similarity 55.6%; Pred. No. 6.3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXDYS 11
|:| | |:
Db 435 VIPPGMDFS 443

RESULT 25

US-09-051-341-7
; Sequence 7, Application US/09051341
; Patent No. 6124528
; GENERAL INFORMATION:
; APPLICANT: Shemmaker, C. K.
; TITLE OF INVENTION: MODIFICATION OF SOLUBLE SOLIDS USING
; TITLE OF INVENTION: SUCROSE PHOSPHATE SYNTHASE ENCODING SEQUENCE
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rae-Venter Law Group, P.C.
; STREET: 260 Sheridan Avenue, Suite 440
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/051,341
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/17351
; FILING DATE: 25-OCT-1996
; APPLICATION NUMBER: US 08/549,016
; FILING DATE: 27-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/372,200
; FILING DATE: 12-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara Rae-Venter, Ph.D.,
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.110.02US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)328-4400

; TELEFAX: (415)328-4477
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1068 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-051-341-7

Query Match 60.0%; Score 30; DB 3; Length 1068;
Best Local Similarity 55.6%; Pred. No. 6.3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGXDYS 11
|:| | |:
Db 435 VIPPGMDFS 443

Search completed: June 10, 2003, 13:51:38
Job time : 9.64286 secs

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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:46:50 ; Search time 15 Seconds
(without alignments)
75.710 Million cell updates/sec

Title: US-09-909-164-46
Perfect score: 50
Sequence: 1 EEVVPXGXDS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues

Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published_Applications_AA.*

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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pap.*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pap.*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pap.*
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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pap.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pap.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pap.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pap.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	34	68.0	283	9	US-09-738-626-4881
2	33	66.0	440	9	US-09-813-408-27
3	32	64.0	3472	9	US-10-027-806-4
4	32	64.0	3472	9	US-10-034-623-4
5	32	64.0	3472	9	US-10-027-801-4
6	31	62.0	299	10	US-09-815-242-10697
7	31	62.0	653	9	US-09-820-843A-26
8	31	62.0	846	10	US-09-815-242-13904
9	30	60.0	7	9	US-09-909-062-1
10	30	60.0	7	9	US-09-909-062-9
11	30	60.0	7	9	US-09-909-062-130
12	30	60.0	11	9	US-09-943-123-22
13	30	60.0	59	10	US-09-948-080-14
14	30	60.0	79	9	US-09-764-891-4601
15	30	60.0	121	9	US-09-852-797-68
16	30	60.0	121	9	US-09-852-797-85
17	30	60.0	121	10	US-09-853-161-68
18	30	60.0	121	10	US-09-853-161-85
19	30	60.0	121	10	US-09-852-659A-68

20	30	60.0	121	10	US-09-852-659A-85	Sequence 85, Appl
21	30	60.0	135	9	US-09-992-598-359	Sequence 359, App
22	30	60.0	135	9	US-09-989-293A-359	Sequence 359, App
23	30	60.0	135	9	US-09-989-735-359	Sequence 359, App
24	30	60.0	135	9	US-09-990-444-359	Sequence 359, App
25	30	60.0	135	9	US-09-989-730-359	Sequence 359, App
26	30	60.0	135	9	US-09-990-436-359	Sequence 359, App
27	30	60.0	135	9	US-09-991-181-359	Sequence 359, App
28	30	60.0	135	9	US-09-993-687-359	Sequence 359, App
29	30	60.0	135	9	US-09-989-734-359	Sequence 359, App
30	30	60.0	135	9	US-09-997-653-359	Sequence 359, App
31	30	60.0	135	9	US-10-174-590-444	Sequence 444, App
32	30	60.0	135	9	US-10-176-758-444	Sequence 444, App
33	30	60.0	135	9	US-10-175-737-444	Sequence 444, App
34	30	60.0	135	9	US-09-993-667-359	Sequence 359, App
35	30	60.0	135	9	US-10-173-706-444	Sequence 444, App
36	30	60.0	135	9	US-10-175-738-444	Sequence 444, App
37	30	60.0	135	9	US-10-175-752-444	Sequence 444, App
38	30	60.0	135	9	US-10-176-482-444	Sequence 444, App
39	30	60.0	135	9	US-10-176-757-444	Sequence 444, App
40	30	60.0	135	9	US-10-176-913-444	Sequence 444, App
41	30	60.0	135	9	US-10-180-552-444	Sequence 444, App
42	30	60.0	135	9	US-10-180-557-444	Sequence 444, App
43	30	60.0	135	9	US-09-990-438-359	Sequence 359, App
44	30	60.0	135	9	US-09-990-562-359	Sequence 359, App
45	30	60.0	135	9	US-09-997-428-359	Sequence 359, App
46	30	60.0	135	9	US-09-997-666-359	Sequence 359, App
47	30	60.0	135	9	US-10-173-700-444	Sequence 444, App
48	30	60.0	135	9	US-10-174-572-444	Sequence 444, App
49	30	60.0	135	9	US-10-174-579-444	Sequence 444, App
50	30	60.0	135	9	US-10-174-582-444	Sequence 444, App
51	30	60.0	135	9	US-10-174-588-444	Sequence 444, App
52	30	60.0	135	9	US-10-175-739-444	Sequence 444, App
53	30	60.0	135	9	US-10-175-740-444	Sequence 444, App
54	30	60.0	135	9	US-10-175-743-444	Sequence 444, App
55	30	60.0	135	9	US-10-176-488-444	Sequence 444, App
56	30	60.0	135	9	US-10-176-492-444	Sequence 444, App
57	30	60.0	135	9	US-10-176-747-444	Sequence 444, App
58	30	60.0	135	9	US-10-176-750-444	Sequence 444, App
59	30	60.0	135	9	US-10-176-985-444	Sequence 444, App
60	30	60.0	135	9	US-10-176-987-444	Sequence 444, App
61	30	60.0	135	9	US-10-176-991-444	Sequence 444, App
62	30	60.0	135	9	US-10-176-993-444	Sequence 444, App
63	30	60.0	135	9	US-10-176-993-444	Sequence 444, App
64	30	60.0	135	9	US-10-184-658-444	Sequence 444, App
65	30	60.0	135	9	US-10-227-884-108	Sequence 108, App
66	30	60.0	135	9	US-09-990-711-359	Sequence 359, App
67	30	60.0	135	9	US-10-173-695-444	Sequence 444, App
68	30	60.0	135	9	US-10-173-697-444	Sequence 444, App
69	30	60.0	135	9	US-10-173-705-444	Sequence 444, App
70	30	60.0	135	9	US-10-174-576-444	Sequence 444, App
71	30	60.0	135	9	US-10-174-585-444	Sequence 444, App
72	30	60.0	135	9	US-10-174-586-444	Sequence 444, App
73	30	60.0	135	9	US-10-175-747-444	Sequence 444, App
74	30	60.0	135	9	US-10-176-481-444	Sequence 444, App
75	30	60.0	135	9	US-10-176-485-444	Sequence 444, App

ALIGNMENTS

RESULT 1

US-09-738-626-4881
; Sequence 4881, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIKOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKO

; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: PatentIn ver. 3.0
; SEQ ID NO 4881
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-4881

Query Match 68.0%; Score 34; DB 9; Length 283;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 VPXGXDYS 11
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Db 56 VPAGADYS 63

RESULT 2

US-09-813-408-27
; Sequence 27, Application US/09813408
; Publication No. US20030049619A1
; GENERAL INFORMATION:
; APPLICANT: Delagrave, Simon
; APPLICANT: Maris, Barry
; TITLE OF INVENTION: Methods For The Synthesis Of Polynucleotides
; TITLE OF INVENTION: Of Polynucleotides
; FILE REFERENCE: HER0041
; CURRENT APPLICATION NUMBER: US/09/813,408
; CURRENT FILING DATE: 2001-03-21
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Aeropyrum pernix
US-09-813-408-27

Query Match 66.0%; Score 33; DB 9; Length 440;
Best Local Similarity 66.7%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGXDY 10
||| |||
Db 120 EVLPWGVY 128

RESULT 3

US-10-027-806-4
; Sequence 4, Application US/10027806
; Patent No. US20020160476A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; APPLICANT: Schleper, Christa
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCOIP.002A
; CURRENT APPLICATION NUMBER: US/10/027,806
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29

; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3472
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-806-4

Query Match 64.0%; Score 32; DB 9; Length 3472;
Best Local Similarity 45.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDYS 11
||| |||
Db 2294 EDVIPRGISFS 2304

RESULT 4

US-10-034-623-4
; Sequence 4, Application US/10034623
; Publication No. US20020198365A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; APPLICANT: Schleper, Christa
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCOIP.002A
; CURRENT APPLICATION NUMBER: US/10/034,623
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/408,020
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/102,294
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3472
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-034-623-4

Query Match 64.0%; Score 32; DB 9; Length 3472;
Best Local Similarity 45.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDYS 11
||| |||
Db 2294 EDVIPRGISFS 2304

RESULT 5

US-10-027-801-4
; Sequence 4, Application US/10027801
; Publication No. US20030054364A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; APPLICANT: Schleper, Christa
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCOIP.002A
; CURRENT APPLICATION NUMBER: US/10/027,801
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3472
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-801-4

Query Match 64.0%; Score 32; DB 9; Length 3472;

Best Local Similarity 45.5%; Pred. NO. 1.1e+03;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDXS 11
Db 2294 EDVIPRGISFS 2304

RESULT 6

US-09-815-242-10697
; Sequence 10697, Application US/09815242
; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.

; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes

; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 10697

; LENGTH: 299

; TYPE: PRT

; ORGANISM: Enterococcus faecalis

US-09-815-242-10697

Query Match 62.0%; Score 31; DB 10; Length 299;

Best Local Similarity 40.0%; Pred. NO. 1.4e+02;

Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDX 10

Db 218 EQITPTGIEY 227

RESULT 7

US-09-820-843A-26

; Sequence 26, Application US/09820843A

; Publication No. US20030039963A1

; GENERAL INFORMATION:

; APPLICANT: Council of Scientific and Industrial Research

; TITLE OF INVENTION: A COMPUTATIONAL METHOD FOR THE IDENTIFICATION OF CANDIDATE PROTEIN

; FILE REFERENCE: Q63915

; CURRENT APPLICATION NUMBER: US/09/820,843A

; CURRENT FILING DATE: 2001-03-30

; NUMBER OF SEQ ID NOS: 118

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 26

; LENGTH: 653

; TYPE: PRT

; ORGANISM: Vibrio cholerae
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Iron(III) ABC transporter, permease protein
; NAME/KEY: misc_feature
; OTHER INFORMATION: gi|9654609
US-09-820-843A-26

Query Match 62.0%; Score 31; DB 9; Length 653;

Best Local Similarity 85.7%; Pred. NO. 3.1e+02;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7

Db 300 EEVVPXG 306

RESULT 8

US-09-815-242-13904

; Sequence 13904, Application US/09815242

; Patent No. US20020061569A1

; GENERAL INFORMATION:

; APPLICANT: Haselbeck, Robert

; APPLICANT: Ohlsen, Kari L.

; APPLICANT: Zyskind, Judith W.

; APPLICANT: Wall, Daniel

; APPLICANT: Trawick, John D.

; APPLICANT: Carr, Grant J.

; APPLICANT: Yamamoto, Robert T.

; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in

; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242

; CURRENT FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; NUMBER OF SEQ ID NOS: 14110

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13904

; LENGTH: 846

; TYPE: PRT

; ORGANISM: Salmonella typhi

US-09-815-242-13904

Query Match 62.0%; Score 31; DB 10; Length 846;

Best Local Similarity 60.0%; Pred. NO. 4.1e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDX 10

Db 762 EDVDMGVY 771

RESULT 9

US-09-909-062-1

; Sequence 1, Application US/09909062

; Publication No. US20030036501A1

; GENERAL INFORMATION:

; APPLICANT: Saksena, Anil K

; APPLICANT: Girijavallabhan, Viyyor M

APPLICANT: Lovey, Raymond G
APPLICANT: Jao, Edwin
APPLICANT: Bennett, Frank
APPLICANT: McCormick, Jinping L
APPLICANT: Pike, Russell E
APPLICANT: Bogen, Stephane L
APPLICANT: Liu, Yi-Tsung
APPLICANT: Arasappan, Ashok
APPLICANT: Pinto, Patrick A
APPLICANT: Njoroge, F George
APPLICANT: Ganguly, Ashit
TITLE OF INVENTION: NOVEL PEPTIDES AS NS3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01157K-US
CURRENT APPLICATION NUMBER: US/09/909,062
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/220,109
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-C(-O)
US-09-909-062-1

Query Match 60.0%; Score 30; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
DB 1 EEVVPXG 7

RESULT 10
US-09-909-062-9
Sequence 9, Application US/09909062
Publication No. US20030036501A1
GENERAL INFORMATION:
APPLICANT: Saksena, Anil K
APPLICANT: Girijavaliabhan, Viyyor M
APPLICANT: Lovey, Raymond G
APPLICANT: Jao, Edwin
APPLICANT: Bennett, Frank
APPLICANT: McCormick, Jinping L
APPLICANT: Pike, Russell E
APPLICANT: Bogen, Stephane L
APPLICANT: Liu, Yi-Tsung
APPLICANT: Arasappan, Ashok
APPLICANT: Pinto, Patrick A
APPLICANT: Njoroge, F George
APPLICANT: Ganguly, Ashit
TITLE OF INVENTION: NOVEL PEPTIDES AS NS3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01157K-US
CURRENT APPLICATION NUMBER: US/09/909,062
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/220,109
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
LENGTH: 7
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-C(-O)
US-09-909-062-9

Query Match 60.0%; Score 30; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
DB 1 EEVVPXG 7

RESULT 11
US-09-909-062-130
Sequence 130, Application US/09909062
Publication No. US20030036501A1
GENERAL INFORMATION:
APPLICANT: Saksena, Anil K
APPLICANT: Girijavaliabhan, Viyyor M
APPLICANT: Lovey, Raymond G
APPLICANT: Jao, Edwin
APPLICANT: Bennett, Frank
APPLICANT: McCormick, Jinping L
APPLICANT: Pike, Russell E
APPLICANT: Bogen, Stephane L
APPLICANT: Liu, Yi-Tsung
APPLICANT: Arasappan, Ashok
APPLICANT: Pinto, Patrick A
APPLICANT: Njoroge, F George
APPLICANT: Ganguly, Ashit
TITLE OF INVENTION: NOVEL PEPTIDES AS NS3-SERINE PROTEASE INHIBITORS OF HEPATITIS C
FILE REFERENCE: IN01157K-US
CURRENT APPLICATION NUMBER: US/09/909,062
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 60/220,109
PRIOR FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIn version 3.1
SEQ ID NO 130
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: ACETYLATION
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (7)..(7)
OTHER INFORMATION: AMIDATION
FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (6)..(6)
OTHER INFORMATION: norvaline-C(-O)
US-09-909-062-130

Query Match 60.0%; Score 30; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 3.5e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEVVPXG 7

Db 1 EEVVPXG 7
|||||||

RESULT 12

US-09-943-123-22
; Sequence 22, Application US/09943123
; Publication No. US20020182701A1
; GENERAL INFORMATION:
; APPLICANT: CHANG, Y-H
; APPLICANT: VETRO, J.A.
; APPLICANT: MICKA, W.S.
; TITLE OF INVENTION: Dominant Negative Variants of Methionine Aminopeptidase
; FILE REFERENCE: 16153-8007
; CURRENT APPLICATION NUMBER: US/09/943,123
; CURRENT FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-943-123-22

Query Match 60.0%; Score 30; DB 9; Length 11;
Best Local Similarity 60.0%; Pred. No. 6.4;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDY 10
:|||||
Db 2 KEVSKGDDY 11

RESULT 13

US-09-948-080-14
; Sequence 14, Application US/09948080
; Patent No. US20020102702A1
; GENERAL INFORMATION:
; APPLICANT: VAN DER OSTEN, CLAUS
; APPLICANT: HALKIER, TORDEN
; APPLICANT: ANDERSEN, CARSTEN
; APPLICANT: BAUDITZ, PETER
; APPLICANT: HANSEN, PETER KAMP
; TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
; FILE REFERENCE: 4946,200-US
; CURRENT APPLICATION NUMBER: US/09/948,080
; CURRENT FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US/08/963,851
; PRIOR FILING DATE: 1997-11-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-948-080-14

Query Match 60.0%; Score 30; DB 10; Length 59;
Best Local Similarity 45.5%; Pred. No. 38;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDYS 11
: :| | :| |
Db 38 EKHIPGLEYS 48

RESULT 14

US-09-764-891-4601
; Sequence 4601, Application US/09764891

; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC006
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 10231
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4601
; LENGTH: 79
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-891-4601

Query Match 60.0%; Score 30; DB 9; Length 79;
Best Local Similarity 50.0%; Pred. No. 52;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EEVVPXGDYS 11
: :| | :| |
Db 41 EIIPIGSDYS 50

RESULT 15

US-09-852-797-68
; Sequence 68, Application US/09852797
; Patent No. US20020172994A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P2
; CURRENT APPLICATION NUMBER: US/09/852,797
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-852-797-68

Query Match 60.0%; Score 30; DB 9; Length 121;
Best Local Similarity 85.7%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXG 7
|||||

Db 28 EEVPPG 34

RESULT 16

US-09-852-797-85
 ; Sequence 85, Application US/09852797
 ; Patent No. US20020172994A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 28 Human Secreted Proteins
 ; FILE REFERENCE: PZ003P2
 ; CURRENT APPLICATION NUMBER: US/09/852,797
 ; CURRENT FILING DATE: 2001-05-11
 ; PRIOR FILING DATE: 1997-03-14
 ; PRIOR APPLICATION NUMBER: 60/265,583
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 09/152,060
 ; PRIOR FILING DATE: 1998-09-11
 ; PRIOR APPLICATION NUMBER: PCT/US98/04858
 ; PRIOR FILING DATE: 1998-03-12
 ; PRIOR APPLICATION NUMBER: 60/040,762
 ; PRIOR FILING DATE: 1997-03-14
 ; PRIOR APPLICATION NUMBER: 60/040,710
 ; PRIOR FILING DATE: 1997-03-14
 ; PRIOR APPLICATION NUMBER: 60/050,934
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,100
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,357
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,189
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/057,765
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/048,970
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/068,368
 ; PRIOR FILING DATE: 1997-12-19
 ; NUMBER OF SEQ ID NOS: 118
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 85
 ; LENGTH: 121
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (67)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 ; NAME/KEY: SITE
 ; LOCATION: (89)
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
 US-09-852-797-85

Query Match 60.0%; Score 30; DB 9; Length 121;
 Best Local Similarity 85.7%; Pred. No. 82;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVPPG 7
 Db 28 EEVPPG 34

RESULT 17

US-09-853-161-68
 ; Sequence 68, Application US/09853161
 ; Patent No. US20020076756A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 28 Human Secreted Proteins
 ; FILE REFERENCE: PZ003P3
 ; CURRENT APPLICATION NUMBER: US/09/853,161
 ; CURRENT FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 60/265,583
 ; PRIOR FILING DATE: 2001-02-02

; PRIOR APPLICATION NUMBER: 09/152,060
 ; PRIOR FILING DATE: 1998-09-11
 ; PRIOR APPLICATION NUMBER: PCT/US98/04858
 ; PRIOR FILING DATE: 1998-03-12
 ; PRIOR APPLICATION NUMBER: 60/040,762
 ; PRIOR FILING DATE: 1997-03-14
 ; PRIOR APPLICATION NUMBER: 60/040,710
 ; PRIOR FILING DATE: 1997-03-14
 ; PRIOR APPLICATION NUMBER: 60/050,934
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,100
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,357
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,189
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/057,765
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/048,970
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/068,368
 ; PRIOR FILING DATE: 1997-12-19
 ; NUMBER OF SEQ ID NOS: 118
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 68
 ; LENGTH: 121
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-853-161-68

Query Match 60.0%; Score 30; DB 10; Length 121;
 Best Local Similarity 85.7%; Pred. No. 82;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVPPG 7
 Db 28 EEVPPG 34

RESULT 18

US-09-853-161-85
 ; Sequence 85, Application US/09853161
 ; Patent No. US20020076756A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 28 Human Secreted Proteins
 ; FILE REFERENCE: PZ003P3
 ; CURRENT APPLICATION NUMBER: US/09/853,161
 ; CURRENT FILING DATE: 2001-05-11
 ; PRIOR APPLICATION NUMBER: 60/265,583
 ; PRIOR FILING DATE: 2001-02-02
 ; PRIOR APPLICATION NUMBER: 09/152,060
 ; PRIOR FILING DATE: 1998-09-11
 ; PRIOR APPLICATION NUMBER: PCT/US98/04858
 ; PRIOR FILING DATE: 1998-03-12
 ; PRIOR APPLICATION NUMBER: 60/040,762
 ; PRIOR FILING DATE: 1997-03-14
 ; PRIOR APPLICATION NUMBER: 60/040,710
 ; PRIOR FILING DATE: 1997-03-14
 ; PRIOR APPLICATION NUMBER: 60/050,934
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,100
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,357
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/048,189
 ; PRIOR FILING DATE: 1997-05-30
 ; PRIOR APPLICATION NUMBER: 60/057,765
 ; PRIOR FILING DATE: 1997-09-05
 ; PRIOR APPLICATION NUMBER: 60/048,970
 ; PRIOR FILING DATE: 1997-06-06
 ; PRIOR APPLICATION NUMBER: 60/068,368
 ; PRIOR FILING DATE: 1997-12-19

; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (89)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-853-161-85

Query Match 60.0%; Score 30; DB 10; Length 121;
Best Local Similarity 85.7%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXG 7
| | | | |
Db 28 EEVPPGG 34

RESULT 19
US-09-852-659A-68
; Sequence 68, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 68
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (89)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-852-659A-68

Query Match 60.0%; Score 30; DB 10; Length 121;
Best Local Similarity 85.7%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXG 7
| | | | |
Db 28 EEVPPGG 34

RESULT 20
US-09-852-659A-85
; Sequence 85, Application US/09852659A
; Patent No. US20020077287A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P4
; CURRENT APPLICATION NUMBER: US/09/852,659A
; CURRENT FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/265,583
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/152,060
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: PCT/US98/04858
; PRIOR FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: 60/040,762
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/040,710
; PRIOR FILING DATE: 1997-03-14
; PRIOR APPLICATION NUMBER: 60/050,934
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,100
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,357
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/048,189
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/057,765
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: 60/048,970
; PRIOR FILING DATE: 1997-06-06
; PRIOR APPLICATION NUMBER: 60/068,368
; PRIOR FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 85
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (89)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-852-659A-85

Query Match 60.0%; Score 30; DB 10; Length 121;
Best Local Similarity 85.7%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXG 7
| | | | |
Db 28 EEVPPGG 34

RESULT 21
US-09-992-598-359
; Sequence 359, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman

; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC20
 ; CURRENT APPLICATION NUMBER: US/09/992,598
 ; CURRENT FILING DATE: 2001-11-14
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/065186
 ; PRIOR FILING DATE: 1997-11-12
 ; PRIOR APPLICATION NUMBER: 60/065311
 ; PRIOR FILING DATE: 1997-11-13
 ; PRIOR APPLICATION NUMBER: 60/066770
 ; PRIOR FILING DATE: 1997-11-24
 ; PRIOR APPLICATION NUMBER: 60/075945
 ; PRIOR FILING DATE: 1998-02-25
 ; PRIOR APPLICATION NUMBER: 60/078910
 ; PRIOR FILING DATE: 1998-03-20
 ; PRIOR APPLICATION NUMBER: 60/083322
 ; PRIOR FILING DATE: 1998-04-28
 ; PRIOR APPLICATION NUMBER: 60/084600
 ; PRIOR FILING DATE: 1998-05-07
 ; PRIOR APPLICATION NUMBER: 60/087106
 ; PRIOR FILING DATE: 1998-05-28
 ; PRIOR APPLICATION NUMBER: 60/087607
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/087609
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/087759
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/087827
 ; PRIOR FILING DATE: 1998-06-03
 ; PRIOR APPLICATION NUMBER: 60/088021
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088025
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088026
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088028
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088029
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088030
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088033
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088326
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088167
 ; PRIOR FILING DATE: 1998-06-05
 ; PRIOR APPLICATION NUMBER: 60/088202
 ; PRIOR FILING DATE: 1998-06-05
 ; PRIOR APPLICATION NUMBER: 60/088212
 ; PRIOR FILING DATE: 1998-06-05
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 ; PRIOR FILING DATE: 1998-07-09

Query Match 60.0%; Score 30; DB 9; Length 135;

Best Local Similarity 85.7%; Pred. No. 93;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPKG 7

|||||

Db 28 EEVVPKG 34

RESULT 22

US-09-989-293A-359

; Sequence 359, Application US/09989293A

; Patent No. US2002017716A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Ban L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Napier, Mary A.
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 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2730PIC66
 ; CURRENT APPLICATION NUMBER: US/09/989,293A
 ; CURRENT FILING DATE: 2001-11-20
 ; PRIOR APPLICATION NUMBER: 60/049787
 ; PRIOR FILING DATE: 1997-06-16
 ; PRIOR APPLICATION NUMBER: 60/062250
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; PRIOR FILING DATE: 1998-07-09

Query Match 60.0%; Score 30; DB 9; Length 135;
Best Local Similarity 85.7%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEWVPG 7
DB 28 EEWVPG 34

RESULT 23

US-09-989-735-359
; Sequence 359, Application US/09989735
; Publication No. US20020193299A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnuyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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CURRENT FILING DATE: 2001-11-19
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 ; PRIOR FILING DATE: 1998-07-09

Query Match 60.0%; Score 30; DB 9; Length 135;

Best Local Similarity 85.7%; Pred. No. 93; Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXG 7
 Db 28 EEVVPXG 34

RESULT 24

US-09-990-444-359
 ; Sequence 359, Application US/09990444
 ; Publication No. US20020193300A1

GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
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 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE OF INVENTION: Acids Encoding the Same
 ; FILE REFERENCE: P2730PIC19
 ; CURRENT APPLICATION NUMBER: US/09/990,444

; CURRENT FILING DATE: 2001-11-14
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 ; PRIOR APPLICATION NUMBER: 60/087607
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; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
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; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091633
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091978
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 60.08; Score 30; DB 9; Length 135;
Best Local Similarity 85.7%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EEVVPXG 7
|||||
Db 28 EEVVPXG 34

RESULT 25

US-09-989-730-359
; Sequence 359, Application US/09989730
; Publication No. US20020197674A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730PIC69
; CURRENT APPLICATION NUMBER: US/09/989,730
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1997-11-12

us-09-909-164-46.rapb

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match 60.0%; Score 30; DB 9; Length 135;
Best Local Similarity 85.7%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 EEVXPXG 7
Db 28 EEVPCG 34

Search completed: June 10, 2003, 14:35:46
Job time : 15.0714 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 10, 2003, 13:31:15 ; Search time 11.2143 Seconds

(without alignments)

94.297 Million cell updates/sec

Title: US-09-909-164-46

Perfect score: 50

Sequence: 1 EEVWPXGDYS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

PIR_73:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	72.0	363	D69551	conserved hypotet
2	35	70.0	290	D98182	6-O-methylguanine-D
3	35	70.0	290	AG3104	succinate dehydrog
4	35	70.0	587	F81138	disease resistance
5	35	70.0	906	T48898	disease resistance
6	35	70.0	908	T48899	V1 protein - tobac
7	34	68.0	102	A42452	hypothetical prote
8	34	68.0	156	S54619	conserved hypotet
9	34	68.0	247	A96001	unknown protein [i
10	34	68.0	257	A96546	ferrisiderophore r
11	34	68.0	394	F82491	peptidoglycan-bind
12	34	68.0	433	H87660	fat facets (fat) s
13	34	68.0	2747	B49132	trans-regulatory s
14	33	66.0	124	VKLJ51	thiol peroxidases
15	33	66.0	165	AG1272	conserved hypotet
16	33	66.0	165	AH1635	hypothetical prote
17	33	66.0	196	AD0454	acyl-CoA dehydroge
18	33	66.0	225	S57810	probable alkaline
19	33	66.0	327	S40753	ATP-dependent DNA
20	33	66.0	421	DEXTCM	hypothetical prote
21	33	66.0	440	H72784	probable chitinase
22	33	66.0	1028	F43286	hypothetical prote
23	33	66.0	1088	D82246	plastocyanin b - L
24	33	66.0	1150	T20173	plastocyanin b pre
25	32	64.0	99	S00210	conserved hypotet
26	32	64.0	155	S38255	hypothetical prote
27	32	64.0	168	S58208	
28	32	64.0	196	AI0931	
29	32	64.0	301	F89957	

30	32	64.0	307	2	F84330
31	32	64.0	314	2	AH1912
32	32	64.0	357	1	G69290
33	32	64.0	366	2	G69350
34	32	64.0	425	2	T24111
35	32	64.0	427	2	F64064
36	32	64.0	565	2	H86665
37	32	64.0	632	2	H84350
38	32	64.0	672	2	G88651
39	32	64.0	1474	2	F69009
40	32	64.0	1472	2	T31308
41	32	64.0	6658	2	T13931
42	31	62.0	117	2	A69487
43	31	62.0	202	2	H97247
44	31	62.0	233	2	E72330
45	31	62.0	296	2	F72745
46	31	62.0	319	2	S03833
47	31	62.0	395	2	H84113
48	31	62.0	421	1	DEHUCM
49	31	62.0	496	2	S76296
50	31	62.0	587	2	D81881
51	31	62.0	622	2	S15009
52	31	62.0	630	2	F85074
53	31	62.0	653	2	D82352
54	31	62.0	840	2	AG0526
55	31	62.0	846	2	S57580
56	31	62.0	1741	2	S74910
57	31	62.0	13055	2	T16580
58	30.5	61.0	668	2	JQ2356
59	30	60.0	21	2	B49042
60	30	60.0	97	2	AW0011
61	30	60.0	97	2	A99427
62	30	60.0	128	2	A90471
63	30	60.0	165	2	D69493
64	30	60.0	175	2	S36749
65	30	60.0	180	2	AG0504
66	30	60.0	184	2	B86192
67	30	60.0	184	2	E90335
68	30	60.0	204	2	S66082
69	30	60.0	231	1	ISECP4
70	30	60.0	231	2	A90637
71	30	60.0	231	2	A85488
72	30	60.0	232	2	AB0515
73	30	60.0	232	2	C71908
74	30	60.0	232	2	C64606
75	30	60.0	248	1	ISEB4T

ALIGNMENTS

RESULT 1

D69551
conserved hypotetral protein AF2411 - Archaeoglobus fulgidus

C:Species: Archaeoglobus fulgidus

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999

C:Accession: D69551

R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.;

; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness

Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.

Nature 390, 364-370, 1997

A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Syk

Smith, H.O.; Woese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing a

A:Reference number: A69250; MUID:98049343; PMID:9389475

A:Accession: D69551

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-363 <KLE>

A:Cross-references: GB:AE001109; GB:AE000782; NID:g26869432; PIDN:AAB91255.1; PID:g

Query Match 72.0%; Score 36; DB 2; Length 363;

Best Local Similarity 54.5%; Pred. No. 9;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDXS 11
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Db 120 ENIVPYGIDFS 130

RESULT 2
D98182
O6-methylguanine-DNA methyltransferase PA2118 [imported] - Agrobacterium tumefaciens (strain C58)
C:Species: Agrobacterium tumefaciens
C:Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
C:Accession: D98182
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, D.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens C58
A:Reference number: A97359; PMID:11743194
A:Accession: D98182
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-290 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK88982.1; PID:g15158766; GSPDB:GN00170
C:Genetics:
A:Gene: AGR_L_818
A:Map position: linear chromosome

Query Match 70.0%; Score 35; DB 2; Length 290;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDX 10
|:|:|:|:|
Db 9 EDITPIGSDY 18

RESULT 3
AG3104
6-O-methylguanine-DNA methyltransferase [imported] - Agrobacterium tumefaciens (strain C58)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C:Accession: AG3104
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, S.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, J.E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; PMID:11743193
A:Accession: AG3104
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-290 <KUR>
A:Cross-references: GB:AE008689; PIDN:AAL45253.1; PID:g17742937; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: ada
A:Map position: linear chromosome

Query Match 70.0%; Score 35; DB 2; Length 290;
Best Local Similarity 50.0%; Pred. No. 12;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDX 10
|:|:|:|:|
Db 9 EDITPIGSDY 18

RESULT 4
F81138
succinate dehydrogenase, flavoprotein chain NMB0950 [imported] - Neisseria meningitidis
C:Species: Neisseria meningitidis

C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: F81138
R:Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisele, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, R.; Qian, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.; Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: F81138
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-587 <TET>
A:Cross-references: GB:AE002446; GB:AE002098; NID:g7226185; PIDN:AAF41356.1; PID:g7226185
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0950
A:Superfamily: fumarate reductase flavoprotein; 3-oxosteroid 1-dehydrogenase homologous

Query Match 70.0%; Score 35; DB 2; Length 587;
Best Local Similarity 70.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDX 10
|:|:|:|:|
Db 366 EVVVPQGEDY 375

RESULT 5
T48898
disease resistance protein RPP8 [validated] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000
C:Accession: T48898
R:McDowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Plant Cell 10, 1861-1874, 1998
A:Title: Intragenic recombination and diversifying selection contribute to the evolution of the Arabidopsis thaliana RPP8 gene
A:Reference number: Z24999; MUID:99030193; PMID:9811794
A:Accession: T48898
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-906 <MCD>
A:Cross-references: EMBL:AF089710; NID:g3928861; PIDN:AAC83165.1; PID:g3928862
A:Experimental source: Landsberg erecta
C:Genetics:
A:Gene: RPP8
A:Introns: 293/1; 342/1
A:Function:
A:Description: promotes resistance to Peronospora parasitica

Query Match 70.0%; Score 35; DB 2; Length 906;
Best Local Similarity 60.0%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXDX 10
|:|:|:|:|
Db 881 EKLVPQGEDY 890

RESULT 6
T48899
disease resistance protein rpp8 [similarity] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 21-Jul-2000
C:Accession: T48899
R:McDowell, J.M.; Dhandaydham, M.; Long, T.A.; Aarts, M.G.; Goff, S.; Holub, E.B.; Plant Cell 10, 1861-1874, 1998
A:Title: Intragenic recombination and diversifying selection contribute to the evolution of the Arabidopsis thaliana rpp8 gene
A:Reference number: Z24999; MUID:99030193; PMID:9811794
A:Accession: T48899
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-908 <MCD>

A:Cross-references: EMBL:AF089711; NID:g3901293; PIDN:AAC78631.1; PID:g3901294
 A:Experimental source: Columbia
 C:Genetics:
 A:Gene: rpp8
 A:Introns: 293/1; 342/1
 C:Function:
 A:Description: susceptible allele of a gene that promotes resistance to Peronospora para

Query Match 70.0%; Score 35; DB 2; Length 908;
 Best Local Similarity 60.0%; Pred. NO. 40;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDY 10
 I:| | | | |
 Db 883 EKLVPGGEDY 892

RESULT 7
 A42452
 V1 protein - tobacco yellow dwarf virus (strain Australia)
 C:Species: tobacco yellow dwarf virus
 C:Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999
 C:Accession: A42452
 R:Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.
 Virology 187, 633-642, 1992
 A:Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yellow
 A:Reference number: A42452; MUID:92188538; PMID:1546458
 A:Accession: A42452
 A:Molecule type: DNA
 A:Residues: 1-102 <MOR>
 A:Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284

Query Match 68.0%; Score 34; DB 2; Length 102;
 Best Local Similarity 60.0%; Pred. NO. 6;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 EVVPXGXDYS 11
 I:| | | | |
 Db 7 QVPSSINYS 16

RESULT 8
 S54619
 hypothetical protein YOR013w - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein O2612; hypothetical protein YOL303.3
 C:Species: Saccharomyces cerevisiae
 C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
 C:Accession: S54619; S66879
 R:de Haan, M.; Maarse, A.C.; Grivell, L.A.
 submitted to the EMBL data Library, May 1995
 A:Reference number: S54617
 A:Accession: S54619
 A:Molecule type: DNA
 A:Residues: 1-156 <DEH>
 A:Cross-references: EMBL:X87331; NID:g1041652; PIDN:CAA60762.1; PID:g829123
 R:de Haan, M.; Grivell, L.A.; Maarse, A.C.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S66877
 A:Accession: S66879
 A:Molecule type: DNA
 A:Residues: 1-156 <DEW>
 A:Cross-references: EMBL:274920; NID:g1420109; PIDN:CAA99201.1; PID:g1420111; MIPS:YOR01
 A:Experimental source: strain S288C
 C:Genetics:
 A:Cross-references: SGD:S0005539
 A:Map position: 15R
 C:Superfamily: hypothetical protein YOR013w

Query Match 68.0%; Score 34; DB 2; Length 156;
 Best Local Similarity 66.7%; Pred. NO. 9.6;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 2 EVVPXGXDY 10

Db 50 EVMPLGMDY 58
 I:| | | | |

RESULT 9
 A96001
 conserved hypothetical protein, homolog to osmotically inducible sensory protein S
 C:Species: Sinorhizobium meliloti
 C:Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2001
 C:Accession: A96001
 R:Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.;
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A:Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing
 A:Reference number: A95842; MUID:21396508; PMID:11481431
 A:Accession: A96001
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-247 <KUR>
 A:Cross-references: GB:AL591985; PIDN:CAC49673.1; PID:g15141160; GSPDB:GN00167
 A:Experimental source: strain 1021, megaplasmid pSymb
 R:Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, P.; Barloy-P
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher,
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A:Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Le
 hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Y
 A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A:Reference number: A96039; MUID:21368234; PMID:11474104
 A:Contents: annotation
 C:Genetics:
 A:Gene: SMB21444
 A:Genome: plasmid

Query Match 68.0%; Score 34; DB 2; Length 247;
 Best Local Similarity 60.0%; Pred. NO. 16;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDY 10
 I:| | | | |
 Db 48 EDVEPRGADY 57

RESULT 10
 A96546
 unknown protein [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: A96546
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; A
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewa
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; K
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Ma
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: A96546
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-257 <STO>
 A:Cross-references: GB:AE005173; NID:g11094688; PIDN:AAG29624.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F8A12.12
 A:Map position: 1

Query Match 68.0%; Score 34; DB 2; Length 257;
 Best Local Similarity 54.5%; Pred. NO. 17;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDYS 11

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Db          217 EELLKAGADYS 227
|||||
RESULT 11
F82491
ferrisiderophore reductase VCA0183 [imported] - Vibrio cholerae (strain N16961 serogroup
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: F82491
R;Heidelber, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: F82491
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <HEI>
A;Cross-references: GB:AE003853; GB:AE003858; NID:g9657566; PIDN:AAF96096.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VCA0183
A;Map position: 2
C;Superfamily: flavohemoglobin; cytochrome-b5 reductase homology; globin homology

Query Match          68.0%; Score 34; DB 2; Length 394;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVPXGXDY 10
|||
DB 194 EVTPGSDY 202
|||

RESULT 12
H87660
peptidoglycan-binding protein, probable [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001
R;Niernann, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: H87660
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-433 <SFO>
A;Cross-references: GB:AE005673; NID:gl3425020; PIDN:AAK25284.1; GSPDB:GN00148
C;Genetics:
A;Gene: CC3322

Query Match          68.0%; Score 34; DB 2; Length 433;
Best Local Similarity 54.5%; Pred. No. 29;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDXYS 11
|||||
DB 266 EVILPPGFDYS 276
|||||

RESULT 13
B49132
fat facets (faf) splice form 1 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 19-Dec-1993 #sequence_revision 25-Apr-1997 #text_change 01-Dec-2000
C;Accession: B49132; A49132
R;Fischer-Vize, J.A.; Rubin, G.M.; Lehmann, R.
Development 116, 985-1000, 1992

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A;Title: The fat facets gene is required for Drosophila eye and embryo development
A;Reference number: A49132; MUID:93202020; PMID:1295747
A;Contents: isogenic st
A;Accession: B49132
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-2747 <FIS>
A;Cross-references: GB:104959; NID:gl57411; PIDN:AAF01345.1; PID:g6013474
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:127836, NCBIN:129008, NCBIP:1
A;Accession: A49132
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-2704, 'VT', 2707, 'ANNV' <FI2>
A;Cross-references: GB:104958; NID:gl57410; PIDN:AAF01346.1; PID:g6013475
A;Note: sequence extracted from NCBI backbone (NCBIN:127836, NCBIN:129008, NCBIP:1
C;Keywords: alternative splicing

Query Match          68.0%; Score 34; DB 2; Length 2747;
Best Local Similarity 54.5%; Pred. No. 2.2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDXYS 11
|||||
DB 1394 EVIVPDGQDFS 1404
|||||

RESULT 14
VKLJST
trans-regulatory splicing protein - simian immunodeficiency virus SIVcpz
N;Alternate names: anti-repression trans-activator; art protein; rev protein; trs
C;Species: simian immunodeficiency virus SIVcpz
A;Note: host Pan troglodytes (chimpanzee)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C;Accession: S09988
R;Huet, T.; Cheynier, R.; Meyerhans, A.; Roelants, G.; Wain-Hobson, S.
Nature 345, 356-359, 1990
A;Title: Genetic organization of a chimpanzee lentivirus related to HIV-1.
A;Reference number: S09983; MUID:90259077; PMID:2188136
A;Accession: S09988
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-124 <HUE>
A;Cross-references: EMBL:X52154; NID:g58866; PIDN:CAA36405.1; PID:g763085
C;Genetics:
A;Gene: rev; trs; art
A;Introns: 27/1
C;Superfamily: AIDS trans-regulatory splicing protein
C;Keywords: AIDS; immunodeficiency; splicing protein; transcription regulation

Query Match          66.0%; Score 33; DB 1; Length 124;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVPXGXDXYS 11
|||||
DB 107 ETVPAGGNYS 116
|||||

RESULT 15
AG1272
thiol peroxidases homolog lmo1583 [imported] - Listeria monocytogenes (strain EGD-
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 17-May-2002
C;Accession: AG1272
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bli
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsi
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Krefl, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wei
ok, C.; Schlutener, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wei
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669

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A:Accession: AG1272
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-165 <GLA>
A:Cross-references: GB:NC_003210; PIDN:CAC99661.1; PID:g16411012; GSPDB:GN00177
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo1583
C:Superfamily: thioredoxin peroxidase

Query Match 66.0%; Score 33; DB 2; Length 165;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPGXGXDY 10
|||||
Db 144 EVVPEGSDH 152

RESULT 16
AH1635
thiol peroxidases homolog lin1625 [imported] - *Listeria innocua* (strain Clip11262)
C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 17-May-2002
C:Accession: AH1635
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Makok, C.; Schluter, T.; Smoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1635
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-165 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC96856.1; PID:g16414112; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin1625
C:Superfamily: thioredoxin peroxidase

Query Match 66.0%; Score 33; DB 2; Length 165;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPGXGXDY 10
|||||
Db 144 EVVPEGSDH 152

RESULT 17
AD0454
conserved hypothetical protein YPO3732 [imported] - *Yersinia pestis* (strain CO92)
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AD0454
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Li, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AD0454
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-196 <KUR>
A:Cross-references: GB:AL590842; PIDN:CAC93200.1; PID:g15981648; GSPDB:GN00175
C:Genetics:
A:Gene: YPO3732

Query Match 66.0%; Score 33; DB 2; Length 196;

Best Local Similarity 45.5%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 EEVVPXGXDXS 11
|||||
Db 76 EEAIPTSSDDYA 86

RESULT 18
S57810
hypothetical protein precursor (clone TP11) - tomato
C:Species: *Lycopersicon esculentum* (tomato)
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000
C:Accession: S57810
R:Milligan, S.B.; Gasser, C.S.
Plant Mol. Biol. 28, 691-711, 1995
A:Title: Nature and regulation of pistil-expressed genes in tomato.
A:Reference number: S57808; MUID:95375233; PMID:7647301
A:Accession: S57810
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-225 <MIL>
A:Cross-references: EMBL:U20592; NID:9924625; PIDN:AAA80497.1; PID:9924626
C:Superfamily: plant kunitz-type proteinase inhibitor

Query Match 66.0%; Score 33; DB 2; Length 225;
Best Local Similarity 54.5%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDXS 11
|||||
Db 32 DEVVPGKTYA 42

RESULT 19
S40753
hypothetical protein C15H7.4 - *Caenorhabditis elegans*
C:Species: *Caenorhabditis elegans*
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Sep-1997
C:Accession: S40753
R:Smith, A.
submitted to the EMBL Data Library, February 1993
A:Reference number: S40750
A:Accession: S40753
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-327 <SMI>
A:Cross-references: EMBL:Z22173; NID:g297944; PID:g297948
C:Genetics:
A:Introns: 14/3; 59/2; 115/2; 188/2; 238/3

Query Match 66.0%; Score 33; DB 2; Length 327;
Best Local Similarity 63.6%; Pred. No. 35;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDXS 11
|||||
Db 175 KEVVPNGDKS 185

RESULT 20
DERTCM
acyl-CoA dehydrogenase (EC 1.3.99.3) precursor, medium-chain-specific, mitochondrial
N:Alternate names: acyl dehydrogenase, medium-chain-specific
C:Species: *Rattus norvegicus* (Norway rat)
C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 01-Dec-2000
C:Accession: A28436; S15128
R:Matsubara, Y.; Kraus, J.P.; Ozasa, H.; Glassberg, R.; Finocchiaro, G.; Ikeda, Y.
J. Biol. Chem. 262, 10104-10108, 1987
A:Title: Molecular cloning and nucleotide sequence of cDNA encoding the entire pre
A:Reference number: A28436; MUID:87280028; PMID:3611054
A:Accession: A28436
A:Molecule type: mRNA

A;Residues: 1-421 <RF1>
A;Cross-references: GB:J02791; NID:q202688; PIDN:AAA40670.1; PID:q202689
R;Inagaki, T.; Ohishi, N.; Tsukagoshi, N.; Uda, S.; Ghisla, S.; Yagi, K.
Biochim. Biophys. Acta 1077, 285-290, 1991
A;Title: Structurally different rat liver medium-chain acyl CoA dehydrogenases directed
A;Reference number: S15128; MUID:91230137; PMID:2029527
A;Accession: S15128
A;Status: preliminary
A;Molecule type: protein
A;Residues: 11-81 <BIO>
C;Superfamily: acyl-CoA dehydrogenase
C;Keywords: fatty acid beta-oxidation; fatty acid metabolism; flavoprotein; mitochondrion
F;1-25/Domain: transit peptide (mitochondrion) #status predicted <TRP>
F;26-421/Product: acyl-CoA dehydrogenase, medium-chain-specific #status predicted <MAT>

Query Match 66.0%; Score 33; DB 1; Length 421;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EVVPKXGXDY 10
DB 58 EEIIPVADPY 67
II::II II

RESULT 21
H72784
Probable alkaline proteinase APE0263 - Aeropyrum pernix (strain K1)
C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Accession: H72784
R;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K
DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr
A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: H72784
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-440 <KAW>
A;Cross-references: DDBJ:AP000058; NID:q5103388; PIDN:BAA79178.1; PID:q5103657
A;Experimental source: strain K1
C;Genetics:
A;Gene: APE0263
C;Superfamily: subtilisin; subtilisin homology

Query Match 66.0%; Score 33; DB 2; Length 440;
Best Local Similarity 66.7%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPKXGXDY 10
DB 120 EVLPKGVVDY 128
II::II II

RESULT 22
AF3286
ATP-dependent DNA helicase BMEI0275 [Imported] - Brucella melitensis (strain 16M)
C;Species: Brucella melitensis
C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C;Accession: AF3286
R;DeiVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Mujeer, C.; Los, T.; Ivanova,
.; Mazur, M.; Goltzman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
A;Reference number: AD3252; PMID:11756688
A;Accession: AF3286
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1028 <KUR>
A;Cross-references: GB:AR008917; PIDN:AAL51457.1; PID:g17982167; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEI0275

A;Map position: 1

Query Match 66.0%; Score 33; DB 2; Length 1028;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EVVPKXGXDYS 11
DB 76 EKIVPPGARYS 86
II::II II

RESULT 23

D82246
Probable chitinase Vcl073 [Imported] - Vibrio cholerae (strain N16961 serogroup O1
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: D82246
R;Heidelberger, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson,
Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sell
I, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: D82246
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1088 <HEI>
A;Cross-references: GB:AE004188; GB:AE003852; NID:g9655530; PIDN:AAF94232.1; GSPDB
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: Vcl073
A;Map position: 1

Query Match 66.0%; Score 33; DB 2; Length 1088;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVPKXGXDYS 11
DB 966 ETIPAGGEYS 975
II::II II

RESULT 24

T20173
Hypothetical protein C53A5.2 - Caenorhabditis elegans.
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T20173; T23857
R;Mortimore, B.
Submitted to the EMBL Data Library, November 1996
A;Reference number: Z19232
A;Accession: T20173
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1150 <WIL>
A;Cross-references: EMBL:Z81486; PIDN:CAB03994.1; GSPDB:GN00023; CESP:C53A5.2
A;Experimental source: clone C53A5
R;Matthews, L.
Submitted to the EMBL Data Library, August 1996
A;Reference number: Z19808
A;Accession: T23857
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1150 <WIT>
A;Cross-references: EMBL:Z78015; PIDN:CAB01437.1; GSPDB:GN00023; CESP:C53A5.2
A;Experimental source: clone R02D5
C;Genetics:
A;Gene: CESP:C53A5.2
A;Map position: 5
A;Introns: 33/3; 63/3; 132/3; 169/3; 221/3; 299/3; 379/2; 423/2; 438/2; 471/1; 513/

Query Match 66.0%; Score 33; DB 2; Length 1150;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 3 VWPXGXDYS 11
I: I I I I I
Db 562 VLPVGIDYS 570

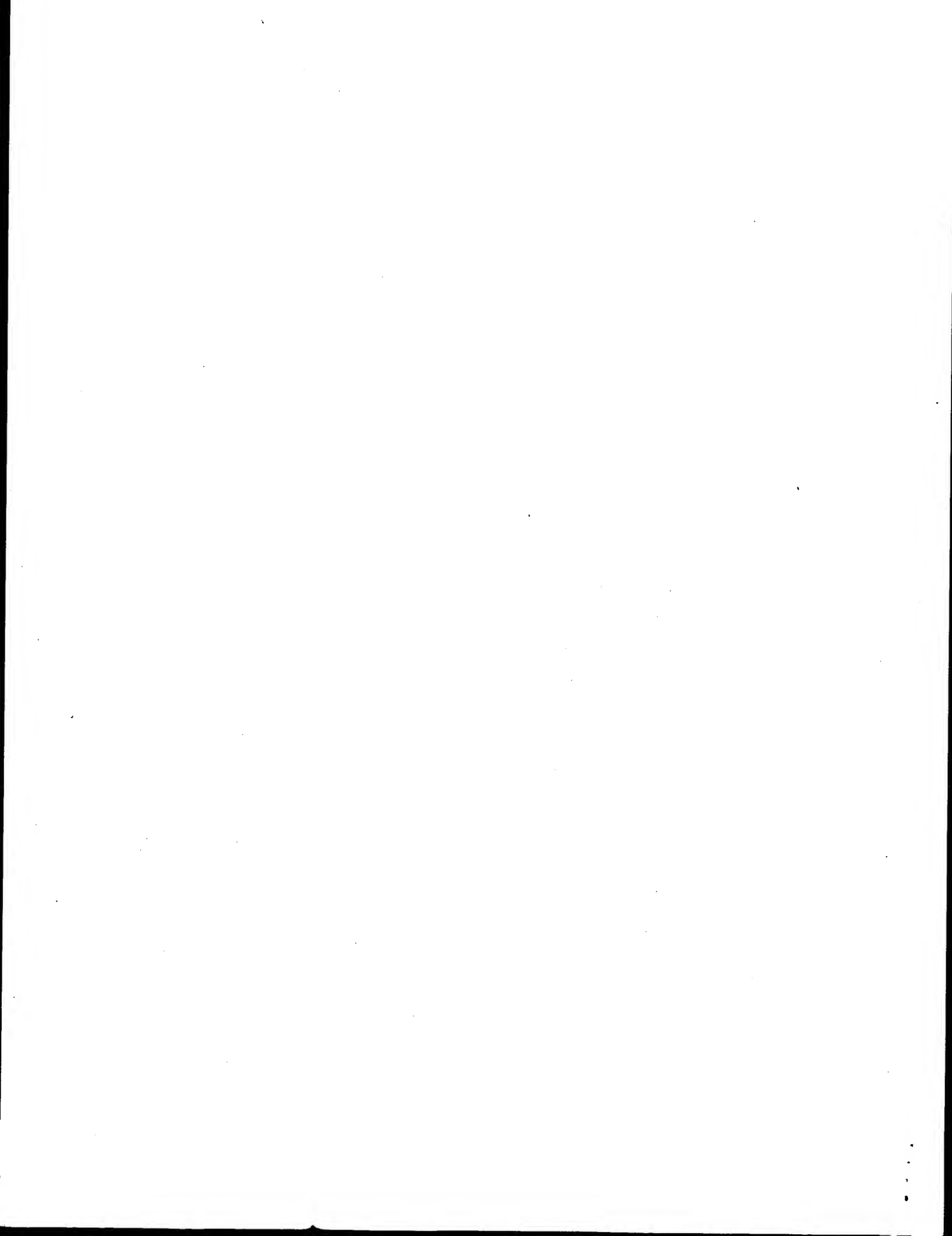
RESULT 25

S00210
C:Species: Populus nigra var. italica (Lombardy poplar)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 20-Apr-2000
C:Accession: S00210
R:Dimitrov, M.I.; Egorov, C.A.; Donchev, A.A.; Atanasov, B.P.
FEBS Lett. 226, 17-22, 1987
A:Title: Complete amino acid sequence of poplar plastocyanin b.
A:Reference number: S00210
A:Accession: S00210
A:Molecule type: protein
A:Residues: 1-99 <blm>
C:Superfamily: plastocyanin
C:Keywords: chloroplast; copper; electron transfer; metalloprotein
F:37,84,87,92/Binding site: copper (His, Cys, His, Met) (type 1) #status predicted

Query Match 64.0%; Score 32; DB 2; Length 99;
Best Local Similarity 54.5%; Pred. NO. 16;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Oy 1 EEVWPXGXDYS 11
I: I I I I I
Db 43 EDVPSGVDVS 53

Search completed: June 10, 2003, 13:49:18
Job time : 11.2143 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:25:04 ; Search time 4.5 Seconds
(without alignments)
101.387 Million cell updates/sec

Title: US-09-909-164-46
Perfect score: 50
Sequence: 1 EEVVPXGXDYS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	35	70.0	1058	1	CARB_FUSNN
2	34	68.0	102	1	Y1LK_TYDVA
3	34	68.0	394	1	HMPA_VIBCH
4	34	68.0	2747	1	FAF_DROME
5	33	66.0	124	1	REV_SIVCZ
6	33	66.0	327	1	YK14_CAEEL
7	33	66.0	421	1	ACDM_RAT
8	32	64.0	154	1	PLAS_ORYSA
9	32	64.0	155	1	PLAS_HORVU
10	32	64.0	168	1	PLAT_POPNI
11	32	64.0	196	1	XJAG_SALTY
12	32	64.0	427	1	TOUR_HAETN
13	32	64.0	1499	1	ALOC_HUMAN
14	32	64.0	3174	1	CHAC_HUMAN
15	31	62.0	233	1	HIS9_THEMEA
16	31	62.0	319	1	YHAI_CRYPA
17	31	62.0	421	1	ACDM_HUMAN
18	31	62.0	421	1	ACDM_PIG
19	31	62.0	562	1	TR2M_ERWHE
20	30	60.0	97	1	PLAS_DAUCA
21	30	60.0	121	1	TKNK_HUMAN
22	30	60.0	175	1	HES3_RAT
23	30	60.0	203	1	CTC_BACSU
24	30	60.0	231	1	ARAD_ECOLI
25	30	60.0	231	1	ARAD_SALTY
26	30	60.0	232	1	SCOA_HELPJ
27	30	60.0	232	1	SCOA_HELPY
28	30	60.0	259	1	OVUH_LYMS
29	30	60.0	421	1	AMP2_YEAST
30	30	60.0	421	1	ECB1_HALEL
31	30	60.0	423	1	ECB1_HALEL
32	30	60.0	430	1	FOLC_BACSU
33	30	60.0	457	1	Z185_HUMAN

34	30	60.0	469	1	LET1_KIULA	p53998	kluyveromy
35	30	60.0	478	1	AMP2_HUMAN	p50379	homo sapien
36	30	60.0	478	1	AMP2_MOUSE	o08663	mus musculus
37	30	60.0	478	1	AMP2_RAT	p38062	rattus norv
38	30	60.0	478	1	GSR2_HUMAN	q9nzm5	homo sapien
39	30	60.0	530	1	AHPF_XANCH	o06465	xanthomonas
40	30	60.0	556	1	APLY_APLKU	q17043	aplysia kur
41	30	60.0	583	1	HEMO_BRARE	q5yht4	brachydanio
42	30	60.0	890	1	BCN5_CLOPE	p08696	clostridium
43	30	60.0	1049	1	SPS_ORYSA	q43802	oryza sativ
44	30	60.0	1068	1	SPS_MAIZE	p19127	zea mays (n
45	30	60.0	1081	1	SPS2_CRAPL	o04933	craterostig
46	30	60.0	1176	1	NIR_NEUCR	p38681	neurospora
47	30	60.0	1401	1	RPOC_VIBCH	q9kv29	vibrio chol
48	30	60.0	1501	1	SNO2_YEAST	p32568	saccharomyc
49	30	60.0	1729	1	TABP_HUMAN	q9c0c2	homo sapien
50	30	60.0	2717	1	ZEP1_HUMAN	p15822	homo sapien
51	30	60.0	3099	1	POLG_PEMVM	o56075	p genome po
52	29.5	59.0	472	1	ET2A_XENLA	p19102	xenopus lae
53	29	58.0	98	1	PLAS_ENTPR	p07465	enteromorph
54	29	58.0	98	1	PLAS_ULVAR	p13133	ulva arasak
55	29	58.0	98	1	PLAS_ULVPE	p56274	ulva pertus
56	29	58.0	99	1	PLAS_RUMOB	p00298	rumex obtus
57	29	58.0	99	1	PLAS_TOBAC	p35476	nicotiana t
58	29	58.0	113	1	Y011_BPT4	p27006	bacteriopho
59	29	58.0	175	1	HES3_MOUSE	q61657	mus musculu
60	29	58.0	230	1	YCAP_ECOLI	p75839	escherichia
61	29	58.0	242	1	PSB4_XENLA	p28024	xenopus lae
62	29	58.0	258	1	YC10_METJA	q58607	methanococ
63	29	58.0	261	1	KLKD_MOUSE	p36368	mus musculus
64	29	58.0	338	1	MTBA_METBA	o30840	methanosarc
65	29	58.0	354	1	VGLI_VZVD	p09258	varicella-z
66	29	58.0	388	1	FEM3_CAEEL	p34691	caenorhabdi
67	29	58.0	389	1	SAT_AERPE	q9yct4	aeropyrum p
68	29	58.0	412	1	DOK2_HUMAN	o60496	homo sapien
69	29	58.0	421	1	ACDM_MOUSE	p45952	mus musculu
70	29	58.0	424	1	MS11_ARATH	o22467	arabidopsis
71	29	58.0	424	1	MS11_LYCES	o22466	lycopersico
72	29	58.0	435	1	HEM1_DESYM	q9kuc1	desulfovibr
73	29	58.0	471	1	TMLH_NEUCR	q96ub1	neurospora
74	29	58.0	472	1	ET2B_XENLA	q91712	xenopus lae
75	29	58.0	477	1	CAP2_RAT	p52481	rattus norv

ALIGNMENTS

RESULT 1

ID	CARB_FUSNN	STANDARD	PRT	1058 AA
AC	Q8RG86			
DT	15-JUN-2002	(Rel. 41, Created)		
DT	15-JUN-2002	(Rel. 41, Last sequence update)		
DT	15-JUN-2002	(Rel. 41, Last annotation update)		
DE	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthase ammonia chain).			
GN	CARB OR FN0422			
OS	Fusobacterium nucleatum (subsp. nucleatum).			
OC	Bacteria; Fusobacteria; Fusobacterium.			
OX	NCBI_TaxID=76856;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-ATCC 25586;			
RX	MEDLINE-21886394; PubMed-11889109;			
RA	Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasileva O., Chu L., Kogan Y., Chaga O., Goltzman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyripides N., Overbeek R.			
RA	"Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586."			
RT	J. Bacteriol. 184:2005-2018(2002).			
RL	-!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O = 2 ADP +			
CC				

phosphate + L-glutamate + carbamoyl phosphate.
 -!- COPACTOR: Binds three manganese ions (By similarity).
 -!- PATHWAY: Arginine biosynthesis.
 -!- SUBUNIT: Pyrimidine biosynthesis; first step.
 -!- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).
 -!- SIMILARITY: BELONGS TO THE CARB FAMILY.

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EMBL; AE010554; AAL94625.1; ALT_INIT.
 InterPro; IPR005483; CPase_L.
 InterPro; IPR005479; CPase_L_D2.
 InterPro; IPR005480; CPase_L_D3.
 InterPro; IPR005481; CPase_L_N.
 InterPro; IPR004362; MGS_like.
 Pfam; PF00289; CPase_L_chain; 2.
 Pfam; PF02786; CPase_L_D2; 2.
 Pfam; PF02787; CPase_L_D3; 1.
 Pfam; PF02142; MGS; 1.
 PRINTS; PR00098; CPASE.
 PROSITE; PS00866; CPASE_1; 2.
 PROSITE; PS00867; CPASE_2; 2.
 Arginine biosynthesis; Pyrimidine biosynthesis; Ligase; Repeat;
 ATP-binding; Manganese; Complete proteome.
 DOMAIN 1 401 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
 DOMAIN 402 546 OLIGOMERIZATION DOMAIN.
 DOMAIN 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
 DOMAIN 930 1058 ALLOSTERIC DOMAIN.
 REPEAT 1 546
 REPEAT 547 1058
 NP_BIND 153 210 ATP (POTENTIAL).
 NP_BIND 302 352 ATP (POTENTIAL).
 METAL 284 298 MANGANESE 1 (BY SIMILARITY).
 METAL 298 298 MANGANESE 1 AND 2 (BY SIMILARITY).
 METAL 300 300 MANGANESE 2 (BY SIMILARITY).
 METAL 820 820 MANGANESE 3 (BY SIMILARITY).
 METAL 832 832 MANGANESE 3 (BY SIMILARITY).
 SEQUENCE 1058 AA; 117451 MW; ED7037AF7C1E339f CRC64;

Query Match 70.0%; Score 35; DB 1; Length 1058;
 Best Local Similarity 60.0%; Pred. No. 17;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGXDYS 11
 : : : : :
 Db 190 EIVPGLNYS 199

RESULT 2
 Y11K_TYDVA
 ID Y11K_TYDVA STANDARD; PRT; 102 AA.
 AC P31619;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE Hypothetical 11.2 kDa protein.
 GN VT.
 OS Tobacco yellow dwarf virus (strain Australia) (TYDV).
 OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
 OX NCBI_TaxID=31599;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92188538; PubMed=1546458;
 RA Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;

"The nucleotide sequence of the infectious cloned DNA component of tobacco yellow dwarf virus reveals features of geminiviruses infecting monocotyledonous plants.";
 Virology 187:633-642(1992).

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EMBL; M81103; AAA47947.1; -.
 PIR; A42452;
 InterPro; IPR002621; Gemini_mov.
 DR Pfam; PF01708; Gemini_mov; 1.
 KW Hypothetical protein
 SQ SEQUENCE 102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;

Query Match 68.0%; Score 34; DB 1; Length 102;
 Best Local Similarity 60.0%; Pred. No. 2.3;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGXDYS 11
 : : : : :
 Db 7 QVVPNGINS 16

RESULT 3
 HMPA_VIBCH
 ID HMPA_VIBCH STANDARD; PRT; 394 AA.
 AC Q9KMY3;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Flavohemoprotein (Hemoglobin-like protein) (Flavohemoglobin).
 GN HMP OR VCA0183.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 SEQUENCE FROM N.A.
 RP STRAIN=El Tor N16961 / Serotype O1;
 RC MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Peterson J.D., Umayam L.A., Dodson R.J., Haft D.H., Hickey E.K., Tettelin H., Richardson D., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardon D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
 RA "DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae".
 RT Nature 406:477-483(2000).
 RL Nature 406:477-483(2000).
 CC -!- DOMAIN: CONSISTS OF TWO DISTINCT DOMAINS; ONE IS A HEME-CONTAINING OXYGEN BINDING DOMAIN IN THE N-TERMINAL REGION AND THE OTHER IS AN FAD-CONTAINING REDUCTASE DOMAIN FOUND IN THE C-TERMINAL REGION.
 CC -!- SIMILARITY: BELONGS TO THE GLOBIN FAMILY. TWO-DOMAIN FLAVOHEMOPROTEINS SUBFAMILY.
 CC -!- SIMILARITY: TO A NUMBER OF FAD/NAD(P) FLAVOPROTEIN OXIDOREDUCTASES.

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EMBL; AE004358; AAF96096.1; -.
 HSSP; P39662; LCQX.

Query Match 66.0%; Score 33; DB 1; Length 124;
 Best Local Similarity 60.0%; Pred. No. 4.6;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EWPVPGXDYS 11
 Db 107 ETVPAGNYS 116

RESULT 6
 YK14_CAEEL STANDARD; PRT: 327 AA.
 AC P34338;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein C15H7.4 in chromosome III.
 GN C15H7.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
 RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
 RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
 RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Shownkeen R.,
 RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
 RA Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
 RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
 RA Whidman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).

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 CC -----
 DR EMBL; Z22173; CAA80126.1; -;
 DR PIR; S40753; S40753.
 DR WormPep; C15H7.4; CE00082.
 KW Hypothetical protein.
 SQ SEQUENCE 327 AA; 35566 MW; 716BC2BDD2E9607E CRC64;

Query Match 66.0%; Score 33; DB 1; Length 327;
 Best Local Similarity 63.6%; Pred. No. 13;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDS 11
 Db 175 KEVVPNGGDKS 185

RESULT 7
 ACDM_RAT STANDARD; PRT: 421 AA.
 AC P08503;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acyl-CoA dehydrogenase, medium-chain specific, mitochondrial precursor
 DE (EC 1.3.99.3) (NCAD).

GN ACDM.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=87280028; PubMed=3611054;
 RA Matsubara Y., Kraus J.P., Ozasa H., Glassberg R., Finocchiaro G.,
 RA Ikeda Y., Mole J., Rosenberg L.E., Tanaka K.;
 RT "Molecular cloning and nucleotide sequence of cDNA encoding the
 RT entire precursor of rat liver medium chain acyl coenzyme A
 RT dehydrogenase.";
 RL J. Biol. Chem. 262:10104-10108(1987).
 CC -1- FUNCTION: THIS ENZYME IS SPECIFIC FOR ACYL CHAIN LENGTHS OF 4 TO
 CC 16.
 CC -1- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
 CC ETF.
 CC -1- COFACTOR: FAD.
 CC -1- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
 CC step.
 CC -1- SUBUNIT: HOMOTETRAMER.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -1- MISCELLANEOUS: A NUMBER OF STRAIGHT-CHAIN ACYL-CoA DEHYDROGENASES
 CC OF DIFFERENT SUBSTRATE SPECIFICITIES ARE PRESENT IN MAMMALIAN
 CC TISSUES.
 CC -1- SIMILARITY: BELONGS TO THE ACYL-CoA DEHYDROGENASE FAMILY.

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 CC -----
 DR EMBL; J02791; AAA40670.1; -;
 DR PIR; A28436; DERTCM.
 DR HSSP; P11310; LEGD.
 DR InterPro; IPR001352; Acyl-CoA_dh.
 DR Pfam; PF00441; Acyl-CoA_dh; 1.
 DR Pfam; PF02770; Acyl-CoA_dh_M; 1.
 DR Pfam; PF02771; Acyl-CoA_dh_N; 1.
 DR PROSITE; PS00072; ACYL-CoA_DH_1; 1.
 DR PROSITE; PS00073; ACYL-CoA_DH_2; 1.
 KW Oxidoreductase; Flavoprotein; FAD; Fatty acid metabolism;
 KW Mitochondrion; Transient peptide.
 FT CHAIN 1 25 MITOCHONDRION.
 FT TRANSIT 26 421 ACYL-CoA DEHYDROGENASE, MEDIUM-CHAIN
 FT SPECIFIC.
 FT ACT_SITE 193 193 FORMS A HYDROGEN-BOND WITH THE FLAVIN
 FT ACT_SITE 401 401 N(5) OF THE FAD COFACTOR (BY SIMILARITY).
 FT SEQUENCE 421 AA; 46555 MW; 2CF076F8C919BDE8 CRC64;

Query Match 66.0%; Score 33; DB 1; Length 421;
 Best Local Similarity 50.0%; Pred. No. 17;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDY 10
 Db 58 EEIIPVADY 67

RESULT 8
 PLAS_ORISA STANDARD; PRT: 154 AA.
 ID PLAS_ORISA
 AC P20423; Q9SBB8;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Plastocyanin, chloroplast precursor.

GN PETE.
OS *Oryza sativa* (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; *Oryza*.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Ilpoom; TISSUE=Leaf;
RA Lee J.-S.;
RT "Molecular cloning and characterization of plastocyanin precursor in
RT rice.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 58-154.
RC STRAIN=cv. Japonica;
RX MEDLINE=89386623; PubMed=2780537;
RA Yano H., Kano M., Tsugita A., Aso K., Nozu Y.;
RT "The amino acid sequence of plastocyanin from rice (*Oryza sativa*,
RT subspecies japonica).";
RL Protein Seq. Data Anal. 2:385-389(1989).
CC -!- FUNCTION: Participates in electron transfer between P700 and the
CC cytochrome b6-f complex in photosystem I.
CC -!- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID
CC MEMBRANE SURFACE IN CHLOROPLASTS.
CC -!- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
CC
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CC
DR EMBL; AF093636; AAC78108.1; -.
DR PIR; S06105; S06105.
DR JTO352; JTO352.
DR HSSP; P00289; 2PCF.
DR InterPro; IPR000923; BlueCu_1.
DR Pfam; PF00127; copper-bind; 1.
DR PRINTS; P00156; COPPERBLUE.
DR ProDom; PD001235; Copper_blue; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
KW Transit peptide.
FT TRANSIT 1 57 CHLOROPLAST.
FT CHAIN 58 154 PLASTOCYANIN.
FT DOMAIN 58 154 PLASTOCYANIN-LIKE.
FT METAL 94 94 COPPER (BY SIMILARITY).
FT METAL 139 139 COPPER (BY SIMILARITY).
FT METAL 142 142 COPPER (BY SIMILARITY).
FT METAL 147 147 COPPER (BY SIMILARITY).
SQ SEQUENCE 154 AA; 15577 MW; E45725D2B5F400D CRC64;
Query Match 64.0%; Score 32; DB 1; Length 154;
Best Local Similarity 54.5%; Pred. No. 9.6;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 EEVVPXGXDYS 11
Db 100 EDAPVSGVDVS 110
RESULT 9
PLAS_HORVU STANDARD; PRT; 155 AA.
AC P08248;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Plastocyanin, chloroplast precursor.

GN PETE.
OS *Hordeum vulgare* (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Triticeae; *Hordeum*.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Boml;
RA Nielsen O.S., Gausing K.;
RT "The precursor of barley plastocyanin: sequence of cDNA clones and
RT gene expression in different tissues.";
RL FEBS Lett. 225:159-162(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. NK 1558;
RX MEDLINE=94039081; PubMed=8223592;
RA Nielsen P., Gausing K.;
RT "In vitro binding of nuclear proteins to the barley plastocyanin gene
RT promoter region.";
RL Eur. J. Biochem. 217:97-104(1993).
CC -!- FUNCTION: Participates in electron transfer between P700 and the
CC cytochrome b6-f complex in photosystem I.
CC -!- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID
CC MEMBRANE SURFACE IN CHLOROPLASTS.
CC -!- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
CC
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CC
DR EMBL; Y00704; CAA68696.1; -.
DR EMBL; Z28347; CAA82201.1; -.
DR PIR; S00206; S00206.
DR HSSP; P00289; 2PCF.
DR InterPro; IPR000923; BlueCu_1.
DR Pfam; PF00127; copper-bind; 1.
DR PRINTS; P00156; COPPERBLUE.
DR ProDom; PD001235; Copper_blue; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
KW Transit peptide.
FT TRANSIT 1 58 CHLOROPLAST.
FT CHAIN 59 155 PLASTOCYANIN.
FT DOMAIN 59 155 PLASTOCYANIN-LIKE.
FT METAL 95 95 COPPER (BY SIMILARITY).
FT METAL 140 140 COPPER (BY SIMILARITY).
FT METAL 143 143 COPPER (BY SIMILARITY).
FT METAL 148 148 COPPER (BY SIMILARITY).
FT VARIANT 120 120 T -> N (IN CV. NK 1558).
SQ SEQUENCE 155 AA; 15709 MW; DAA7EAB5F6F91 CRC64;
Query Match 64.0%; Score 32; DB 1; Length 155;
Best Local Similarity 54.5%; Pred. No. 9.6;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 EEVVPXGXDYS 11
Db 101 EDAPVSGVDVS 111
RESULT 10
PLAT_POPNI STANDARD; PRT; 168 AA.
AC P11970;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Plastocyanin B, chloroplast precursor.
 OS PEST.
 ON Populus nigra (Lombardy poplar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eucosids I; Malpighiales; Salicaceae; Populus.
 OX NCBI_TaxID=3691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Italica; TISSUE=Leaf;
 RA Reichert J., Jenzewski V., Haehnel W.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 70-168.
 RC STRAIN=cv. Italica;
 RA Dmitrov M.I., Egorov C.A., Donchev A.A., Atanasov B.P.;
 RL FEBS Lett. 226:17-22(1987).
 CC -1- FUNCTION: Participates in electron transfer between P700 and the
 CC cytochrome b6-f complex in photosystem I.
 CC -1- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID
 CC MEMBRANE SURFACE IN CHLOROPLASTS.
 CC -1- SIMILARITY: THERE ARE 12 DIFFERENCES BETWEEN THE SEQUENCE OF
 CC POPULAR PLASTOCYANINS A AND B.
 CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
 CC -----
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 CC -----
 CC EMBL; Z50186; CAA90565.1; -
 DR PIR; S00210; S00210.
 DR HSP; P00299; 1PLC.
 DR InterPro; IPR000923; BlueCu1.
 DR InterPro; IPR001235; Copper_blue.
 DR Pfam; PF00127; copper-bind; 1.
 DR PRINTS; PR00156; COPPERBLUE.
 DR PRODOM; PD001235; Copper blue; 1.
 DR PROSITE; PS00196; COPPER_BLUE; 1.
 KW Chloroplast; Electron transport; Copper; Thylakoid; Membrane;
 KW Transit peptide; Multigene family.
 FT TRANSIT 1 69
 FT CHAIN 70 168
 FT DOMAIN 70 168 PLASTOCYANIN B.
 FT METAL 106 106 PLASTOCYANIN-LIKE.
 FT METAL 153 153 COPPER.
 FT METAL 156 156 COPPER.
 FT METAL 161 161 COPPER.
 SQ SEQUENCE 168 AA; 16981 MW; F20DA6EA038AEEA CRC64;
 Query Match 64.0%; Score 32; DB 1; Length 168;
 Best Local Similarity 54.5%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDYS 11
 Db 112 EDVPSGVDS 122
 I: | | | | |
 RESULT 11
 YJAG_SALTY
 ID YJAG_SALTY STANDARD; PRT; 196 AA.
 AC Q9L9I2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hypothetical protein yJag.
 GN YJAG OR STM4169 OR STM1.23 OR STV3716.
 OS Salmonella typhimurium, and

OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 OX NCBI_TaxID=602, 601;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609;
 RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
 RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 LT2";
 RL Nature 413:852-856(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhi; STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagers K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrall B.G.;
 RT "Complete genome sequence of a multiple drug resistant Salmonella
 enterica serovar Typhi CT18";
 RL Nature 413:848-852(2001).
 CC -1- SIMILARITY: STRONG, TO H.INFLUENZAE HI0431.
 CC -----
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 CC -----
 CC EMBL; AF170176; AAF33519.1; -
 DR EMBL; AE008894; AAL22997.1; -
 DR EMBL; AL67279; CAD09475.1; -
 DR StyGene; SG?????; yJag.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 196 AA; 22704 MW; E40049CE5EE64150 CRC64;
 Query Match 64.0%; Score 32; DB 1; Length 196;
 Best Local Similarity 50.0%; Pred. No. 12;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDY 10
 Db 76 EEAIPAADY 85
 I: | | | | |
 RESULT 12
 TOLB_HAEIN
 ID TOLB_HAEIN STANDARD; PRT; 427 AA.
 AC P44677; P94811;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE TOLB protein precursor.
 GN TOLB OR HI0382.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
 OC Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KW20 / ATCC 51907;

RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uitterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
 RA Gnehm C.D., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RL Rd.";
 RL Science 269:496-512(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1479;
 RA MEDLINE=97080550; PubMed=8921895;
 RA Sen K., Sikkema D.J., Murphy T.F.;
 RT "Isolation and characterization of the Haemophilus influenzae tolQ,
 RT tolR, tolA and tolB genes.";
 RL Gene 178:75-81(1996).
 CC -!- FUNCTION: INVOLVED IN THE TONB-INDEPENDENT UPTAKE OF PROTEINS
 CC (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE TOLB FAMILY.
 CC -----
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 CC -----
 CC DR EMBL; U32722; AAC22040.1; -
 CC DR EMBL; U32470; AAC44597.1; -
 CC DR HSSP; P19935; 1CRZ.
 CC TIGR: HI0382; -
 KW Transport; Protein transport; Periplasmic; Signal; Complete proteome.
 FT SIGNAL 1 23
 FT CHAIN 24 427
 FT VARIANT 6 6 R -> H (IN STRAIN 1479).
 FT VARIANT 14 14 V -> I (IN STRAIN 1479).
 FT VARIANT 17 19 VGS -> ITH (IN STRAIN 1479).
 FT VARIANT 21 21 A -> V (IN STRAIN 1479).
 FT VARIANT 79 79 R -> H (IN STRAIN 1479).
 FT VARIANT 129 129 T -> A (IN STRAIN 1479).
 FT VARIANT 160 160 A -> G (IN STRAIN 1479).
 FT VARIANT 237 237 A -> T (IN STRAIN 1479).
 FT VARIANT 322 322 S -> N (IN STRAIN 1479).
 FT VARIANT 326 326 A -> V (IN STRAIN 1479).
 FT VARIANT 328 328 A -> S (IN STRAIN 1479).
 SQ SEQUENCE 427 AA; 44967 MW; 0882201AE5254B9 CRC64;
 Query Match 64.0%; Score 32; DB 1; Length 427;
 Best Local Similarity 60.0%; Pred. No. 29;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 EVVPGXDYS 11
 Db 103 QVVPNGGYS 112
 RESULT 13
 ID A10C.HUMAN STANDARD; PRT; 1499 AA.
 AC O60312: Q96914;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Potential phospholipid-transporting ATPase VC (EC 3.6.3.1) (ATPVC)
 DE (Aminophospholipid translocase VC).
 GN ATP10C OR ATPVC OR KIAA0566.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21225279; PubMed=11326269;
 RA Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S.,
 RA Oshimura M.;
 RT "A novel maternally expressed gene, ATP10C, encodes a putative
 RT aminophospholipid translocase associated with Angelman syndrome.";
 RL Nat. Genet. 28:19-20(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21313119; PubMed=11353404;
 RA Herzog L.B.K., Kim S.-J., Cook E.H. Jr., Ledbetter D.H.;
 RT "The human aminophospholipid-transporting ATPase gene ATP10C maps
 RT adjacent to UBE3A and exhibits similar imprinted expression.";
 RL Am. J. Hum. Genet. 68:1501-1505(2001).
 RN [3]
 RP SEQUENCE OF 337-1499 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98290545; PubMed=9628581;
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:31-39(1998).
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O -> ADP + phosphate.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -!- TISSUE SPECIFICITY: Wide expression, with highest levels in
 CC kidney, followed by lung, brain, prostate, testis, ovary, and
 CC small intestine.
 CC -!- DISEASE: Defects in ATP10C may be a cause of Angelman syndrome
 CC (AS), also known as 'happy puppet syndrome'.
 CC -!- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
 CC ATPASES). SUBFAMILY IV.
 CC -----
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 CC -----
 CC DR EMBL; AB051358; BAB47392.1; -
 CC DR EMBL; AY029504; AAK33100.1; -
 CC DR EMBL; AY029487; AAK33100.1; JOINED.
 CC DR EMBL; AY029488; AAK33100.1; JOINED.
 CC DR EMBL; AY029489; AAK33100.1; JOINED.
 CC DR EMBL; AY029490; AAK33100.1; JOINED.
 CC DR EMBL; AY029491; AAK33100.1; JOINED.
 CC DR EMBL; AY029492; AAK33100.1; JOINED.
 CC DR EMBL; AY029493; AAK33100.1; JOINED.
 CC DR EMBL; AY029494; AAK33100.1; JOINED.
 CC DR EMBL; AY029495; AAK33100.1; JOINED.
 CC DR EMBL; AY029496; AAK33100.1; JOINED.
 CC DR EMBL; AY029497; AAK33100.1; JOINED.
 CC DR EMBL; AY029498; AAK33100.1; JOINED.
 CC DR EMBL; AY029499; AAK33100.1; JOINED.
 CC DR EMBL; AY029500; AAK33100.1; JOINED.
 CC DR EMBL; AY029501; AAK33100.1; JOINED.
 CC DR EMBL; AY029502; AAK33100.1; JOINED.
 CC DR EMBL; AY029503; AAK33100.1; JOINED.
 CC DR EMBL; AB011138; BAA25492.1; -
 CC DR Genew; HGNC:13547; ATP10C.
 CC MIM; 605855; -
 CC MIM; 105830; -
 CC InterPro; IPR001757; ATPase_E1-E2.
 CC InterPro; IPR001454; Hlgase/hydrlase.
 CC Pfam; PF00702; Hydrolase; 1.


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FT CONFLICT 2127 2129 GIE -> VSA (IN REF. 4).
FT CONFLICT 2281 2281 G -> E (IN REF. 5).
FT CONFLICT 2413 2413 T -> R (IN REF. 5).
FT CONFLICT 2567 2567 K -> E (IN REF. 5).
SQ SEQUENCE 3174 AA; 360299 MW; FD2AB895B4A7149E CRC64;

Query Match
Best Local Similarity 64.0%; Score 32; DB 1; Length 3174;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDY 10
Db 242 ENIVPEGYDF 251

RESULT 15
HIS9_THEME
ID HIS9_THEME STANDARD; PRT; 233 AA.
AC Q9WZRL;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable histidinol-phosphatase (EC 3.1.3.15) (HolPase).
GN HISK OR TW0804.
OS Thermotoga maritima.
OC Bacteria; Thermotogae; Thermotogae (class); Thermotogales;
OC Thermotogaceae; Thermotoga.
OX NCBI_TaxID=2336;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=99287316; PubMed=10360571;
RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA McDonald L., Utterback F.R., Malek J.A., Linher K.D., Garrett M.M.,
RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT "Evidence for lateral gene transfer between Archaea and Bacteria from
RT genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
CC -!- CATALYTIC ACTIVITY: L-histidinol-phosphate + H(2)O = L-histidinol
CC + phosphate.
CC -!- PATHWAY: Histidine biosynthesis; eighth step.
CC -!- SIMILARITY: BELONGS TO THE PHP FAMILY OF HYDROLASE. HISK FAMILY.
CC -----
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RESULT 16
YHAL_CRYPA
ID YHAL_CRYPA STANDARD; PRT; 319 AA.
AC P10941;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein 1 in hypovirulence-associated DS-RNA genetic
DE element [Contains: P29 proteinase].
OS Cryphonectria parasitica (Chesnut blight fungus) (Endothia
OS parasitica).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Diaporthales; Valsaceae; Cryphonectria.
OX NCBI_TaxID=5116;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=EP713;
RC MEDLINE=89251594; PubMed=2721496;
RX Rae B.P., Hillman B.I., Tartaglia J., Nuss D.L.;
RT "Characterization of double-stranded RNA genetic elements associated
RT with biological control of chestnut blight: organization of terminal
RT domains and identification of gene products.";
RL EMBO J. 8:657-663(1989).
CC -!- MISCELLANEOUS: DOUBLE-STRANDED RNA GENETIC ELEMENTS ARE ASSOCIATED
CC WITH BIOLOGICAL CONTROL OF THE FUNGAL DISEASE CHESTNUT BLIGHT.
CC THIS DS-RNA ARE ASSOCIATED WITH HYPOVIRULENCE. THEY ARE LOCALIZED
CC IN THE CYTOPLASM.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C7.
CC -----
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- RA Strauss A.W.:
RT "Nucleotide sequence of medium-chain acyl-CoA dehydrogenase mRNA and
its expression in enzyme-deficient human tissue.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4068-4072(1987).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Sun F., Wang Y., Block G.D.;
RT "Medium-chain acyl-CoA dehydrogenase.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 314-342 FROM N.A., AND VARIANT MCAD GLU-329.
RX MEDLINE-90365752; PubMed-2393404;
RA Matsubara Y., Narisawa K., Miyabayashi S., Tada K., Coates P.M.,
BAchmann C., Elsas L.J. II, Pollitt R.J., Rhead W.J., Roe C.R.;
RT "Identification of a common mutation in patients with medium-chain
acyl-CoA dehydrogenase deficiency.";
RL Biochem. Biophys. Res. Commun. 171:498-505(1990).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE-96420477; PubMed-8823176;
RA Lee H.J., Wang M., Paschke R., Nandy A., Ghisla S., Kim J.J.;
RT "Crystal structures of the wild type and the Glu376Gly/Thr255Glu
mutant of human medium-chain acyl-CoA dehydrogenase: influence of the
location of the catalytic base on substrate specificity.";
RL Biochemistry 35:12412-12420(1996).
RN [6]
RP REVIEW ON VARIANTS MCAD.
RX MEDLINE-93250819; PubMed-1363805;
RA Tanaka K., Yokota I., Coates P.M., Strauss A.W., Kelly D.P.,
RA Zhang Z.F., Gregersen N., Andresen B.S., Matsubara Y., Curtis D.,
RA Chen Y.-T.;
RT "Mutations in the medium chain acyl-CoA dehydrogenase (MCAD) gene.";
RL Hum. Mutat. 1:271-279(1992).
RN [7]
RP VARIANT MCAD GLU-329.
RX MEDLINE-90368980; PubMed-2394825;
RA Yokota I., Indo Y., Coates P.M., Tanaka K.;
RT "Molecular basis of medium chain acyl-coenzyme A dehydrogenase
deficiency. An A to G transition at position 985 that causes a
lysine-304 to glutamate substitution in the mature protein is the
single prevalent mutation.";
RL J. Clin. Invest. 86:1000-1003(1990).
RN [8]
RP VARIANT MCAD GLU-329.
RX MEDLINE-91067682; PubMed-2251268;
RA Kelly D.P., Whelan A.J., Ogden M.L., Alpers R., Zhang Z.F., Bellus G.,
RA Gregersen N., Dorland L.J., Strauss A.W.;
RT "Molecular characterization of inherited medium-chain acyl-CoA
dehydrogenase deficiency.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:9236-9240(1990).
RN [9]
RP VARIANTS MCAD ILE-149; ARG-244; ARG-267 AND THR-375.
RX MEDLINE-92081773; PubMed-1664086;
RA Yokota I., Coates P.M., Hale D.E., Rinaldo P., Tanaka K.;
RT "Molecular survey of a prevalent mutation, 985A-to-G transition, and
identification of five infrequent mutations in the medium-chain acyl-
CoA dehydrogenase (MCAD) gene in 55 patients with MCAD deficiency.";
RL Am. J. Hum. Genet. 49:1280-1291(1991).
RN [10]
RP VARIANT MCAD GLU-329.
RX MEDLINE-91224627; PubMed-1902818;
RA Gregersen N., Andresen B.S., Bross P., Winter V., Ruediger N.,
RA Engst S., Christensen E., Kelly D., Strauss A.W., Koelvræ S.,
RA Bolund L., Ghisla S.;
RT "Molecular characterization of medium-chain acyl-CoA dehydrogenase
(MCAD) deficiency: identification of a lys329 to glu mutation in the
MCAD gene, and expression of inactive mutant enzyme protein in E.
- RT coli.";
RL Hum. Genet. 86:545-551(1991).
RN [11]
RP VARIANT MCAD GLU-329 FREQUENCY.
RX MEDLINE-91109464; PubMed-1671131;
RA Blakemore A.I., Singleton H., Pollitt R.J., Engel P.C., Kolvræ S.,
RA Gregersen N., Curtis D.;
RT "Frequency of the G985 MCAD mutation in the general population.";
RL Lancet 337:298-299(1991).
RN [12]
RP VARIANTS MCAD THR-326 AND ARG-336.
RX MEDLINE-94256509; PubMed-8198141;
RA Andresen B.S., Jensen T.G., Bross P., Knudsen I., Winter V.,
RA Koelvræ S., Bolund L., Ding J.-H., Chen Y.-T., van Hove J.L.K.,
RA Curtis D., Yokota I., Tanaka K., Kim J.-J.P., Gregersen N.;
RT "Disease-causing mutations in exon 11 of the medium-chain acyl-CoA
dehydrogenase gene.";
RL Am. J. Hum. Genet. 54:975-988(1994).
RN [13]
RP VARIANT MCAD I15-GLY-CYS-116 DEL.
RX MEDLINE-95327425; PubMed-7603790;
RA Ziaadeh R., Hoffman E.P., Finegold D.N., Hoop R.C., Brackett J.C.,
RA Strauss A.W., Naylor E.W.;
RT "Medium chain acyl-CoA dehydrogenase deficiency in Pennsylvania:
neonatal screening shows high incidence and unexpected mutation
frequencies.";
RL Pediatr. Res. 37:675-678(1995).
RN [14]
RP VARIANT MCAD ARG-195.
RX MEDLINE-95015014; PubMed-7929823;
RA Brackett J.C., Sims H.F., Steiner R.D., Nunge M., Zimmerman E.M.,
RA Demartinville B., Rinaldo P., Slaughter P., Strauss A.W.;
RT "A novel mutation in medium chain acyl-CoA dehydrogenase causes sudden
neonatal death.";
RL J. Clin. Invest. 94:1477-1483(1994).
RN [15]
RP VARIANT MCAD ALA-193.
RX MEDLINE-97301766; PubMed-9158144;
RA Andresen B.S., Bross P., Udvari S., Kirk J., Gray G., Kmoch S.,
RA Chamoles N., Knudsen I., Winter V., Wilcken B., Yokota I., Hart K.,
RA Packman S., Harpey J.P., Saudubray J.M., Hale D.E., Bolund L.,
RA Koelvræ S., Gregersen N.;
RT "The molecular basis of medium-chain acyl-CoA dehydrogenase (MCAD)
deficiency in compound heterozygous patients: is there correlation
between genotype and phenotype?";
RL Hum. Mol. Genet. 6:695-707(1997).
RN [16]
RP CHARACTERIZATION OF VARIANT MCAD ALA-193.
RX MEDLINE-99102080; PubMed-9882619;
RA Kuchler B., Abdel-Ghany A.G., Bross P., Nandy A., Rasched I.,
RA Ghisla S.;
RT "Biochemical characterization of a variant human medium-chain acyl-CoA
dehydrogenase with a disease-associated mutation localized in the
active site.";
RL Biochem. J. 337:225-230(1999).
RN [17]
RP VARIANT HIS-67.
RX PubMed-11349232;
RA Andresen B.S., Dobrowolski S.F., O'Reilly L., Muenzer J.,
RA McCandless S.E., Frazier D.M., Udvari S., Bross P., Knudsen I.,
RA Banas R., Chace D.H., Engel P.C., Naylor E.W., Gregersen N.;
RT "Medium-chain acyl-CoA dehydrogenase (MCAD) mutations identified by
MS/MS-based prospective screening of newborns differ from those
observed in patients with clinical symptoms: identification and
characterization of a new, prevalent mutation that results in mild
MCAD deficiency.";
RL Am. J. Hum. Genet. 68:1408-1418(2001).
RN [18]
RP VARIANT MCAD LEU-245.
RX PubMed-11409868;
RA Zschocke J., Schulze A., Lindner M., Fiesel S., Olgemöller K.,
RA Hoffmann G.F., Penzien J., Ruiter J.P.N., Wanders R.J.A.,
RA Mayatepek E.;

RT Molecular and functional characterization of mild MCAD deficiency.";
 RL Hum. Genet. 108:404-408(2001).
 RN [19]
 RP VARIANT THR-281.
 RX PubMed=11486912;
 RA Albers S., Levy H.L., Irons M., Strauss A.W., Marsden D.;
 RT "Compound heterozygosity in four asymptomatic siblings with
 medium-chain acyl-CoA dehydrogenase deficiency.";
 RL J. Inher. Metab. Dis. 24:417-418(2001).
 CC -!- FUNCTION: THIS ENZYME IS SPECIFIC FOR ACYL CHAIN LENGTHS OF 4 TO
 16.
 CC -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
 CC ETF.
 CC -!- COFACTOR: FAD.
 CC -!- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
 CC step.
 CC -!- SUBUNIT: HOMOTETRAMER.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -!- MISCELLANEOUS: A NUMBER OF STRAIGHT-CHAIN ACYL-CoA DEHYDROGENASES
 CC OF DIFFERENT SUBSTRATE SPECIFICITIES ARE PRESENT IN MAMMALIAN
 CC TISSUES.
 CC -!- SIMILARITY: BELONGS TO THE ACYL-CoA DEHYDROGENASE FAMILY.
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 CC -----
 DR EMBL; M91432; AAA59567.1; -;
 DR EMBL; M91421; AAA59567.1; JOINED.
 DR EMBL; M91422; AAA59567.1; JOINED.

Query Match 62.0%; Score 31; DB 1; Length 421;
 Best Local Similarity 40.0%; Pred. No. 46;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDY 10
 Db 58 EEIIPVAAEY 67
 ID ACDCM_PIG STANDARD; PRT; 421 AA.
 AC P41367;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Acyl-CoA dehydrogenase, medium-chain specific, mitochondrial precursor
 DE (EC 1.3.99.3) (MCAD).
 GN ACADM.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Suzuki H., Kimura M., Ito T., Murakami Y., Hamasima N., Yasue H.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ÅNGSTRÖMS).
 RC TISSUE=Liver;
 RX MEDLINE=93361479; PubMed=8356049;
 RA Kim J.-J.P., Wang M., Paschke R.;
 RT "Crystal structures of medium-chain acyl-CoA dehydrogenase from pig
 liver mitochondria with and without substrate.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:7523-7527(1993).
 CC -!- FUNCTION: THIS ENZYME IS SPECIFIC FOR ACYL CHAIN LENGTHS OF 4 TO
 CC 16.
 CC -!- CATALYTIC ACTIVITY: Acyl-CoA + ETF = 2,3-dehydroacyl-CoA + reduced
 CC ETF.
 CC -!- COFACTOR: FAD.
 CC -!- PATHWAY: Mitochondrial fatty acid beta-oxidation system; first
 CC step.
 CC -!- SUBUNIT: HOMOTETRAMER.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial matrix.
 CC -!- MISCELLANEOUS: A NUMBER OF STRAIGHT-CHAIN ACYL-CoA DEHYDROGENASES
 CC OF DIFFERENT SUBSTRATE SPECIFICITIES ARE PRESENT IN MAMMALIAN
 CC TISSUES.
 CC -!- SIMILARITY: BELONGS TO THE ACYL-CoA DEHYDROGENASE FAMILY.
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 CC -----
 DR EMBL; U40845; AAA83759.1; -;
 DR PDB; 3MDD; 30-SEP-94.
 DR PDB; 3MDE; 30-SEP-94.
 DR InterPro; IPR001552; Acyl-CoA_dh.
 DR Pfam; PF00441; Acyl-CoA_dh; 1.
 DR Pfam; PF02770; Acyl-CoA_dh.M; 1.
 DR Pfam; PF02771; Acyl-CoA_dh.N; 1.
 DR PROSITE; PS00072; ACYL-CoA_DH_1; 1.
 DR PROSITE; PS00073; ACYL-CoA_DH_2; 1.
 KW Oxidoreductase; Flavoprotein; FAD; Fatty acid metabolism;
 KW Mitochondrion; Transit peptide; 3D-structure.
 FT TRANSIT 1 25 MITOCHONDRION.
 FT CHAIN 26 421 ACYL-CoA DEHYDROGENASE, MEDIUM-CHAIN
 FT SPECIFIC.
 FT ACT_SITE 193 193 FORMS A HYDROGEN-BOND WITH THE FLAVIN
 FT N(5) OF THE FAD COFACTOR (BY SIMILARITY).
 FT ACT_SITE 401 401 BASE.
 FT CONFLICT 40 40 K -> E (IN REF. 2).
 FT CONFLICT 283 283 S -> P (IN REF. 2).
 FT CONFLICT 305 305 G -> E (IN REF. 2).
 FT CONFLICT 331 331 D -> E (IN REF. 2).
 SQ SEQUENCE 421 AA; 46358 MW; 27347B0C9F2B7C3 CRC64;
 Query Match 62.0%; Score 31; DB 1; Length 421;
 Best Local Similarity 40.0%; Pred. No. 46;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDY 10
 Db 58 EEIIPVAAEY 67
 ID TR2M_ERWHE STANDARD; PRT; 562 AA.
 AC Q47861;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Tryptophan 2-monooxygenase (EC 1.13.12.3).
 GN IAAM.
 OS Erwinia herbicola.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Pantoea.
 OX NCBI_TaxID=549;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=py. gypsophilae / PD713;
 RA Ophir Y., Kunik T., Manulis S., Lichter A., Barash I., Gafni Y.;
 RT Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.

```
CC -1- CATALYTIC ACTIVITY: L-tryptophan + O(2) = indole-3-acetamide +
CC CO(2) + H(2)O
CC -1- PATHWAY: FIRST STEP IN THE BIOSYNTHESIS OF AUXINS FROM TRYPTOPHAN.
CC -----
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CC -----
CC EMBL; L33867; AAC17187.1;
CC InterPro: IPR002937; Amino_oxidase.
CC InterPro: IPR000205; NAD_binding.
CC Pfam: PF01593; Amino_Oxidase; 1.
CC Oxidoreductase; Monooxygenase; Auxin biosynthesis.
CC SEQUENCE 562 AA; 62513 MW; 621E7AA389DDF886 CRC64;
CC -----
CC Query Match 62.0%; Score 31; DB 1; Length 562;
CC Best Local Similarity 62.5%; Pred. No. 63;
CC Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
CC -----
CC QY 3 VVPXGXDY 10
CC Db :|||
CC 456 LVPAGADY 463
CC -----
CC RESULT 20
CC PLAS_DAUCA STANDARD; PRT; 97 AA.
CC AC P20422;
CC DT 01-FEB-1991 (Rel. 17, Created)
CC DT 01-FEB-1991 (Rel. 17, Last sequence update)
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC DE Plastocyanin.
CC GS PETE.
CC OS Daucus carota (Carrot).
CC OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
CC OC Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
CC OX NCBI_TaxID=4039;
CC RN [1]
CC RP SEQUENCE.
CC RA Shoji A., Yoshizaki F., Karahashi A., Sugimura Y., Shimokoriyama M.;
CC RT "Complete amino acid sequence of plastocyanin from Daucus carota.";
CC RL Seikagaku 57:1036-1036(1985).
CC CC -1- FUNCTION: Participates in electron transfer between P700 and the
CC cytochrome b6-f complex in photosystem I.
CC CC -1- SUBCELLULAR LOCATION: LOOSELY BOUND TO THE INNER THYLAKOID
CC MEMBRANE SURFACE IN CHLOROPLASTS.
CC CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
CC PIR; JW0011; JW0011.
CC HSSP; P17341; IPLB.
CC DR InterPro: IPR000923; BlueCu_1.
CC DR InterPro: IPR001235; Copper_blue.
CC DR Pfam; PF00127; Copper_bind; 1.
CC DR PRINTS; PR00156; COPPERBLUE.
CC DR ProDom; PD001235; Copper_blue; 1.
CC DR PROSITE; PS00196; COPPER_BLUE; 1.
CC KW Chloroplast; Electron transport; Copper; Thylakoid; Membrane.
CC DOMAIN 1 97 PLASTOCYANIN-LIKE.
CC FT METAL 37 37 COPPER (BY SIMILARITY).
CC FT METAL 82 82 COPPER (BY SIMILARITY).
CC FT METAL 85 85 COPPER (BY SIMILARITY).
CC FT METAL 90 90 COPPER (BY SIMILARITY).
CC FT METAL 90 90 COPPER (BY SIMILARITY).
CC SQ SEQUENCE 97 AA; 10181 MW; B15DE6B8428F72D4 CRC64;
CC -----
CC Query Match 60.0%; Score 30; DB 1; Length 97;
CC Best Local Similarity 54.5%; Pred. No. 16;
CC Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
CC -----
CC QY 1 EEVVPXGXDYS 11
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Db 43 EDEVPAGVDVS 53
:|:|:|:|
RESULT 21
TKNK_HUMAN STANDARD; PRT; 121 AA.
AC Q9UHF0;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurokinin B precursor (NKB) (Neuromedin K) (2NEUROK1).
GN TAC3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sheppard P., Jelinek L., Whitmore T., Blumberg H., Lehner J.,
RA O'Hara P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=20322570; PubMed=1086201;
RA Page N.M., Woods R.J., Gardiner S.M., Lomthasong K., Gladwell R.T.,
RA Butlin D.J., Manyonda I.T., Lowry P.J.;
RT "Excessive placental neurokinin B secretion during the third trimester
RT causes pre-eclampsia.";
RL Nature 405:797-800(2000).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DEVELOPMENTAL STAGE: In pregnancy, the expression of NKB is
CC confined to the outer syncytiotrophoblast of the placenta,
CC significant concentrations of NKB can be detected in plasma as
CC early as week 9, and plasma concentrations of NKB are grossly
CC elevated in pregnancy-induced hypertension and pre-eclampsia.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC -----
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CC -----
CC EMBL; AF186112; AAF01430.1;
CC EMBL; AF216586; AAF76980.1;
CC Genew; HGNC:11521; TAC3.
CC MIM; 162330;
CC InterPro: IPR003635; Neurokinin.
CC InterPro: IPR002040; Tachykinin.
CC ProDom; PD020370; Neurokinin; 1.
CC PROSITE; PS00267; TACHYKININ; 1.
CC Tachykinin; Neuropeptide; Cleavage on pair of basic residues;
CC Amidation; Signal.
CC SIGNAL 1 16 POTENTIAL.
CC FT PROPEP 17 78 BY SIMILARITY.
CC FT PEPTIDE 81 90 NEUROKININ B.
CC FT PROPEP 94 121 BY SIMILARITY.
CC FT MOD_RES 90 90 AMIDATION (G-91 PROVIDE AMIDE GROUP) (BY
CC SIMILARITY).
CC SQ SEQUENCE 121 AA; 13438 MW; 14C9AFE2EE9EDECA CRC64;
CC -----
CC Query Match 60.0%; Score 30; DB 1; Length 121;
CC Best Local Similarity 85.7%; Pred. No. 20;
CC Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 EEWVPGX 7
 DB 28 EEWVPGG 34

RESULT 22
 HES3_RAT
 ID HES3_RAT STANDARD; PRT; 175 AA.
 AC Q04667;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Transcription factor HES-3 (Hairy and enhancer of split 3).
 GN HES3 OR HES-3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=94040724; PubMed=1340473;
 RA Sasai Y., Kageyama R., Tagawa Y., Shigemoto R., Nakanishi S.;
 RT "Two mammalian helix-loop-helix factors structurally related to
 Drosophila hairy and Enhancer of split.";
 RL Genes Dev. 6:2620-2634(1992).
 CC -1- FUNCTION: TRANSCRIPTIONAL REPRESSOR OF GENES THAT REQUIRE A BHLH
 PROTEIN FOR THEIR TRANSCRIPTION.
 CC -1- SUBUNIT: TRANSCRIPTION REPRESSION REQUIRES FORMATION OF A COMPLEX
 WITH A CO-REPRESSOR PROTEIN (GROUCHO).
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN PURKINJE CELLS.
 CC -1- DOMAIN: HAS A PARTICULAR TYPE OF BASIC DOMAIN (PRESENCE OF A
 HELIX-INTERRUPTING PROLINE) THAT BINDS TO THE N-BOX (CACNAG),
 RATHER THAN THE CANONICAL E-BOX (CANNTG).
 CC -1- DOMAIN: THE CARBOXYL-TERMINAL WRPW MOTIF IS A TRANSCRIPTIONAL
 REPRESSION DOMAIN NECESSARY FOR THE INTERACTION WITH GROUCHO, A
 TRANSCRIPTIONAL CO-REPRESSOR RECRUITED TO SPECIFIC TARGET DNA BY
 HAIRY-RELATED PROTEINS.
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 TRANSCRIPTION FACTORS. "HAIRY" SUBFAMILY.

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 DR EMBL: D13418; BAA02683.1; -
 DR PIR: S36749; S36749.
 DR TRANSFAC: T01651; -
 DR InterPro: IPR001092; HLH_basic.
 DR Pfam: PF00010; HLH; 1.
 DR SMART: SM00353; HLH; 1.
 DR PROSITE: PS00038; HLH_1; 1.
 DR PROSITE: PS00888; HLH_2; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein; Repressor.
 FT DNA_BIND 1 6
 FT DOMAIN 7 50 BASIC DOMAIN.
 FT DOMAIN 108 167 HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
 FT DOMAIN 172 175 PRO-RICH.
 FT WRPW MOTIF (REQUIRED FOR ACTIVITY)
 FT (BY SIMILARITY).
 SQ SEQUENCE 175 AA; 19137 MW; D490663869155CB3 CRC64;

Query Match 60.0%; Score 30; DB 1; Length 175;
 Best Local Similarity 62.5%; Pred. No. 30;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 VVPXGXDY 10
 DB 58 LVPBGVDY 65

RESULT 23
 CTC_BACSU
 ID CTC_BACSU STANDARD; PRT; 203 AA.
 AC P14194;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE General stress protein ctc.
 GN CTC.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=96051385; PubMed=7584024;
 RA Ogasawara N., Nakai S., Yoshikawa H.;
 RT "Systematic sequencing of the 180 kilobase region of the Bacillus
 subtilis chromosome containing the replication origin.";
 RL DNA Res. 1:1-14(1994).
 CC [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer L., Albertini A.M., Alloni G.,
 Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 Denzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 Ghim S.F., Glaser P., Goffeau A., Golligly E.J., Grandi G.,
 Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
 Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadale Y.,
 Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
 Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 Tosato V., Uchiyama S., Vandenberg M., Vannier F., Vassarotti A.,
 Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus
 subtilis.";
 RL Nature 390:249-256(1997).
 RN [3]
 RP SEQUENCE OF 1-185 FROM N.A.
 RX MEDLINE=90066361; PubMed=2555671;
 RA Nilsson D., Hove-Jensen B., Arnvig K.;
 RT "Primary structure of the tms and prs genes of Bacillus subtilis.";
 RL Mol. Gen. Genet. 218:565-571(1989).
 RN [4]
 RP SEQUENCE OF 1-13.
 RC STRAIN=168 / IS58;
 RX Voelker U., Engelmann S., Maul B., Riethdorf S., Voelker A.,
 Schmidt R., Mach H., Hecker M.;
 RT "Analysis of the induction of general stress proteins of Bacillus
 subtilis.";
 RL Microbiology 140:741-752(1994).
 CC -1- FUNCTION: NOT KNOWN.

CC -!- DEVELOPMENTAL STAGE: EXPRESSED AT THE END OF EXPONENTIAL GROWTH
 CC UNDER CONDITIONS IN WHICH THE ENZYMES OF THE TCA CYCLE ARE
 CC REPRESSED.
 CC -!- INDUCTION: BY HEAT SHOCK, SALT STRESS, OXIDATIVE STRESS, GLUCOSE
 CC LIMITATION AND OXYGEN LIMITATION.
 CC -!- SIMILARITY: BELONGS TO THE L25P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 CC EMBL: D26185; BAA05287.1; -
 CC EMBL: Z99104; CAB11828.1; -
 CC EMBL: X16518; CAA34524.1; -
 CC PIR: S05373; S05373.
 CC Subtilist; BG10115; etc.
 CC InterPro: IPR001021; Ribosomal_L25.
 CC Pfam: PF01386; Ribosomal_L25p; 1.
 CC ProDom: PD012503; Ribosomal_L25; 1.
 CC TIGRFAMs: TIGR00731; ctc_TL5; 1.
 CC Heat shock; Complete proteome.
 CC INIT MET 0
 CC VARIAT 1 1 A -> R (IN STRAIN IS58).
 CC VARIAT 9 9 T -> Q (IN STRAIN IS58).
 CC VARIAT 12 12 T -> I (IN STRAIN IS58).
 CC SEQUENCE 203 AA; 21924 MW; 5130A404D0B86247 CRC64;
 CC
 CC Query Match 60.0%; Score 30; DB 1; Length 203;
 CC Best Local Similarity 62.5%; Pred. No. 35;
 CC Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 CC
 CC QY 4 VPGXGDYS 11
 CC : | | | |
 CC Db 157 LPAGGDYS 164
 CC
 CC RESULT 24
 CC ARAD_ECOLI STANDARD; PRT; 231 AA.
 CC ID ARAD_ECOLI STANDARD; PRT; 231 AA.
 CC AC P08203;
 CC DT 01-AUG-1988 (Rel. 08, Created)
 CC DT 01-AUG-1991 (Rel. 19, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE L-ribulose 5-phosphate 4-epimerase (EC 5.1.3.4) (Phosphoribulose
 CC isomerase).
 CC GN ARAD OR B0061.
 CC OS Escherichia coli.
 CC OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC OC Escherichia.
 CC OX NCBI_TaxID:562;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN-B;
 CC RX MEDLINE=87163495; PubMed=3549454;
 CC RA Lee N., Gielow W., Martin R., Hamilton E., Fowler A.;
 CC RT "The organization of the arabad operon of Escherichia coli.";
 CC RL Gene 47:231-244(1986).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN-K12;
 CC RX MEDLINE=91083835; PubMed=2261080;
 CC RA Chen H., Sun Y., Stark T., Beattie W., Moses R.E.;
 CC RT "Nucleotide sequence and deletion analysis of the polb gene of
 CC Escherichia coli.";
 CC RL DNA Cell Biol. 9:631-635(1990).
 CC RN [3]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN-K12;
 CC RX MEDLINE=91067495; PubMed=2251150;

RA Mineno J., Fukui H., Ishino Y., Kato I., Shinagawa H.;
 RT "Nucleotide sequence of the arad gene of Escherichia coli K12
 RT encoding the L-ribulose 5-phosphate 4-epimerase.";
 RN Nucleic Acids Res. 18:6722-6722(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=92334977; PubMed=1630901;
 RA Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
 RA Isono K., Mizobuchi K., Nakata A.;
 RT "Systematic sequencing of the Escherichia coli genome: analysis of
 RT the 0-2.4 min region.";
 RL Nucleic Acids Res. 20:3305-3308(1992).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [6]
 RP SEQUENCE OF 222-231 FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=91017565; PubMed=2217198;
 RA Bonner C.A., Hays S., McEntee K., Goodman M.F.;
 RT "DNA polymerase II is encoded by the DNA damage-inducible dinA gene
 RT of Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:7663-7667(1990).
 RN [7]
 RP SEQUENCE OF 158-231 FROM N.A.
 RC STRAIN-K12 / W3110;
 RX MEDLINE=91238699; PubMed=2034216;
 RA Iwasaki H., Ishino Y., Toh H., Nakata A., Shinagawa H.;
 RT "Escherichia coli DNA polymerase II is homologous to alpha-like DNA
 RT polymerases.";
 RL Mol. Gen. Genet. 226:24-33(1991).
 CC -!- CATALYTIC ACTIVITY: L-ribulose 5-phosphate = D-xylulose 5-
 CC phosphate.
 CC -!- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
 CC -!- PATHWAY: L-arabinose catabolism; third step.
 CC -!- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY. ARAD/FUCA
 CC SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: M15263; AAA23464.1; -
 CC EMBL: M35371; -; NOT_ANNOTATED_CDS.
 CC EMBL: M62646; AAA24405.1; -
 CC EMBL: D10483; BAA01332.1; -
 CC EMBL: AE000116; AAC73172.1; -
 CC EMBL: M37737; AAA23683.1; -
 CC EMBL: M38283; AAA63763.1; -
 CC EMBL: X56048; CAA39519.1; -
 CC PIR: D29022; ISECP4.
 CC PIR: S13593; ISECK4.
 CC PIR: A36236; A36236.
 CC PIR: S40577; S40577.
 CC ECO2DBASE: G028.1; 6TH EDITION.
 CC EcoGene: Egl0055; arad.
 CC InterPro: IPR001303; Aldolase_II_N.
 CC InterPro: IPR004661; Arab.
 CC Pfam: PF00596; Aldolase_II; 1.
 CC TIGRFAMs: TIGR00760; arad; 1.
 CC Arabinose catabolism; Isomerase; Zinc; Complete proteome.
 CC KW


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FT METAL          76 76 ZINC (BY SIMILARITY).
FT METAL          95 95 ZINC (BY SIMILARITY).
FT METAL          97 97 ZINC (BY SIMILARITY).
FT METAL         171 171 ZINC (BY SIMILARITY).
FT VARIANT        50 50 V -> I.
FT VARIANT        70 70 T -> A.
FT VARIANT        216 216 D -> N.
SQ SEQUENCE      231 AA; 25519 MW; 1753F75958332163 CRC64;

Query Match          60.0%; Score 30; DB 1; Length 231;
Best Local Similarity 55.6%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 VVPXGXDYS 11
   : | | | | |
DB 41 IKPSGVDYS 49

RESULT 25
ARAD_SALTY
ID ARAD_SALTY STANDARD; PRT; 231 AA.
AC P06190;
DT 01-JAN-1988 (Rel. 06, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4) (Phosphoribulose
isomerase).
GN ARAD OR STM0101.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RA Lin H.-C., Lei S.-P., Studnicka G., Wilcox G.;
MEDLINE=85232046; PubMed=3891514;
RT "The arabid operon of Salmonella typhimurium LT2. III. Nucleotide
sequence of arab and its flanking regions, and primary structure of
its product, L-ribulose-5-phosphate 4-epimerase."
RL Gene 34:129-134(1985).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2."
RL Nature 413:852-856(2001).
CC -|- CATALYTIC ACTIVITY: L-ribulose 5-phosphate = D-xylulose 5-
phosphate.
CC -|- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
CC -|- PATHWAY: L-arabinose catabolism; third step.
CC -|- SIMILARITY: BELONGS TO THE ALDOLASE CLASS II FAMILY. ARAD/FUCA
SUBFAMILY.
CC -|- CAUTION: Ref.1 sequence differs from that shown due to a
frameshift in position 202.
-----
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-----
CC
CC EMBL; M11047; AAA27025.1; ALT_FRAME.
CC EMBL; AE008698; AAL19065.1; -.
CC PIR; A24986; ISEB47.

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DR StyGene: SG10015; arad.
DR InterPro; IPR001303; Aldolase_II_N.
DR InterPro; IPR004661; Arad.
DR Pfam; PF00596; Aldolase_II; 1.
DR TIGRFAMs; TIGR00760; arad; 1.
KW Arabinose catabolism; isomerase; zinc; Complete proteome.
FT METAL          76 76 ZINC (BY SIMILARITY).
FT METAL          95 95 ZINC (BY SIMILARITY).
FT METAL          97 97 ZINC (BY SIMILARITY).
FT METAL         171 171 ZINC (BY SIMILARITY).
SQ SEQUENCE      231 AA; 25531 MW; DA473505739284F9 CRC64;

Query Match          60.0%; Score 30; DB 1; Length 231;
Best Local Similarity 55.6%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 VVPXGXDYS 11
   : | | | | |
DB 41 IKPSGVDYS 49

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Search completed: June 10, 2003, 13:40:25
Job time : 5.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:30:25 ; Search time 25.7857 Seconds

(without alignments)

87.898 Million cell updates/sec

Title: US-09-909-164-46

Perfect score: 50

Sequence: 1 EEVVPXGDYS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Lasting first 75 summaries

Database :

SPTREMBL21.*

1: sp.archaea.*

2: sp.bacteria.*

3: sp.fungi.*

4: sp.human.*

5: sp.invertebrate.*

6: sp.mammal.*

7: sp.mhc.*

8: sp.organelle.*

9: sp.phage.*

10: sp.plant.*

11: sp.podent.*

12: sp.virus.*

13: sp.vertbrate.*

14: sp.unclassified.*

15: sp.rvirus.*

16: sp.bacteriap.*

17: sp.bacteriap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36	72.0	298	2	O52367 rhizobium t
2	36	72.0	363	17	O30260 archaeoglob
3	35	70.0	78	6	Q9XST4 canis faml
4	35	70.0	143	5	Q9VSY8 drosophila
5	35	70.0	217	4	O00404 homo sapien
6	35	70.0	290	16	Q8U7J0 agrobacteri
7	35	70.0	299	4	Q9UEE9 homo sapien
8	35	70.0	587	16	Q9JZP8 neisseria m
9	35	70.0	692	5	Q9V190 drosophila
10	35	70.0	906	10	Q9ZSY4 arabidopsis
11	35	70.0	908	10	Q9FJK8 arabidopsis
12	35	70.0	908	10	Q8W4J9 arabidopsis
13	35	70.0	908	10	Q9ZSY3 arabidopsis
14	35	70.0	909	10	Q9M5A1 arabidopsis
15	35	70.0	1063	16	Q8RG86 fusobacteri
16	34	68.0	156	3	Q12479 saccharomyc

17	34	68.0	175	10	Q8VY88
18	34	68.0	247	16	Q92U66
19	34	68.0	257	10	Q9C6J0
20	34	68.0	433	16	Q9A382
21	34	68.0	1442	17	Q96YH5
22	34	68.0	2778	5	Q9V9T6
23	33	66.0	143	17	Q8TX62
24	33	66.0	165	16	Q92BC5
25	33	66.0	165	16	Q8Y6U8
26	33	66.0	196	16	Q8ZAQ9
27	33	66.0	210	10	Q6S890
28	33	66.0	225	10	Q40129
29	33	66.0	253	16	Q8XPA8
30	33	66.0	312	11	Q9D876
31	33	66.0	440	17	Q9YF13
32	33	66.0	471	11	Q8RL26
33	33	66.0	484	11	Q8VD18
34	33	66.0	517	16	Q8XZL5
35	33	66.0	563	13	Q9DDJ4
36	33	66.0	563	16	Q99XL5
37	33	66.0	678	12	Q9ELX6
38	33	66.0	1028	16	Q8YJ11
39	33	66.0	1088	16	Q9KT32
40	33	66.0	1150	5	O17704
41	33	66.0	1828	16	Q98K29
42	32	64.0	105	11	Q9CRG3
43	32	64.0	140	17	Q8TNG3
44	32	64.0	154	10	Q9SBB8
45	32	64.0	219	5	Q9GQ04
46	32	64.0	253	15	P88362
47	32	64.0	266	11	Q9JMA5
48	32	64.0	275	5	Q9VIX6
49	32	64.0	280	5	Q9VMN9
50	32	64.0	295	11	O70565
51	32	64.0	295	11	O88271
52	32	64.0	301	16	Q99TD4
53	32	64.0	307	17	Q9HP60
54	32	64.0	314	16	Q8YIJ8
55	32	64.0	336	11	Q9D8M6
56	32	64.0	336	11	Q9CX34
57	32	64.0	354	11	Q9CRE7
58	32	64.0	357	17	O29920
59	32	64.0	366	17	O29451
60	32	64.0	405	17	Q8TY23
61	32	64.0	423	16	Q92M00
62	32	64.0	425	5	Q9XVK4
63	32	64.0	511	2	O52680
64	32	64.0	543	3	O8TF44
65	32	64.0	564	17	Q8U2A4
66	32	64.0	565	16	Q9CIN1
67	32	64.0	632	17	Q9HNP8
68	32	64.0	672	5	O45063
69	32	64.0	745	5	Q9SP46
70	32	64.0	873	10	Q9LKL4
71	32	64.0	884	10	Q94F60
72	32	64.0	1031	5	Q9U6A3
73	32	64.0	1082	10	O94D25
74	32	64.0	1410	2	O52673
75	32	64.0	1420	2	O52666

ALIGNMENTS

RESULT 1
O52367
ID O52367; PRELIMINARY; PRT; 298 AA.
AC O52367; (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-1998 (TrEMBLrel. 20, Last annotation update)
DE Aryl-alcohol dehydrogenase homolog (Fragment).
GN XYL81.

OS Rhizobium tropici.
 OG Plasmid pRtCFN299a.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=398;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CFN299;
 RA Rosenblueth M., Hynes M.F., Martinez-Romero E.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -|- COFACTOR: ZINC (BY SIMILARITY).
 CC -|- SIMILARITY: BELONGS TO THE ZINC-CONTAINING ALCOHOL DEHYDROGENASE
 CC FAMILY
 DR EMBL; AF036920; AAC04779.1; -.
 DR HSP; P07846; ISDG.
 DR InterPro; IPR002328; ADH_zinc.
 DR InterPro; IPR002085; Adh_zn_family.
 DR Pfam; PF00107; adh_zinc; 1.
 DR PROSITE; PS00059; ADH_ZINC; 1.
 KW Oxidoreductase; Plasmid; Zinc.
 FT NON_TER 298
 SQ SEQUENCE 298 AA; 31092 MW; 49B2F8117C33AE87 CRC64;
 Query Match 72.0%; Score 36; DB 2; Length 298;
 Best Local Similarity 50.0%; Pred. No. 12;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 2 EVVPGXGXDYS 11
 Db [1] [1] [1] [1]
 250 EIIPEGADFS 259
 RESULT 2
 O30260 PRELIMINARY; PRT; 363 AA.
 AC O30260;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Hypothetical protein AF2411.
 GN AF2411.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OX NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
 RC MEDLINE-98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Richardson D.D., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
 RA Fleischmann R.D., Kerlavage A.R., Graham D.E., Kyrpides N.C.,
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Uitterback T.,
 RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
 RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 DR EMBL; AE001109; AAB91255.1; -.
 DR TIGR; AF2411; -.
 DR InterPro; IPR002103; Bac_luciferase.
 DR Pfam; PF00296; bac_luciferase; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 363 AA; 41736 MW; 0E976EAE78F4803 CRC64;
 Query Match 72.0%; Score 36; DB 17; Length 363;
 Best Local Similarity 54.5%; Pred. No. 15;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EEVVPXGXGXDYS 11
 Db [1] [1] [1] [1]
 120 ENIVPYGIDFS 130
 RESULT 3
 Q9XST4 PRELIMINARY; PRT; 78 AA.
 AC Q9XST4;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE p97 homologous protein (Fragment).
 GN P97.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=THYROID;
 RX MEDLINE-20422104; PubMed=10964405;
 RA Pichon B., Mercan D., Pouillon V., Christophe-Hobertus C.,
 RA Christophe D.;
 RT "A method for the large-scale cloning of nuclear proteins and nuclear
 RT targeting sequences on a functional basis.";
 RL Anal. Biochem. 284:231-239(2000).
 DR EMBL; AJ388531; CAB46833.1; -.
 FT NON_TER 78
 SQ SEQUENCE 78 AA; 8895 MW; B62486313555FBA1 CRC64;
 Query Match 70.0%; Score 35; DB 6; Length 78;
 Best Local Similarity 54.5%; Pred. No. 4.4;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 EEVVPXGXGXDYS 11
 Db [1] [1] [1] [1]
 16 EDVVPSSGGEYS 26
 RESULT 4
 Q9VSY8 PRELIMINARY; PRT; 143 AA.
 AC Q9VSY8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
 DE CG3911 protein.
 GN CG3911.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE-20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Ballif J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glassman K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector R., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR EMBL; AE003552; AAF50270.1; -.
 DR FlyBase; FBgn0035992; CG3911.
 SQ SEQUENCE 143 AA; 16471 MW; 1DC346DC22C02AA2 CRC64;

Query Match 70.0%; Score 35; DB 5; Length 143;
 Best Local Similarity 66.7%; Pred. No. 8.7;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGXD 9
 Db 135 EEVVPAGED 143

RESULT 5
 ID 000404 PRELIMINARY; PRT; 217 AA.
 AC 000404;
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE P97 homologous protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=FLACENTA;
 RX MEDLINE=97160586; PubMed=9006920;
 RA Nobukuni T., Kobayashi M., Omori A., Ichinose S., Iwanaga T.,
 RA Takahashi I., Hashimoto K., Hattori S., Kaibuchi K., Miyata Y.,
 RT "An Alu-linked repetitive sequence corresponding to 280 amino acids is
 expressed in a novel bovine protein, but not in its human homologue."
 RL J. Biol. Chem. 272:2801-2807(1997).
 DR EMBL; D85939; BAA20069.1; -.
 SQ SEQUENCE 217 AA; 24061 MW; E404BA2E35497828 CRC64;

Query Match 70.0%; Score 35; DB 4; Length 217;
 Best Local Similarity 54.3%; Pred. No. 14;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDYS 11
 Db 16 EDVVPSGEYS 26

RESULT 6
 Q8U7J0

ID Q8U7J0 PRELIMINARY; PRT; 290 AA.
 AC Q8U7J0;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 6-O-methylguanine-DNA methyltransferase.
 GN ADA OR ATU4459 OR AGR_L_818.
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 C58."
 RL Science 294:2317-2323(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Qucillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Roumieu K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
 RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 Agrobacterium tumefaciens C58."
 RL Science 294:2323-2328(2001).
 DR EMBL; AE009374; AAL45253.1; -.
 DR EMBL; AE008240; AAK8982.1; -.
 KW Methyltransferase; Transferase; Complete proteome.
 SQ SEQUENCE 290 AA; 31587 MW; B626592EF519977F CRC64;
 Query Match 70.0%; Score 35; DB 16; Length 290;
 Best Local Similarity 50.0%; Pred. No. 19;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDY 10
 Db 9 EDITPIGSDY 18

RESULT 7
 ID Q8U7J0 PRELIMINARY; PRT; 299 AA.
 AC Q8U7J0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE BCNT protein (CRANIOFACIAL development protein 1).
 GN BCNT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98267221; PubMed=9602175;
 RA Takahashi I., Nobukuni T., Omori H., Kobayashi M., Tanaka S.,
 RA Ohshima K., Okada N., Masui T., Hashimoto K., Iwashita S.;
 RT "Existence of a bovine LINE repetitive insert that appears in the CDNA
 of bovine protein BCNT in ruminant, but not in human, genomes.";

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RL Gene 211:387-394(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB09285; BAA31867.1; -
DR EMBL; BC000991; AAH00991.1; -
SQ SEQUENCE 299 AA; 33593 MW; F4A9E928B669451A CRC64;

Query Match
Best Local Similarity 70.0%; Score 35; DB 4; Length 299;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDS 11
Db 16 EDYVPSGGEYS 26

RESULT 8
Q9JZP8 PRELIMINARY; PRT; 587 AA.
AC Q9JZP8
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Succinate dehydrogenase, flavoprotein subunit.
GN NM00950.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN SEQUENCE FROM N.A.
RC STRAIN=MC58; SEROGROUP B;
RX MEDLINE=20175755; PubMed=10710307;
RA Tetelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Cittoni E., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Pizzo M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
RT *Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.
RL Science 287:1809-1815(2000).
CC -I- COFACTOR: FAD (BY SIMILARITY).
DR EMBL; AE002446; AAF41356.1; -
DR HSSP; P00363; 1FUM.
DR TIGR; NMB0950; -
DR InterPro; IPR003953; FAD_bind2.
DR InterPro; IPR001327; FAD_Pyr_redox.
DR InterPro; IPR003952; FRD/SDH_FAD.
DR InterPro; IPR001100; Pyr_redox.
DR InterPro; IPR004112; Succ_DH_flav_C.
DR Pfam; PF00890; FAD_binding_2; 1.
DR Pfam; PF02910; succ_DH_flav_C; 1.
DR PRINTS; PR00368; FADPNR.
DR PRINTS; PR00411; PNRDTASEI.
DR PROSITE; PS00504; FRD_SDH_FAD_BINDING; 1.
DR PROSITE; PS00504; Oxidoreductase; Complete proteome.
KW FAD; Flavoprotein; Oxidoreductase; Complete proteome.
SQ SEQUENCE 587 AA; 64502 MW; 9581701B08069003 CRC64;

Query Match
Best Local Similarity 70.0%; Score 35; DB 16; Length 587;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDS 10
Db 366 EVVVPQGEDY 375

RESULT 9
Q9VI90 PRELIMINARY; PRT; 692 AA.
AC Q9VI90
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CG10040 protein (Roughened eye).
GN RN OR CG10040 OR CG14600 OR CG14601.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.I., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Flier C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harst N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasok P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rehnert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC St Pierre S.E., Galindo M.I., Couso J.P., Thor S.;
RT "Control of Drosophila imaginal disc development by rotund and
RT roughened eye: differentially expressed transcripts of the same gene
RT encoding distinct zinc finger proteins."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003672; AAF54035.1; -
DR EMBL; AF395904; AAL59598.1; -
DR HSSP; P08153; 1ZFD.
DR FlyBase; FBgn0037494; rn.
DR InterPro; IPR000822; znf_C2H2.
DR Pfam; PF00096; zf-C2H2; 5.
DR ProDom; PD000003; znf_C2H2; 1.
DR SMART; SM00355; znf_C2H2; 5.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 5.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 5.
KW DNA-binding; Metal-binding; Zinc-binding; Zinc-finger.

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SQ SEQUENCE 692 AA; 75774 MW; BD010502BB65042E CRC64;
 Query Match 70.0%; Score 35; DB 5; Length 692;
 Best Local Similarity 60.0%; Pred. No. 52;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVVPXGXDYS 11
 I:| | | | |
 Db 26 EIPPAGGDYS 35

RESULT 10
 Q9ZSY4 PRELIMINARY; PRT; 906 AA.
 AC Q9ZSY4;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Disease resistance protein RPP8.
 GN RPP8.
 OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LA-ER;
 RX MEDLINE=99030193; PubMed=9811794;
 RA McDowell J.M., Dhandaaydham M., Long T.A., Aarts M.G., Goff S.,
 RA Holub E.B., Dangl J.L.;
 RT "Intragenic recombination and diversifying selection contribute to the
 RT evolution of downy mildew resistance at the RPP8 locus of
 RT Arabidopsis.";
 RL Plant Cell 10:1861-1874 (1998).
 DR EMBL; AF089710; AAC83165.1; -;
 DR InterPro; IPR000767; Disease_resist.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR002182; NB-ARC.
 DR Pfam; PF00560; LRR; 1.
 DR Pfam; PF00931; NB-ARC; 1.
 DR PRINTS; PR00364; DISEASERSIST.
 SQ SEQUENCE 906 AA; 104201 MW; 52905EB143676F8F CRC64;

Query Match 70.0%; Score 35; DB 10; Length 906;
 Best Local Similarity 60.0%; Pred. No. 70;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVVVPXGXDY 10
 I:| | | | |
 Db 881 EKLVPGGEDY 890

RESULT 11
 Q9FJK8 PRELIMINARY; PRT; 908 AA.
 AC Q9FJK8;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Disease resistance protein.
 OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=99087489; PubMed=9872454;
 RA Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VII.

RT Sequence features of the regions of 1,013,767 bp covered by sixteen
 RT physically assigned P1 and TAC clones.";
 RL DNA Res. 5:297-308 (1998).
 DR EMBL; AB015468; BAB10695.1; -;
 DR InterPro; IPR000767; Disease_resist.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR002182; NB-ARC.
 DR Pfam; PF00560; LRR; 2.
 DR Pfam; PF00931; NB-ARC; 1.
 DR PRINTS; PR00364; DISEASERSIST.
 SQ SEQUENCE 908 AA; 104448 MW; 3111991B17239693 CRC64;

Query Match 70.0%; Score 35; DB 10; Length 908;
 Best Local Similarity 60.0%; Pred. No. 70;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVVVPXGXDY 10
 I:| | | | |
 Db 883 EKLVPGGEDY 892

RESULT 12
 Q8W4J9 PRELIMINARY; PRT; 908 AA.
 AC Q8W4J9;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Disease resistance protein RPP8.
 GN AT5G43470, MW20.19.
 OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
 RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
 RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
 RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
 RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
 RA Ecker J., Theologis A., Davis R.W.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY062514; AAL32592.1; -;
 DR InterPro; IPR000767; Disease_resist.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR002182; NB-ARC.
 DR Pfam; PF00560; LRR; 2.
 DR Pfam; PF00931; NB-ARC; 1.
 DR PRINTS; PR00364; DISEASERSIST.
 SQ SEQUENCE 908 AA; 104649 MW; 4461F553128F3A15 CRC64;

Query Match 70.0%; Score 35; DB 10; Length 908;
 Best Local Similarity 60.0%; Pred. No. 70;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVVVPXGXDY 10
 I:| | | | |
 Db 883 EKLVPGGEDY 892

RESULT 13
 Q9ZSY3 PRELIMINARY; PRT; 908 AA.
 AC Q9ZSY3;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE RPP8 (Disease resistance protein RPP8).
 OS Arabidopsis thaliana (Mouse-ear cross).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COL;
 RX MEDLINE=99030193; PubMed=9811794;
 RA McDowell J.M., Dhandaydham M., Long T.A., Aarts M.G.M., Goff S.,
 RA Holub E.B., Dangl J.L.;
 RT "Intragenic recombination and diversifying selection contribute to the
 RT evolution of downy mildew resistance at the RPP8 locus of
 RT Arabidopsis.";
 RL Plant Cell 10:1861-1874(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20181125; PubMed=10718197;
 RA Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
 RT features of the regions of 3,076,755 bp covered by sixty p1 and TAC
 RT clones.";
 RL DNA Res. 7:31-63(2000).
 DR EMBL; AF089711; AAC78631.1; -;
 DR EMBL; AB025638; BAA97426.1; -;
 DR InterPro; IPR000767; Disease_resist.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR002182; NB-ARC.
 DR Pfam; PF00560; LRR; 2.
 DR Pfam; PF00931; NB-ARC; 1.
 DR PRINTS; PR00364; DISEASERSIST.
 SQ SEQUENCE 908 AA; 104681 MW; 1BFA35BB6B0CB5CD CRC64;
 Query Match 70.0%; Score 35; DB 10; Length 908;
 Best Local Similarity 60.0%; Pred. No. 70;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDY 10
 Db 883 EKLVPGGEDY 892
 RESULT 14
 Q9M5A1
 ID Q9M5A1 PRELIMINARY; PRT; 909 AA.
 AC Q9M5A1
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Viral resistance protein.
 GN HRT.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DI-17;
 RA Cooley M.B., Pathirana S., Wu H., Kachroo P., Klessig D.F.;
 RT "Members of the Arabidopsis HRT/RPP8 family of resistance genes confer
 RT resistance to both viral and oomycete pathogens.";
 RL Plant Cell 0:0-0(2000).
 DR EMBL; AF234174; AAR36987.1; -;
 DR InterPro; IPR000767; Disease_resist.
 DR InterPro; IPR001611; LRR.
 DR InterPro; IPR002182; NB-ARC.
 DR Pfam; PF00560; LRR; 2.
 DR Pfam; PF00931; NB-ARC; 1.
 DR PRINTS; PR00364; DISEASERSIST.
 SQ SEQUENCE 909 AA; 105052 MW; 06262B71A2B3037F CRC64;
 Query Match 70.0%; Score 35; DB 10; Length 909;
 Best Local Similarity 60.0%; Pred. No. 70;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGXDY 10
 Db 884 EKLVPGGEDY 893
 RESULT 15
 Q9RG86
 ID Q9RG86 PRELIMINARY; PRT; 1063 AA.
 AC Q9RG86;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Carbamoyl-phosphate synthase large chain (EC 6.3.5.5).
 GN FN0422
 OS Fusobacterium nucleatum (subsp. nucleatum).
 OC Bacteria; Fusobacteriia; Fusobacterium.
 OX NCBI_TaxID=76856;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 25586;
 RX MEDLINE=21886394; PubMed=11889109;
 RA Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
 RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
 RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
 RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
 RA Fongstien M., Kyripides N., Overbeek R.;
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium
 RT nucleatum strain ATCC 25586.";
 RL J. Bacteriol. 184:2005-2018(2002).
 DR EMBL; AE010554; AAL94625.1; -;
 KW Ligase; Complete proteome.
 SQ SEQUENCE 1063 AA; 118008 MW; 39700E10B7CCB411 CRC64;
 Query Match 70.0%; Score 35; DB 16; Length 1063;
 Best Local Similarity 60.0%; Pred. No. 84;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 EVVPXGXDYS 11
 Db 195 EIVPGLNYS 204
 RESULT 16
 Q12479
 ID Q12479 PRELIMINARY; PRT; 156 AA.
 AC Q12479;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE ORF YOR013W.
 GN YOR013W.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC De haan M., Grivell L.A., Maarse A.C.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MIPS;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FY1679;
 RA De haan M., Maarse A.C., Grivell L.A.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FY1679;


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RX MEDLINE=94010918; PubMed=8413243;
RA Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlenny G.,
RA Sherman F.;
RT "CYC2 encodes a factor involved in mitochondrial import of yeast
RT cytochrome c.";
RL Mol. Cell. Biol. 13:6442-6451(1993).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RX MEDLINE=94169519; PubMed=7764548;
RA Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
RT "Molecular cloning of a gene, DHS1, which complements a drug-
RT hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
RL Biosci. Biotechnol. Biochem. 58:391-395(1994).
DR EMBL; Z74920; CAA99201.1; -
DR EMBL; X87331; CAA60762.1; -
DR SGD; S0005539; YOR013W.
SQ SEQUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;

Query Match 68.0%; Score 34; DB 3; Length 156;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVVPXGXDY 10
||:| | | |
Db 50 EVVPLGMDY 58

RESULT 17
Q8VY88 PRELIMINARY; PRT; 175 AA.
AC Q8VY88;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Hypothetical 19.2 kDa protein.
GN ATIC50910.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY072348; AAL61955.1; -
DR InterPro; IPR002110; ANK.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW Hypothetical protein.
SQ SEQUENCE 175 AA; 19189 MW; 7F72AB1EC82C4190 CRC64;

Query Match 68.0%; Score 34; DB 10; Length 175;
Best Local Similarity 54.5%; Pred. No. 18;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EVVVPXGXDYS 11
||:| | | |
Db 135 EELLKAGADYS 145

RESULT 18
Q92U66 PRELIMINARY; PRT; 247 AA.
ID Q92U66
AC Q92U66;
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)

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DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Hypothetical protein RBL273.
GN RBL273 OR SMB21444.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396508; PubMed=11481431;
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA Vorholter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA Golding B., Puehler A.;
RT "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
DR EMBL; AL603646; CAC49673.1; -
KW Plasmid; Hypothetical protein; Complete proteome.
SQ SEQUENCE 247 AA; 28930 MW; 2F14F383E66D420 CRC64;

Query Match 68.0%; Score 34; DB 16; Length 247;
Best Local Similarity 60.0%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGXDX 10
||:| | | |
Db 48 EDVEPRGADY 57

RESULT 19
Q9C670 PRELIMINARY; PRT; 257 AA.
ID Q9C670
AC Q9C670;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE Hypothetical 28.6 kDa protein.
GN F8A12.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.V.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W., Dewar K.,
RA Chung M.K., Conn L., Conway A.B., Feng J.-D., Fong B., Fujii C.Y.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Hansen N.F., Huizar L.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzilli A.,
RA Maltisheva J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana.";
RL Nature 408:816-820(2000).
DR EMBL; AC079284; RAG50930.1; -
DR InterPro; IPR002110; ANK.
DR PROSITE; PS50088; ANK_REPEAT; 1.
DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
KW ANK repeat; Hypothetical protein; Repeat.

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SQ SEQUENCE 257 AA; 28578 MW; 714C7A4387F32B5C CRC64;
 Query Match 68.0%; Score 34; DB 10; Length 257;
 Best Local Similarity 54.5%; Pred. No. 28;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

 QY 1 EEVVPXGXDXYS 11
 Db 217 EELLKAGADYS 227

 RESULT 20
 Q9A382 PRELIMINARY; PRT; 433 AA.
 AC Q9A382;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DE 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Peptidoglycan-binding protein, putative.
 GN CC3322
 OS Caulobacter crescentus.
 OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
 OC Caulobacter.
 OX NCBI_TaxID=155892;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 19089 / CB15;
 RX MEDLINE=21173698; PubMed=11259647;
 RA Eisen J., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
 RA Kolonay J.F., Smt J., Craven M.B., Khouri H., Shetty J., Berry K.,
 RA Uitterback J., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;
 RT "Complete genome sequence of Caulobacter crescentus";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
 DR EMBL; AE005994; AAK25284.1;
 DR HSSP; P41052; 1LTM.
 DR TIGR; CC3322;
 DR InterPro; IPR002477; PG_binding.
 DR Pfam; PF01471; PG_binding_1;
 KW Complete proteome.
 SQ SEQUENCE 433 AA; 46169 MW; F7DD18B9F4CA10A7 CRC64;

 Query Match 68.0%; Score 34; DB 16; Length 433;
 Best Local Similarity 54.5%; Pred. No. 51;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

 QY 1 EEVVPXGXDXYS 11
 Db 266 EVILPPGFDYS 276

 RESULT 21
 Q96YH5 PRELIMINARY; PRT; 1442 AA.
 AC Q96YH5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical protein ST2195.
 GN ST2195.
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=111955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-JCM 10545 / 7;
 RX PubMed=11572479;
 RA Kavarabiyasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermoacidophilic
 RT Crenarchaeon, Sulfolobus tokodaii strain7";
 RL DNA Res. 8:123-140(2001).
 DR EMBL; AP000989; BAB67302.1;
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 1442 AA; 156497 MW; D63EC2C35228121F CRC64;

Query Match 68.0%; Score 34; DB 17; Length 1442;
 Best Local Similarity 50.0%; Pred. No. 2e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

 QY 1 EEVVPXGXDX 10
 Db 863 EEITPGANY 872

RESULT 22

Q9V9T6 PRELIMINARY; PRT; 2778 AA.
 ID Q9V9T6
 AC Q9V9T6; Q9Y0Z7;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2002 (TrEMBLrel. 20, Last annotation update)
 DE FAF protein (BCDNA:LD22582)
 DE FAF OR BCDNA:LD22582 OR CCI945.
 GN Drosophila melanogaster (fruit fly).
 OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.-H.C., Blaise R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Bereman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Flesler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Liang D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Ljung Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter G.M., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

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RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE OF 1090-2778 FROM N.A.
RA Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,
RA Agbayani A., Arcina T.T., Baxter E., Blazej R.G., Butenhoff C.,
RA Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,
RA Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,
RA Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M.,
RA Park S., Sequeira A., Sethi H., Snir E., Svirkas R.R., Weinburg T.,
RA Celniker S.E.;
RT "Full length Drosophila melanogaster cDNA sequence.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003779; AAF57198.1; -
DR EMBL; AF145677; AAD38652.1; -
DR FlyBase; FBgn0005632; raf.
DR InterPro; IPR001394; UCH-2.
DR Pfam; PF00442; UCH-1; 1.
DR Pfam; PF00443; UCH-2; 1.
DR PROSITE; PS00972; UCH_2.1; 1.
DR PROSITE; PS00973; UCH_2.2; 1.
DR PROSITE; PS0235; UCH_2.3; 1.
SQ SEQUENCE 2778 AA; 311140 MW; FFB90438BA53A02B CRC64;

Query Match 68.0%; Score 34; DB 5; Length 2778;
Best Local Similarity 54.5%; Pred. No. 4.1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGXDXS 11
| : || | | :
Db 1394 EVIVPDGDQFS 1404

RESULT 23
Q8TX62 PRELIMINARY; PRT; 143 AA.
ID Q8TX62
AC Q8TX62;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Uncharacterized conserved protein.
GN MK0814.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
OX NCBI_TaxID=2320;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-AV19 / DSM 6324 / JCM 9639;
RX MEDLINE-21927647; PubMed-11930014;
RA Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natale D.A., Rogozin I.B., Tatusov R.D., Wolf Y.I., Stetter K.O.,
RA Malykh A.G., Koonin E.V., Kozyavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR EMBL; AE010372; AAM0207.1; -
KW Complete proteome.
SQ SEQUENCE 143 AA; 15734 MW; 4C8B28A1FBEBDD0B CRC64;

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Query Match 66.0%; Score 33; DB 17; Length 143;
Best Local Similarity 60.0%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGXDX 10
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Db 75 EELVPQAGY 84

RESULT 24
Q92BC5

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ID Q92BC5 PRELIMINARY; PRT; 165 AA.
AC Q92BC5;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Hypothetical protein lin1625.
GN LIN1625.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-CLIP 11262 / SEROVAR 6A;
RX PubMed-11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueder T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
DR EMBL; AL596169; CAC96856.1; -
DR ListList; LIN01625; -
DR InterPro; IPR000866; AhpC-TSA.
DR InterPro; IPR02065; TPX.
DR Pfam; PF00578; AhpC-TSA; 1.
DR PROSITE; PS01265; TPX; UNKNOWN_1.
DR KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 165 AA; 18162 MW; 77705B7CD8BC8F4D CRC64;

Query Match 66.0%; Score 33; DB 16; Length 165;
Best Local Similarity 66.7%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 EVVVPXGXDX 10
| : || | | :
Db 144 EVVPEGSDH 152

RESULT 25
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ID Q8Y608
AC Q8Y608;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical protein lmo1583.
GN LMO1583.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-EGD-E / SEROVAR 1/2A;
RX MEDLINE-21537279; PubMed-11679669;
RA Baquero F., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schlueder T., Simoes N., Tierrez A.,

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RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
 RT "Comparative genomics of *Listeria species*."
 RL Science 294:849-852(2001).
 DR EMBL; AL591979; CAC99661.1; -.
 DR ListiList; LMO01583; -.
 DR InterPro; IPR000866; AhpC-TSA.
 DR InterPro; IPR002065; TPX.
 DR Pfam; PF00578; AhpC-TSA; 1.
 DR PROSITE; PS01265; TPX; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 165 AA; 18133 MW; 77705B7CC46D424D CRC64;

Query Match 66.0%; Score 33; DB 16; Length 165;
 Best Local Similarity 66.7%; Pred. No. 28;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 EVWPXGXDY 10
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Search completed: June 10, 2003, 13:46:39
 Job time : 26.7857 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:24:45 ; Search time 31.3571 Seconds

(without alignments)

46.744 Million cell updates/sec

Title: US-09-909-164-47

Perfect score: 52

Sequence: 1 EGVVPXGMSYS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	96.2	11	23	ABB80521 Hepatitis C virus
2	50	96.2	11	23	ABB80522 Hepatitis C virus
3	50	96.2	11	23	ABB80525 Hepatitis C virus
4	50	96.2	11	23	ABB80526 Hepatitis C virus
5	50	96.2	11	23	ABB80529 Hepatitis C virus
6	50	96.2	11	23	ABB80563 Hepatitis C virus
7	50	96.2	11	23	ABB80564 Hepatitis C virus
8	50	96.2	11	23	ABB80565 Hepatitis C virus
9	50	96.2	11	23	ABB80566 Hepatitis C virus
10	50	96.2	11	23	ABB80567 Hepatitis C virus

11	50	96.2	11	23	ABB80568 Hepatitis C virus
12	46	88.5	11	23	ABB80524 Hepatitis C virus
13	46	88.5	11	23	ABB80528 Hepatitis C virus
14	46	88.5	11	23	ABB80529 Hepatitis C virus
15	46	88.5	11	23	ABB80561 Hepatitis C virus
16	46	88.5	11	23	ABB80562 Hepatitis C virus
17	45	86.5	11	23	ABB80523 Hepatitis C virus
18	45	86.5	11	23	ABB80527 Hepatitis C virus
19	45	86.5	11	23	ABB80535 Hepatitis C virus
20	45	86.5	11	23	ABB80536 Hepatitis C virus
21	45	86.5	11	23	ABB80539 Hepatitis C virus
22	45	86.5	11	23	ABB80540 Hepatitis C virus
23	45	86.5	11	23	ABB80558 Hepatitis C virus
24	45	86.5	11	23	ABB80560 Hepatitis C virus
25	44	84.6	11	23	ABB80544 Hepatitis C virus
26	44	84.6	11	23	ABB80545 Hepatitis C virus
27	44	84.6	11	23	ABB80549 Hepatitis C virus
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29	44	84.6	11	23	ABB80553 Hepatitis C virus
30	42	80.8	11	23	ABB80530 Hepatitis C virus
31	41	78.8	11	23	ABB80538 Hepatitis C virus
32	41	78.8	11	23	ABB80542 Hepatitis C virus
33	41	78.8	11	23	ABB80543 Hepatitis C virus
34	40	76.9	11	23	ABB80537 Hepatitis C virus
35	40	76.9	11	23	ABB80541 Hepatitis C virus
36	40	76.9	11	23	ABB80547 Hepatitis C virus
37	40	76.9	11	23	ABB80548 Hepatitis C virus
38	40	76.9	11	23	ABB80551 Hepatitis C virus
39	40	76.9	11	23	ABB80556 Hepatitis C virus
40	40	76.9	11	23	ABB80557 Hepatitis C virus
41	40	76.9	20	20	AAU76810 Novel human diago
42	40	76.9	1022	22	ABG03621 Novel human diago
43	40	76.9	1022	22	ABG03826 Novel human diago
44	40	76.9	1022	22	ABG08173 Hepatitis C virus
45	39	75.0	11	23	ABB80546 Hepatitis C virus
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48	39	75.0	11	23	ABB80555 Hepatitis C virus
49	38	73.1	11	23	ABB80533 Hepatitis C virus
50	38	73.1	11	23	ABB80534 Hepatitis C virus
51	38	73.1	3472	21	AAU90913 Hepatitis C virus
52	37	71.2	11	23	ABB80531 Hepatitis C virus
53	37	71.2	11	23	ABB80532 Hepatitis C virus
54	36	69.2	244	21	AA112881 Murine JNK3 bindin
55	36	69.2	484	21	AA112882 Murine JNK3 bindin
56	35	67.3	11	18	AAW99288 Peptide N424 from
57	34	65.4	842	21	AAU44359 P. chrysogenum sut
58	34	65.4	947	21	AAU44359 Pinus radiata cell
59	34	65.4	1070	22	AAU14378 Human novel protei
60	33	63.5	12	21	AAV83772 HCV NS3 protease s
61	33	63.5	12	21	AAV83772 HCV NS3 protease s
62	33	63.5	13	18	AAW99276 Peptide D4 from WO
63	33	63.5	13	18	AAW99276 Peptide 5 used in
64	33	63.5	14	18	AAW99275 Peptide C0 from WO
65	33	63.5	14	18	AAW99277 Peptide 4 used in
66	33	63.5	14	18	AAW99277 Peptide 6 used in
67	33	63.5	14	18	AAW99277 Peptide D2 from WO
68	33	63.5	16	18	AAW99274 Peptide 3 used in
69	33	63.5	16	18	AAW99274 Peptide D1 from WO
70	33	63.5	18	18	AAW99273 Peptide 2 used in
71	33	63.5	18	18	AAW99273 Peptide 1 used in
72	33	63.5	18	19	AAW71281 Cleavable substrate
73	33	63.5	20	18	AAW99272 Peptide PS from WO
74	33	63.5	20	18	AAW99272 Peptide 1 used in
75	33	63.5	20	20	AAU14511 HCV NS3 protease t

ALIGNMENTS

RESULT 1
ABB80521
ID ABB80521 standard; peptide; 11 AA.

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XX AC ABB80521;
XX DT 08-OCT-2002 (first entry)
XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #1.
XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX RW virucide.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1
XX FT Modified-site 6 /note= "N-terminal acetyl"
XX FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
XX FT residue 7"
XX FT Misc-difference 9 /note= "D-form residue"
XX FT Modified-site 11 /note= "C-terminal amide"
XX PN WO200208251-A2.
XX PD 31-JAN-2002.
XX PF 19-JUL-2001; 2001WO-US23169.
XX PR 21-JUL-2000; 2000US-220101P.
XX PA (CORV-) CORVAS INT INC.
XX PI Lim-wilby M, Levy OE, Brunck TK;
XX DR WPI; 2002-361643/39.
XX CC Novel peptide compound having hepatitis C virus protease inhibitory
XX PT activity useful for treating disorders associated with hepatitis C
XX PT virus protease
XX PS Claim 17; Page 64; 69pp; English.
XX CC The sequence represents a peptide compound of the invention having
XX CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
XX CC invention are alpha-ketoamide peptide analogues. The peptides have
XX CC virucide activity, and are useful for treating and in the manufacture of
XX CC a medicament to treat disorders associated with HCV protease. A
XX CC pharmaceutical composition comprising the peptide as an active ingredient
XX CC is useful for treating disorders associated with hepatitis C virus.
XX SQ Sequence 11 AA;
XX Query Match 96.2%; Score 50; DB 23; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 0.0011;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEVVPXGMSYS 11
Db 1 EEVVPXGMSYS 11
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ID ABB80522 standard; peptide; 11 AA.
XX AC ABB80522;
XX DT 08-OCT-2002 (first entry)
XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #2.
XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX RW virucide.

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OS Synthetic.
XX Key Location/Qualifiers
XX FT Modified-site 1 /note= "N-terminal acetyl"
XX FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
XX FT residue 7"
XX FT Misc-difference 9 /note= "D-form residue"
XX FT Modified-site 11 /note= "C-terminal amide"
XX PN WO200208251-A2.
XX PD 31-JAN-2002.
XX PF 19-JUL-2001; 2001WO-US23169.
XX PR 21-JUL-2000; 2000US-220101P.
XX PA (CORV-) CORVAS INT INC.
XX PI Lim-wilby M, Levy OE, Brunck TK;
XX DR WPI; 2002-361643/39.
XX CC Novel peptide compound having hepatitis C virus protease inhibitory
XX PT activity useful for treating disorders associated with hepatitis C
XX PT virus protease
XX PS Claim 17; Page 64; 69pp; English.
XX CC The sequence represents a peptide compound of the invention having
XX CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
XX CC invention are alpha-ketoamide peptide analogues. The peptides have
XX CC virucide activity, and are useful for treating and in the manufacture of
XX CC a medicament to treat disorders associated with HCV protease. A
XX CC pharmaceutical composition comprising the peptide as an active ingredient
XX CC is useful for treating disorders associated with hepatitis C virus.
XX SQ Sequence 11 AA;
XX Query Match 96.2%; Score 50; DB 23; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 0.0011;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEVVPXGMSYS 11
Db 1 EEVVPXGMSYS 11
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ID ABB80525 standard; peptide; 11 AA.
XX AC ABB80525;
XX DT 08-OCT-2002 (first entry)
XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #5.
XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX RW virucide.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1 /note= "N-terminal acetyl"
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FT Misc-difference 8
FT FT Modified-site 11 /note= "D-form residue"
FT FT Modified-site 11 /note= "C-terminal amide"
XX WO200208251-A2.
XX 31-JAN-2002.
XX 19-JUL-2001; 2001WO-US23169.
XX 21-JUL-2000; 2000US-220101P.
XX (CORV-) CORVAS INT INC.
XX Lim-wilby M, Levy OE, Brunck TK;
XX WPI; 2002-361643/39.
XX Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
XX Claim 17; Page 64; 69pp; English.
XX The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
XX Sequence 11 AA;
XX Query Match 96.2%; Score 50; DB 23; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 0.0011;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EEVVPXGMSYS 11
DB 1 EEVVPXGMSYS 11
RESULT 4
ABB80526
ID ABB80526 standard; peptide; 11 AA.
XX AC ABB80526;
XX 08-OCT-2002 (first entry)
XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #6.
XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
FT Misc-difference 8 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 11 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
XX WO200208251-A2.

FT Misc-difference 8
FT FT Modified-site 11 /note= "D-form residue"
FT FT Modified-site 11 /note= "C-terminal amide"
XX WO200208251-A2.
XX 31-JAN-2002.
XX 19-JUL-2001; 2001WO-US23169.
XX 21-JUL-2000; 2000US-220101P.
XX (CORV-) CORVAS INT INC.
XX Lim-wilby M, Levy OE, Brunck TK;
XX WPI; 2002-361643/39.
XX Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease
XX Claim 17; Page 64; 69pp; English.
XX The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.
XX Sequence 11 AA;
XX Query Match 96.2%; Score 50; DB 23; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 0.0011;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 EEVVPXGMSYS 11
DB 1 EEVVPXGMSYS 11
RESULT 5
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ID ABB80559 standard; peptide; 11 AA.
XX AC ABB80559;
XX 08-OCT-2002 (first entry)
XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #39.
XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
FT Misc-difference 8 /note= "D-form residue"
FT Modified-site 8 /note= "Oxymethionine"
FT Modified-site 11 /note= "C-terminal amide"
XX WO200208251-A2.
XX 31-JAN-2002.
XX 19-JUL-2001; 2001WO-US23169.
XX 21-JUL-2000; 2000US-220101P.

XX (CORV-) CORVAS INT INC.
 XX
 PI Lim-wilby M, Levy OE, Brunck TK;
 XX
 DR WPI; 2002-361643/39.
 XX
 DR Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease -
 XX
 XX
 PS Claim 17; Page 65; 69pp; English.
 XX
 CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX
 SQ Sequence 11 AA;
 XX
 Query Match 96.2%; Score 50; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEVVPXGMSYS 11
 Db | | | | | | | | | |
 1 EEVVPXGMSYS 11
 RESULT 6
 ABB80563
 ID ABB80563 standard; peptide; 11 AA.
 XX
 AC ABB80563;
 XX
 DT 08-OCT-2002 (first entry)
 XX
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #43.
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 KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Valyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Modified-site 11 /note= "C-terminal amide"
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 PN WO200208251-A2.
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 PD 31-JAN-2002.
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 PF 19-JUL-2001; 2001WO-US23169.
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 PR 21-JUL-2000; 2000US-220101P.
 XX
 PA (CORV-) CORVAS INT INC.
 XX
 PI Lim-wilby M, Levy OE, Brunck TK;
 XX
 DR WPI; 2002-361643/39.
 XX
 DR Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease -
 XX

XX Claim 17; Page 65; 69pp; English.
 XX
 CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX
 SQ Sequence 11 AA;
 XX
 Query Match 96.2%; Score 50; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0011;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EEVVPXGMSYS 11
 Db | | | | | | | | | |
 1 EEVVPXGMSYS 11
 RESULT 7
 ABB80564
 ID ABB80564 standard; peptide; 11 AA.
 XX
 AC ABB80564;
 XX
 DT 08-OCT-2002 (first entry)
 XX
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #44.
 XX
 KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Leucyl carbonyl forming keto-amide linkage with
 FT residue 7"
 FT Modified-site 11 /note= "C-terminal amide"
 FT
 PN WO200208251-A2.
 XX
 PD 31-JAN-2002.
 XX
 PF 19-JUL-2001; 2001WO-US23169.
 XX
 PR 21-JUL-2000; 2000US-220101P.
 XX
 PA (CORV-) CORVAS INT INC.
 XX
 PI Lim-wilby M, Levy OE, Brunck TK;
 XX
 DR WPI; 2002-361643/39.
 XX
 DR Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease -
 XX
 PS Claim 17; Page 65; 69pp; English.
 XX
 CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.


```

XX SQ Sequence 11 AA;
Query Match 96.2%; Score 50; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEVVPXGMSYS 11
DB 1 EEVVPXGMSYS 11

RESULT 8
ABB80565
ID ABB80565 standard; peptide; 11 AA.
XX AC ABB80565;
XX DT 08-OCT-2002 (first entry)
XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #45.
XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX KW virucide.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1
XX FT /note= "N-terminal acetyl"
XX FT Modified-site 6
XX FT /note= "Norleucyl carbonyl forming keto-amide linkage
XX FT Modified-site 11 with residue 7"
XX FT /note= "C-terminal amide"
XX PN WO200208251-A2.
XX PD 31-JAN-2002.
XX PF 19-JUL-2001; 2001WO-US23169.
XX PR 21-JUL-2000; 2000US-220101P.
XX PA (CORV-) CORVAS INT INC.
XX PI Lim-wilby M, Levy OE, Brunck TK;
XX DR WPI; 2002-361643/39.
XX CC Novel peptide compound having hepatitis C virus protease inhibitory
XX PT activity useful for treating disorders associated with hepatitis C
XX PT virus protease
XX PS Claim 17; Page 65; 69pp; English.
XX CC The sequence represents a peptide compound of the invention having
XX CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
XX CC invention are alpha-ketoamide peptide analogues. The peptides have
XX CC virucide activity, and are useful for treating and in the manufacture of
XX CC a medicament to treat disorders associated with HCV protease. A
XX CC pharmaceutical composition comprising the peptide as an active ingredient
XX CC is useful for treating disorders associated with hepatitis C virus.

SQ Sequence 11 AA;
Query Match 96.2%; Score 50; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEVVPXGMSYS 11
DB 1 EEVVPXGMSYS 11

RESULT 9
ABB80566
ID ABB80566 standard; peptide; 11 AA.
XX AC ABB80566;
XX DT 08-OCT-2002 (first entry)
XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46.
XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX KW virucide.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1
XX FT /note= "N-terminal acetyl"
XX FT Modified-site 6
XX FT /note= "2-aminoisobutyl carbonyl residue forming a
XX FT Modified-site 11 keto-amide linkage with residue 7"
XX FT /note= "C-terminal amide"
XX PN WO200208251-A2.
XX PD 31-JAN-2002.
XX PF 19-JUL-2001; 2001WO-US23169.
XX PR 21-JUL-2000; 2000US-220101P.
XX PA (CORV-) CORVAS INT INC.
XX PI Lim-wilby M, Levy OE, Brunck TK;
XX DR WPI; 2002-361643/39.
XX CC Novel peptide compound having hepatitis C virus protease inhibitory
XX PT activity useful for treating disorders associated with hepatitis C
XX PT virus protease
XX PS Claim 17; Page 65; 69pp; English.
XX CC The sequence represents a peptide compound of the invention having
XX CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
XX CC invention are alpha-ketoamide peptide analogues. The peptides have
XX CC virucide activity, and are useful for treating and in the manufacture of
XX CC a medicament to treat disorders associated with HCV protease. A
XX CC pharmaceutical composition comprising the peptide as an active ingredient
XX CC is useful for treating disorders associated with hepatitis C virus.

SQ Sequence 11 AA;
Query Match 96.2%; Score 50; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEVVPXGMSYS 11
DB 1 EEVVPXGMSYS 11

RESULT 10
ABB80567
ID ABB80567 standard; peptide; 11 AA.
XX AC ABB80567;
XX DT 08-OCT-2002 (first entry)

```

```

XX SQ Sequence 11 AA;
Query Match 96.2%; Score 50; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEVVPXGMSYS 11
DB 1 EEVVPXGMSYS 11

RESULT 9
ABB80566
ID ABB80566 standard; peptide; 11 AA.
XX AC ABB80566;
XX DT 08-OCT-2002 (first entry)
XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #46.
XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX KW virucide.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Modified-site 1
XX FT /note= "N-terminal acetyl"
XX FT Modified-site 6
XX FT /note= "2-aminoisobutyl carbonyl residue forming a
XX FT Modified-site 11 keto-amide linkage with residue 7"
XX FT /note= "C-terminal amide"
XX PN WO200208251-A2.
XX PD 31-JAN-2002.
XX PF 19-JUL-2001; 2001WO-US23169.
XX PR 21-JUL-2000; 2000US-220101P.
XX PA (CORV-) CORVAS INT INC.
XX PI Lim-wilby M, Levy OE, Brunck TK;
XX DR WPI; 2002-361643/39.
XX CC Novel peptide compound having hepatitis C virus protease inhibitory
XX PT activity useful for treating disorders associated with hepatitis C
XX PT virus protease
XX PS Claim 17; Page 65; 69pp; English.
XX CC The sequence represents a peptide compound of the invention having
XX CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
XX CC invention are alpha-ketoamide peptide analogues. The peptides have
XX CC virucide activity, and are useful for treating and in the manufacture of
XX CC a medicament to treat disorders associated with HCV protease. A
XX CC pharmaceutical composition comprising the peptide as an active ingredient
XX CC is useful for treating disorders associated with hepatitis C virus.

SQ Sequence 11 AA;
Query Match 96.2%; Score 50; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EEVVPXGMSYS 11
DB 1 EEVVPXGMSYS 11

RESULT 10
ABB80567
ID ABB80567 standard; peptide; 11 AA.
XX AC ABB80567;
XX DT 08-OCT-2002 (first entry)

```

DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #47.
KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX Synthetic.
OS
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT Modified-site 6 /note= "N-terminal acetyl"
FT Modified-site 6
FT Modified-site 11 /note= "(s,s)allothreonyl carbonyl residue forming a
FT keto-amide linkage with residue 7"
FT Modified-site 11
FT /note= "C-terminal amide"
FT
PN WO200208251-A2.
XX
XX 31-JAN-2002.
XX
PF 19-JUL-2001; 2001WO-US23169.
XX
PR 21-JUL-2000; 2000US-220101P.
XX
PA (CORV-) CORVAS INT INC.
XX
PI Lim-wilby M, Levy OE, Brunck TK;
XX
DR WPI; 2002-361643/39.
XX
XX Novel peptide compound having hepatitis C virus protease inhibitory
FT activity useful for treating disorders associated with hepatitis C
FT virus protease
XX
XX Claim 17; Page 65; 69pp; English.
XX
XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
XX
PS Sequence 11 AA;
XX
XX Query Match 96.2%; Score 50; DB 23; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 0.0011;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEVVPXGMSYS 11
DB 1 EEVVPXGMSYS 11
RESULT 11
ABB80568
ID ABB80568 standard; peptide; 11 AA.
XX
AC ABB80568;
XX
DT 08-OCT-2002 (first entry)
XX
DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #48.
XX
KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX Synthetic.
OS
XX Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminal acetyl"
FT
PN WO200208251-A2.
FT

FT Modified-site 6
FT /note= "Alpha-propynyl-glycyl-carbonyl residue forming
FT a keto-amide linkage with residue 7"
FT Modified-site 11
FT /note= "C-terminal amide"
XX
XX WO200208251-A2.
XX
XX 31-JAN-2002.
XX
PF 19-JUL-2001; 2001WO-US23169.
XX
PR 21-JUL-2000; 2000US-220101P.
XX
PA (CORV-) CORVAS INT INC.
XX
XX Lim-wilby M, Levy OE, Brunck TK;
XX
XX WPI; 2002-361643/39.
XX
XX Novel peptide compound having hepatitis C virus protease inhibitory
FT activity useful for treating disorders associated with hepatitis C
FT virus protease
XX
XX Claim 17; Page 65; 69pp; English.
XX
XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
XX
PS Sequence 11 AA;
XX
XX Query Match 96.2%; Score 50; DB 23; Length 11;
XX Best Local Similarity 100.0%; Pred. No. 0.0011;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EEVVPXGMSYS 11
DB 1 EEVVPXGMSYS 11
RESULT 12
ABB80524
ID ABB80524 standard; peptide; 11 AA.
XX
AC ABB80524;
XX
DT 08-OCT-2002 (first entry)
XX
DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #4.
XX
KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX Synthetic.
OS
XX Key Location/Qualifiers
FT Modified-site 1
FT /note= "N-terminal acetyl"
FT Modified-site 6
FT /note= "Norvalyl carbonyl residue forming keto-amide linkage with
FT residue 7"
FT Misc-difference 9
FT /note= "D-form residue"
FT Modified-site 11
FT /note= "C-terminal amide"
XX
XX WO200208251-A2.
XX

PD 31-JAN-2002.
XX
PF 19-JUL-2001; 2001WO-US23169.
XX
PR 21-JUL-2000; 2000US-220101P.
XX
PA (CORV-) CORVAS INT INC.
XX
XX Lim-wilby M, Levy OE, Brunck TK;
XX
XX WPI; 2002-361643/39.
DR
XX Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease -
XX
XX Claim 17; Page 64; 69pp; English.
PS
XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
XX Sequence 11 AA;
Query Match 88.5%; Score 46; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EEVVPXGMSYS 11
DB 1 EEVVPXGMDYS 11
RESULT 13
ABB80528
ID ABB80528 standard; peptide; 11 AA.
XX
AC ABB80528;
XX
DT 08-OCT-2002 (first entry)
XX
DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #8.
XX
KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT residue 7"
FT Misc-difference 8 /note= "D-form residue"
FT Modified-site 11 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
PN WO200208251-A2.
XX
PD 31-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-US23169.
XX
PF 21-JUL-2000; 2000US-220101P.
XX
PR (CORV-) CORVAS INT INC.
XX
PA Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT activity useful for treating disorders associated with hepatitis C

PI Lim-wilby M, Levy OE, Brunck TK;
XX
DR WPI; 2002-361643/39.
XX
PT Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT virus protease -
XX
XX Claim 17; Page 64; 69pp; English.
PS
XX The sequence represents a peptide compound of the invention having
CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
CC invention are alpha-ketoamide peptide analogues. The peptides have
CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.
XX
XX Sequence 11 AA;
Query Match 88.5%; Score 46; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 EEVVPXGMSYS 11
DB 1 EEVVPXGMDYS 11
RESULT 14
ABB80529
ID ABB80529 standard; peptide; 11 AA.
XX
AC ABB80529;
XX
DT 08-OCT-2002 (first entry)
XX
DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #9.
XX
KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
KW virucide.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT residue 7"
FT Misc-difference 8 /note= "D-form residue"
FT Modified-site 9 /note= "D-form residue"
FT Modified-site 11 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
PN WO200208251-A2.
XX
PD 31-JAN-2002.
XX
XX 19-JUL-2001; 2001WO-US23169.
XX
PR 21-JUL-2000; 2000US-220101P.
XX
PA (CORV-) CORVAS INT INC.
XX
PI Lim-wilby M, Levy OE, Brunck TK;
XX
XX WPI; 2002-361643/39.
DR
XX Novel peptide compound having hepatitis C virus protease inhibitory
PT activity useful for treating disorders associated with hepatitis C
PT activity useful for treating disorders associated with hepatitis C

PT virus protease -
 PS Claim 17; Page 64; 69pp; English.
 XX
 CC The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX SQ Sequence 11 AA;
 Query Match 88.5%; Score 46; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0075;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGMSYS 11
 DB 1 EEVVPXGMDYS 11
 RESULT 15
 ID ABB80561 standard; peptide; 11 AA.
 XX ABB80561;
 DT 08-OCT-2002 (first entry)
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #41.
 KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT Misc-difference 8 residue 7"
 FT Modified-site 8 /note= "D-form residue"
 FT Modified-site 8 /note= "Oxymethionine"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 XX WO200208251-A2.
 PN 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 XX 21-JUL-2000; 2000US-220101P.
 XX (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease -
 XX Claim 17; Page 65; 69pp; English.
 PS The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.

CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX SQ Sequence 11 AA;
 Query Match 88.5%; Score 46; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.0075;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGMSYS 11
 DB 1 EEVVPXGMDYS 11
 RESULT 16
 ID ABB80562 standard; peptide; 11 AA.
 XX ABB80562;
 DT 08-OCT-2002 (first entry)
 DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #42.
 KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX Synthetic.
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT Misc-difference 8 residue 7"
 FT Modified-site 8 /note= "D-form residue"
 FT Modified-site 8 /note= "Oxymethionine"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 XX WO200208251-A2.
 PN 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 XX 21-JUL-2000; 2000US-220101P.
 XX (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease -
 XX Claim 17; Page 65; 69pp; English.
 PS The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.

CC is useful for treating disorders associated with hepatitis C virus.

XX Sequence 11 AA;

SQ Query Match 88.5%; Score 46; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0075;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEWVPXGMSYS 11
Db ||||||| ||

RESULT 17
ABB80523
ID ABB80523 standard; peptide; 11 AA.

XX AC ABB80523;

XX DT 08-OCT-2002 (first entry)

XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #3.

XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"

FT Misc-difference 9 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

XX WO200208251-A2.

XX PD 31-JAN-2002.

XX PF 19-JUL-2001; 2001WO-US23169.

XX PR 21-JUL-2000; 2000US-220101P.

XX PA (CORV-) CORVAS INT INC.

XX PI Lim-wilby M, Levy OE, Brunck TK;

XX DR WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory
activity useful for treating disorders associated with hepatitis C
virus protease

PS Claim 17; Page 64; 69pp; English.

XX The sequence represents a peptide compound of the invention having
hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
invention are alpha-ketoamide peptide analogues. The peptides have
virucide activity, and are useful for treating and in the manufacture of
a medicament to treat disorders associated with HCV protease. A
pharmaceutical composition comprising the peptide as an active ingredient
is useful for treating disorders associated with hepatitis C virus.

SQ Sequence 11 AA;

Query Match 86.5%; Score 45; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEWVPXGMSYS 11
Db ||||||| ||

RESULT 18

ABB80527
ID ABB80527 standard; peptide; 11 AA.

XX AC ABB80527;

XX DT 08-OCT-2002 (first entry)

XX DE Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #7.

XX KW Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
virucide.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal acetyl"

FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
residue 7"

FT Misc-difference 8 /note= "D-form residue"

FT Modified-site 11 /note= "C-terminal amide"

XX WO200208251-A2.

XX PD 31-JAN-2002.

XX PF 19-JUL-2001; 2001WO-US23169.

XX PR 21-JUL-2000; 2000US-220101P.

XX PA (CORV-) CORVAS INT INC.

XX PI Lim-wilby M, Levy OE, Brunck TK;

XX DR WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory
activity useful for treating disorders associated with hepatitis C
virus protease

PS Claim 17; Page 64; 69pp; English.

XX The sequence represents a peptide compound of the invention having
hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
invention are alpha-ketoamide peptide analogues. The peptides have
virucide activity, and are useful for treating and in the manufacture of
a medicament to treat disorders associated with HCV protease. A
pharmaceutical composition comprising the peptide as an active ingredient
is useful for treating disorders associated with hepatitis C virus.

SQ Sequence 11 AA;

Query Match 86.5%; Score 45; DB 23; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEWVPXGMSYS 11
Db ||||||| ||

RESULT 19

ABB80535
ID ABB80535 standard; peptide; 11 AA.

OS	Synthetic.	
XX	Key	Location/Qualifiers
PH	Modified-site	1 /note= "N-terminal acetyl"
FT	Modified-site	6 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"
FT	Misc-difference	9 /note= "D-form residue"
FT	Modified-site	11 /note= "C-terminal amide"
FT	WO200208251-A2.	
XX	31-JAN-2002.	
XX	19-JUL-2001; 2001WO-US23169.	
PF	21-JUL-2000; 2000US-220101P.	
XX	(CORV-) CORVAS INT INC.	
PA	Lim-wilby M, Levy OE, Brunck TK;	
XX	WPI; 2002-361643/39.	
DR	Novel peptide compound having hepatitis C virus protease inhibitory activity useful for treating disorders associated with hepatitis C virus protease	
PT	Claim 17; Page 64; 69pp; English.	
PS	The sequence represents a peptide compound of the invention having hepatitis C virus (HCV) protease inhibitory activity. The peptides of the invention are alpha-ketoamide peptide analogues. The peptides have virucide activity, and are useful for treating and in the manufacture of a medicament to treat disorders associated with HCV protease. A pharmaceutical composition comprising the peptide as an active ingredient is useful for treating disorders associated with hepatitis C virus.	
XX	Sequence 11 AA;	
CC	Query Match	86.5%; Score 45; DB 23; Length 11;
CC	Best Local Similarity	90.9%; Pred. No. 0.012;
CC	Matches 10; Conservative	0; Mismatches 1; Indels 0; Gaps 0
QY	1 EEVVPXGMSYS 11	
DB	1 EEVVPXGQSYS 11	
RESULT 21		
ABB80539	ID ABB80539 standard; peptide; 11 AA.	
XX	AC ABB80539;	
XX	08-OCT-2002 (first entry)	
XX	Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #19.	
XX	Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide; virucide.	
KW	Synthetic.	
XX		
XX	Key	Location/Qualifiers
PH	Modified-site	1 /note= "N-terminal acetyl"
FT	Modified-site	6 /note= "Norvalyl carbonyl forming keto-amide linkage with residue 7"

FT Misc-difference 8
FT Modified-site 11 /note= "D-form residue"
FT /note= "C-terminal amide"
XX WO200208251-A2.
XX 31-JAN-2002.
XX 19-JUL-2001; 2001WO-US23169.
XX 21-JUL-2000; 2000US-220101P.
XX (CORV-) CORVAS INT INC.
XX Lim-wilby M, Levy OE, Brunck TK;
XX WPI; 2002-361643/39.
XX Novel peptide compound having hepatitis C virus protease inhibitory
XX activity useful for treating disorders associated with hepatitis C
XX virus protease -
XX Claim 17; Page 65; 69pp; English.
XX The sequence represents a peptide compound of the invention having
XX hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
XX invention are alpha-ketoamide peptide analogues. The peptides have
XX virucide activity, and are useful for treating and in the manufacture of
XX a medicament to treat disorders associated with HCV protease. A
XX pharmaceutical composition comprising the peptide as an active ingredient
XX is useful for treating disorders associated with hepatitis C virus.
XX Sequence 11 AA;
XX Query Match 86.5%; Score 45; DB 23; Length 11;
XX Best Local Similarity 90.9%; Pred. NO. 0.012;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 EEVVPXGMSYS 11
Db 1 EEVVPXGMSYS 11
RESULT 22
ABB80540
ID ABB80540 standard; peptide; 11 AA.
XX AC ABB80540;
XX DT 08-OCT-2002 (first entry)
XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #20.
XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX virucide.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "D-form residue"
FT Misc-difference 8 /note= "D-form residue"
FT Misc-difference 9 /note= "D-form residue"
FT Modified-site 11 /note= "C-terminal amide"
XX WO200208251-A2.
XX 31-JAN-2002.
XX 19-JUL-2001; 2001WO-US23169.
XX 21-JUL-2000; 2000US-220101P.
XX (CORV-) CORVAS INT INC.

XX 31-JAN-2002.
XX 19-JUL-2001; 2001WO-US23169.
XX 21-JUL-2000; 2000US-220101P.
XX (CORV-) CORVAS INT INC.
XX Lim-wilby M, Levy OE, Brunck TK;
XX WPI; 2002-361643/39.
XX Novel peptide compound having hepatitis C virus protease inhibitory
XX activity useful for treating disorders associated with hepatitis C
XX virus protease -
XX Claim 17; Page 65; 69pp; English.
XX The sequence represents a peptide compound of the invention having
XX hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
XX invention are alpha-ketoamide peptide analogues. The peptides have
XX virucide activity, and are useful for treating and in the manufacture of
XX a medicament to treat disorders associated with HCV protease. A
XX pharmaceutical composition comprising the peptide as an active ingredient
XX is useful for treating disorders associated with hepatitis C virus.
XX Sequence 11 AA;
XX Query Match 86.5%; Score 45; DB 23; Length 11;
XX Best Local Similarity 90.9%; Pred. NO. 0.012;
XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 EEVVPXGMSYS 11
Db 1 EEVVPXGMSYS 11
RESULT 23
ABB80558
ID ABB80558 standard; peptide; 11 AA.
XX AC ABB80558;
XX DT 08-OCT-2002 (first entry)
XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #38.
XX Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
XX virucide.
XX Synthetic.
XX Key Location/Qualifiers
FH Modified-site 1 /note= "N-terminal acetyl"
FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
FT Modified-site 8 residue 7"
FT Modified-site 11 /note= "Oxymethionine"
FT Modified-site 11 /note= "C-terminal amide"
XX WO200208251-A2.
XX 31-JAN-2002.
XX 19-JUL-2001; 2001WO-US23169.
XX 21-JUL-2000; 2000US-220101P.
XX (CORV-) CORVAS INT INC.

XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease -
 XX Claim 17; Page 65; 69pp; English.
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX Sequence 11 AA;
 SQ Query Match 86.5%; Score 45; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.012; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGMSYS 11
 DB 1 EEVVPXGMHYS 11
 RESULT 24
 ABB80560
 ID ABB80560 standard; peptide; 11 AA.
 XX AC ABB80560;
 XX DT 08-OCT-2002 (first entry)
 XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #40.
 DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 XX virucide.
 KW Synthetic.
 OS Key Location/Qualifiers
 XX Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT Modified-site 6 residue 7"
 FT Misc-difference 8 /note= "D-form residue"
 FT Modified-site 8 /note= "Oxymethionine"
 FT Misc-difference 9 /note= "D-form residue"
 FT Modified-site 11 /note= "C-terminal amide"
 FT WO200208251-A2.
 XX 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 XX 21-JUL-2000; 2000US-220101P.
 XX (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.

XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease -
 XX Claim 17; Page 65; 69pp; English.
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.
 XX Sequence 11 AA;
 SQ Query Match 86.5%; Score 45; DB 23; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.012; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EEVVPXGMSYS 11
 DB 1 EEVVPXGMHYS 11
 RESULT 25
 ABB80544
 ID ABB80544 standard; peptide; 11 AA.
 XX AC ABB80544;
 XX DT 08-OCT-2002 (first entry)
 XX Hepatitis C virus NS3/NS4a serine protease inhibitor peptide #24.
 DE Hepatitis C virus; HCV; serine protease; inhibitor; alpha-ketoamide;
 KW virucide.
 XX Synthetic.
 OS Key Location/Qualifiers
 XX Modified-site 1 /note= "N-terminal acetyl"
 FT Modified-site 6 /note= "Norvalyl carbonyl forming keto-amide linkage with
 FT Modified-site 11 /note= "C-terminal amide"
 FT WO200208251-A2.
 XX 31-JAN-2002.
 XX 19-JUL-2001; 2001WO-US23169.
 XX 21-JUL-2000; 2000US-220101P.
 XX (CORV-) CORVAS INT INC.
 XX Lim-wilby M, Levy OE, Brunck TK;
 XX WPI; 2002-361643/39.
 XX Novel peptide compound having hepatitis C virus protease inhibitory
 PT activity useful for treating disorders associated with hepatitis C
 PT virus protease -
 XX Claim 17; Page 65; 69pp; English.
 XX The sequence represents a peptide compound of the invention having
 CC hepatitis C virus (HCV) protease inhibitory activity. The peptides of the
 CC invention are alpha-ketoamide peptide analogues. The peptides have
 CC virucide activity, and are useful for treating and in the manufacture of
 CC a medicament to treat disorders associated with HCV protease. A
 CC pharmaceutical composition comprising the peptide as an active ingredient
 CC is useful for treating disorders associated with hepatitis C virus.

CC virucide activity, and are useful for treating and in the manufacture of
CC a medicament to treat disorders associated with HCV protease. A
CC pharmaceutical composition comprising the peptide as an active ingredient
CC is useful for treating disorders associated with hepatitis C virus.

XX
SQ Sequence 11 AA;

Query Match 84.6%; Score 44; DB 23; Length 11;
Best Local Similarity 90.9%; Pred No. 0.019;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXGMSYS 11
|||||
Db 1 EEVVPXGTSYS 11

Search completed: June 10, 2003, 13:39:12
Job time : 31.3571 secs

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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:31:45 ; Search time 9.64286 seconds

(without alignments)
33.564 Million cell updates/sec

Title: US-09-909-164-47

Perfect score: 52

Sequence: 1 EEVVPKXGMSYS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2.6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2.6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2.6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2.6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2.6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2.6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	65.4	947	US-09-228-986-73	Sequence 73, Appl
2	33	63.5	45	US-08-637-759B-236	Sequence 236, App
3	33	63.5	45	US-08-871-355A-236	Sequence 236, App
4	33	63.5	45	US-09-201-945-236	Sequence 236, App
5	33	63.5	65	5177197-51	Patent No. 5177197
6	33	63.5	410	5177197-1	Patent No. 5177197
7	33	63.5	1394	6 5177197-30	Patent No. 5177197
8	32	61.5	10	US-09-357-952-66	Sequence 66, Appl
9	32	61.5	10	US-09-521-650-66	Sequence 66, Appl
10	32	61.5	10	US-09-168-888-66	Sequence 66, Appl
11	32	61.5	102	US-08-580-988A-23	Sequence 23, Appl
12	32	61.5	152	US-08-460-694-4	Sequence 4, Appl
13	32	61.5	152	US-08-460-744-4	Sequence 4, Appl
14	32	61.5	152	US-07-667-711B-4	Sequence 4, Appl
15	32	61.5	173	US-08-193-977-7	Sequence 7, Appl
16	32	61.5	189	US-08-464-517-21	Sequence 21, Appl
17	32	61.5	189	US-08-246-361A-21	Sequence 21, Appl
18	32	61.5	189	US-08-463-772-21	Sequence 21, Appl
19	32	61.5	189	PCT-US93-05000-21	Sequence 21, Appl
20	32	61.5	236	US-08-464-517-22	Sequence 22, Appl
21	32	61.5	236	US-08-246-361A-22	Sequence 22, Appl
22	32	61.5	236	US-08-463-772-22	Sequence 22, Appl
23	32	61.5	236	PCT-US93-05000-22	Sequence 22, Appl
24	32	61.5	280	US-08-464-517-6	Sequence 6, Appl
25	32	61.5	280	US-08-463-772-6	Sequence 6, Appl
26	32	61.5	289	US-08-246-361A-4	Sequence 4, Appl
27	32	61.5	289	PCT-US93-05000-4	Sequence 4, Appl

28	32	61.5	291	5	PCT-US93-05000-6	Sequence 6, Appl
29	32	61.5	292	2	US-08-464-517-23	Sequence 23, Appl
30	32	61.5	292	2	US-08-246-361A-6	Sequence 6, Appl
31	32	61.5	292	2	US-08-246-361A-23	Sequence 23, Appl
32	32	61.5	292	3	US-08-463-772-23	Sequence 23, Appl
33	32	61.5	292	5	PCT-US93-05000-23	Sequence 23, Appl
34	32	61.5	295	1	US-07-947-120-8	Sequence 8, Appl
35	32	61.5	295	1	US-08-472-893A-8	Sequence 8, Appl
36	32	61.5	295	2	US-08-460-694-2	Sequence 2, Appl
37	32	61.5	295	2	US-08-464-517-19	Sequence 19, Appl
38	32	61.5	295	2	US-08-464-517-20	Sequence 20, Appl
39	32	61.5	295	2	US-08-246-361A-19	Sequence 19, Appl
40	32	61.5	295	2	US-08-246-361A-20	Sequence 20, Appl
41	32	61.5	295	3	US-08-463-772-19	Sequence 19, Appl
42	32	61.5	295	3	US-08-463-772-20	Sequence 20, Appl
43	32	61.5	295	3	US-08-460-744-2	Sequence 2, Appl
44	32	61.5	295	3	US-07-667-711B-2	Sequence 2, Appl
45	32	61.5	295	3	US-08-947-492-8	Sequence 8, Appl
46	32	61.5	295	5	PCT-US93-05000-2	Sequence 2, Appl
47	32	61.5	295	5	PCT-US93-05000-19	Sequence 19, Appl
48	32	61.5	295	5	PCT-US93-05000-20	Sequence 20, Appl
49	32	61.5	309	2	US-08-464-517-4	Sequence 4, Appl
50	32	61.5	309	3	US-08-463-772-4	Sequence 4, Appl
51	32	61.5	529	4	US-09-240-639-4	Sequence 4, Appl
52	32	61.5	618	2	US-08-770-761A-3	Sequence 3, Appl
53	32	61.5	647	2	US-08-770-761A-8	Sequence 8, Appl
54	32	61.5	660	2	US-08-770-761A-2	Sequence 2, Appl
55	32	61.5	662	2	US-08-770-761A-5	Sequence 5, Appl
56	32	61.5	705	2	US-08-770-761A-7	Sequence 7, Appl
57	32	61.5	819	2	US-08-464-517-7	Sequence 7, Appl
58	32	61.5	819	3	US-08-246-361A-7	Sequence 7, Appl
59	32	61.5	819	3	US-08-463-772-7	Sequence 7, Appl
60	32	61.5	819	5	PCT-US93-05000-7	Sequence 7, Appl
61	31	59.6	59	4	US-08-963-851-14	Sequence 14, Appl
62	31	59.6	622	2	US-08-459-146-2	Sequence 2, Appl
63	31	59.6	622	2	US-08-459-065-2	Sequence 2, Appl
64	30	57.7	13	4	US-09-288-391-22	Sequence 22, Appl
65	30	57.7	13	4	US-09-288-391-23	Sequence 23, Appl
66	30	57.7	117	4	US-08-444-818-44	Sequence 44, Appl
67	30	57.7	121	4	US-09-152-060-68	Sequence 68, Appl
68	30	57.7	121	4	US-09-152-060-85	Sequence 85, Appl
69	30	57.7	122	4	US-08-879-995A-1	Sequence 1, Appl
70	30	57.7	122	3	US-09-215-096-1	Sequence 1, Appl
71	30	57.7	132	4	US-08-444-818-52	Sequence 52, Appl
72	30	57.7	159	2	US-08-844-086-4	Sequence 4, Appl
73	30	57.7	159	3	US-09-018-211-4	Sequence 4, Appl
74	30	57.7	211	5	PCT-US94-0417A-18	Sequence 18, Appl
75	30	57.7	241	3	US-08-834-776A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-228-986-73
; Sequence 73, Application US/09228986
; Patent No. 6359198
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Niels
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
; FILE REFERENCE: 11000/1020
; CURRENT APPLICATION NUMBER: US/09/228,986
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 73
; LENGTH: 947
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-228-986-73

Query Match 65.4%; Score 34; DB 4; Length 947;

Best Local Similarity 66.7%; Pred. No. 1e+02;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMSYS 11

Db 686 VMPSGISYS 694

RESULT 2

US-08-637-759B-236

; Sequence 236, Application US/08637759B

; Patent No. 5876931

; GENERAL INFORMATION:

; APPLICANT: David William Holden

; TITLE OF INVENTION: Identification of Genes

; NUMBER OF SEQUENCES: 501

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst

; STREET: 2800 One Atlantic Center

; CITY: Atlanta

; STATE: Georgia

; COUNTRY: USA

; ZIP: 30309-3450

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/637,759B

; FILING DATE: 03-MAY-1996

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB95/02875

; FILING DATE: 11-DEC-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Pabst, Patrea L.

; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: RPMS 101

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404) 873-8794

; TELEFAX: (404) 873-8795

; INFORMATION FOR SEQ ID NO: 236:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 45 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

US-08-637-759B-236

Query Match 63.5%; Score 33; DB 2; Length 45;

Best Local Similarity 60.0%; Pred. No. 5.1;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10

Db 1 EEISPLGWSY 10

RESULT 3

US-08-671-355A-236

; Sequence 236, Application US/08871355A

; Patent No. 6015669

; GENERAL INFORMATION:

; APPLICANT: David William Holden

; TITLE OF INVENTION: Identification of Genes

; NUMBER OF SEQUENCES: 501

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst

; STREET: 2800 One Atlantic Center

; CITY: Atlanta

; STATE: Georgia

; COUNTRY: USA

; ZIP: 30309-3450

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/201,945

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/637,759

;
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMs 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 236:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-09-201-945-236

Query Match 63.5%; Score 33; DB 4; Length 45;
Best Local Similarity 60.0%; Pred. No. 5.1;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGMSY 10
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Db 1 EEISPLGWSY 10

RESULT 5
517197-51
; Patent No. 5177197
; APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;
; WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAES-
; SON-WELSH, LENA; HELDIN, CARL-HENRIK
; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
; NUMBER OF SEQUENCES: 53
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/487,343
; FILING DATE: 27-FEB-1990
; SEQ ID NO: 51:
; LENGTH: 65
5177197-51

Query Match 63.5%; Score 33; DB 6; Length 65;
Best Local Similarity 45.5%; Pred. No. 7.8;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGMSY 11
||: ||| |
Db 52 KEICPGMGYT 62

RESULT 6
5177197-1
; Patent No. 5177197
; APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;
; WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAES-
; SON-WELSH, LENA; HELDIN, CARL-HENRIK
; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
; NUMBER OF SEQUENCES: 53
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/487,343
; FILING DATE: 27-FEB-1990
; SEQ ID NO: 1:
; LENGTH: 410
5177197-1

Query Match 63.5%; Score 33; DB 6; Length 410;
Best Local Similarity 45.5%; Pred. No. 63;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGMSY 11
||: ||| |
Db 399 KEICPGMGYT 409

RESULT 7
5177197-30
; Patent No. 5177197
; APPLICANT: KANZAKI, TETSUTO; OLOFSSON, ANDERS; MOREN, ANITA;
; WERNSTEDT, CHRISTER; HELLMAN, ULF; MIYAZONO, KOHEI; CLAES-
; SON-WELSH, LENA; HELDIN, CARL-HENRIK
; TITLE OF INVENTION: ISOLATED NUCLEOTIDE SEQUENCE EXPRESSING
; HUMAN TRANSFORMING GROWTH FACTOR-BETAL-BINDING PROTEIN
; NUMBER OF SEQUENCES: 53
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/487,343
; FILING DATE: 27-FEB-1990
; SEQ ID NO: 30:
; LENGTH: 1394
5177197-30

Query Match 63.5%; Score 33; DB 6; Length 1394;
Best Local Similarity 45.5%; Pred. No. 2.6e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGMSY 11
||: ||| |
Db 399 KEICPGMGYT 409

RESULT 8
US-09-357-952-66
; Sequence 66, Application US/09357952
; Patent No. 6248904
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Pro
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
; CURRENT APPLICATION NUMBER: US/09/357,952
; CURRENT FILING DATE: 1999-07-21
; EARLIER APPLICATION NUMBER: US 60/093,642
; EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 66
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-357-952-66

Query Match 61.5%; Score 32; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.5;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EEVVPXGMSY 10
||: ||| |
Db 1 DDIVPCMSY 10

RESULT 9
US-09-521-650-66
; Sequence 66, Application US/09521650
; Patent No. 6335429
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard

; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/521,650
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 09/168,888
; EARLIER FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-521-650-66

Query Match 61.5%; Score 32; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.5;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EEVVPXGMSY 10
Db 1 DDIVPCMSY 10

RESULT 10
US-09-168-888-66
; Sequence 66, Application US/09168888
; Patent No. 6342611
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290002
; CURRENT APPLICATION NUMBER: US/09/168,888
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,582
; EARLIER FILING DATE: 1997-10-10
; EARLIER APPLICATION NUMBER: US 09/033,661
; EARLIER FILING DATE: 1998-03-03
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 66
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-168-888-66

Query Match 61.5%; Score 32; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.5;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EEVVPXGMSY 10
Db 1 DDIVPCMSY 10

RESULT 11
US-08-580-988A-23
; Sequence 23, Application US/08580988A
; Patent No. 5856161
; GENERAL INFORMATION:
; APPLICANT: Aggarwal et al.
; TITLE OF INVENTION: Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor-I-Associated Protein Kinase And Methods
; TITLE OF INVENTION: For Its Use
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dr. Benjamin A. Adler
; STREET: 8011 Candle Lane
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77071

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 Mb floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word for Macintosh
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,988A
; FILING DATE: January 3, 1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benjamin Aaron Adler, Ph.D., J.D.
; REGISTRATION NUMBER: 35,423
; REFERENCE/DOCKET NUMBER: D5721CIP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-777-2321
; TELEFAX: 713-777-6908
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; HYPOTHEICAL: no
; ANTI-SENSE: no
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; US-08-580-988A-23

Query Match 61.5%; Score 32; DB 2; Length 102;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGMSY 10
Db 24 EEVFLAMNY 33

RESULT 12
US-08-460-694-4
; Sequence 4, Application US/08460694
; Patent No. 5858655
; GENERAL INFORMATION:
; APPLICANT: Arnold, Andrew
; TITLE OF INVENTION: PRAD1 Cyclin and its cDNA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,694
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-694-4

Query Match 61.5%; Score 32; DB 2; Length 152;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10
Db 20 EEVFFPLAMNY 29

RESULT 13
US-08-460-744-4
Sequence 4, Application US/08460744
Patent No. 6107541
GENERAL INFORMATION:
APPLICANT: Arnold, Andrew
TITLE OF INVENTION: Pradi Cyclin and its cdna
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 New York Avenue, N.W., Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,744
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McConathy, Evelyn H.
REGISTRATION NUMBER: 35,279
REFERENCE/DOCKET NUMBER: 0609.4070005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-460-744-4

Query Match 61.5%; Score 32; DB 3; Length 152;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10
Db 20 EEVFFPLAMNY 29

RESULT 14
US-07-667-711B-4
Sequence 4, Application US/07667711B
Patent No. 6110700
GENERAL INFORMATION:
APPLICANT: ARNOLD, ANDREW
TITLE OF INVENTION: Pradi Cyclin and its cdna
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/667,711B
FILING DATE: 11-MAR-1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCPHAIL, DONALD R.
REGISTRATION NUMBER: 35,811
REFERENCE/DOCKET NUMBER: 0609.4070000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 152 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-07-667-711B-4

Query Match 61.5%; Score 32; DB 3; Length 152;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10
Db 20 EEVFFPLAMNY 29

RESULT 15
US-08-193-977-7
Sequence 7, Application US/08193977
Patent No. 5625031
GENERAL INFORMATION:
APPLICANT: WEBSTER, KEVIN R.
APPLICANT: COLEMAN, KEVIN G.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF THE P33CDK2 AND

;; TITLE OF INVENTION: P34CDC2 CELL CYCLE REGULATORY KINASES AND HUMAN
;; TITLE OF INVENTION: PAPILLOMAVIRUS E7 ONCOPROTEIN
;; NUMBER OF SEQUENCES: 34
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: REED & ROBINS
;; STREET: 635 BRYANT STREET
;; CITY: PALO ALTO
;; STATE: CALIFORNIA
;; COUNTRY: UNITED STATES OF AMERICA
;; ZIP: 94301
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentip Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/193,977
;; FILING DATE: 08-FEB-1994
;; CLASSIFICATION: 530
;; ATTORNEY/AGENT INFORMATION:
;; NAME: ROBINS, ROBERTA L.
;; REGISTRATION NUMBER: 33,208
;; REFERENCE/DOCKET NUMBER: 5998-0016
;; TELEPHONE: (415) 617-8999
;; TELEFAX: (415) 327-3231
;; INFORMATION FOR SEQ ID NO: 7:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 173 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-193-977-7

Query Match 61.5%; Score 32; DB 1; Length 173;
Best Local Similarity 60.0%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10
||| | | | | |
DB 55 EEVFPPLAMNY 64

RESULT 16
US-08-464-517-21
; Sequence 21, Application US/08464517
; Patent No. 5869640
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,517
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/701,514
;; FILING DATE: 16-MAY-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Matthew P. Vincent
;; REGISTRATION NUMBER: 36,709
;; REFERENCE/DOCKET NUMBER: MII-004C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 227-7400
;; TELEFAX: (617) 227-5941
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 189 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-464-517-21

Query Match 61.5%; Score 32; DB 2; Length 189;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10
||| | | | | |
DB 74 EEVFPPLAMNY 83

RESULT 17
US-08-246-361A-21
; Sequence 21, Application US/08246361A
; Patent No. 5998582
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246,361A
; FILING DATE: 19-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/701,514
;; FILING DATE: 16-MAY-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Matthew P. Vincent
;; REGISTRATION NUMBER: 36,709
;; REFERENCE/DOCKET NUMBER: MII-004C
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 227-7400
;; TELEFAX: (617) 227-5941
;; INFORMATION FOR SEQ ID NO: 21:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 189 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-246-361A-21

Query Match 61.5%; Score 32; DB 2; Length 189;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10
||| | | |
Db 74 EEVFLPMNY 83

RESULT 18

US-08-463-772-21
; Sequence 21, Application US/08463772
; Patent No. 6066501

; GENERAL INFORMATION:

; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,772
; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew P. Vincent
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-004C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 21:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-463-772-21

Query Match 61.5%; Score 32; DB 3; Length 189;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10
||| | | |
Db 74 EEVFLPMNY 83

RESULT 19

PCT-US93-05000-21
; Sequence 21, Application PC/TUS9305000

; GENERAL INFORMATION:
; APPLICANT: MITOTIX
; TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05000
; FILING DATE: 19930525
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/888,178
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL91-02A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 616-861-9540
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 189 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
PCT-US93-05000-21

; Query Match

Best Local Similarity 61.5%; Score 32; DB 5; Length 189;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10
||| | | |

Db 74 EEVFLPMNY 83

RESULT 20

US-08-464-517-22
; Sequence 22, Application US/08464517
; Patent No. 5869640

; GENERAL INFORMATION:

; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,517
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308

; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew P. Vincent
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-004C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-464-517-22

Query Match 61.5%; Score 32; DB 2; Length 236;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10
||| | | |
Db 20 EEVFPPLAMNY 29

RESULT 21
US-08-246-361A-22
; Sequence 22, Application US/08246361A
; Patent No. 5998582
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246,361A
; FILING DATE: 19-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew P. Vincent
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-004C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-246-361A-22

Query Match 61.5%; Score 32; DB 2; Length 236;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10
||| | | |
Db 20 EEVFPPLAMNY 29

RESULT 22
US-08-463-772-22
; Sequence 22, Application US/08463772
; Patent No. 6066501
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,772
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew P. Vincent
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-004C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-463-772-22

Query Match 61.5%; Score 32; DB 3; Length 236;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10
||| | | |
Db 20 EEVFPPLAMNY 29

RESULT 23
PCT-US93-05000-22
; Sequence 22, Application PC/TUS9305000
; GENERAL INFORMATION:
; APPLICANT: MITOTIX
; TITLE OF INVENTION: D-Type Cyclin and Uses Related Thereto
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/05000
; FILING DATE: 19930525
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/888,178
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL91-02A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-861-6240
; TELEFAX: 616-861-9540
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
PCT-US93-05000-22
Query Match 61.5%; Score 32; DB 5; Length 236;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 EEVVPXGMSY 10
Db 20 EEVFLPMNY 29

RESULT 24
US-08-464-517-6
; Sequence 6, Application US/08464517
; Patent No. 5869640
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/464,517
; FILING DATE:

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew P. Vincent
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-004C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 280 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-464-517-6
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Best Local Similarity 60.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 EEVVPXGMSY 10
Db 75 EEVFLPMNY 84

RESULT 25
US-08-463-772-6
; Sequence 6, Application US/08463772
; Patent No. 6066501
; GENERAL INFORMATION:
; APPLICANT: BEACH, David H.
; TITLE OF INVENTION: D-TYPE CYCLIN AND USES RELATED THERETO
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII(text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,772
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/963,308
; FILING DATE: 16-OCT-1992
; APPLICATION NUMBER: US 07/888,178
; FILING DATE: 26-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/701,514
; FILING DATE: 16-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Matthew P. Vincent
; REGISTRATION NUMBER: 36,709
; REFERENCE/DOCKET NUMBER: MII-004C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 280 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-463-772-6

Query Match 61.5%; Score 32; DB 3; Length 280;

Best Local Similarity 60.0%; Pred. NO. 65;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10

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Db 75 EEVFPPLAMNY 84

Search completed: June 10, 2003, 13:51:38

Job time : 9.64286 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:46:50 ; Search time 15 seconds
(without alignments)
75.710 Million cell updates/sec

Title: US-09-909-164-47
Perfect score: 52
Sequence: 1 BEVVPXGMSYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 392085 seqs, 103240269 residues
Total number of hits satisfying chosen parameters: 392085

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published_Applications_AA:*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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10: /cgn2_6/ptodata/2/pubpaa/US03_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38	73.1	3472	9	US-10-027-806-4
2	38	73.1	3472	9	US-10-034-623-4
3	38	73.1	3472	9	US-10-027-801-4
4	34	65.4	947	9	US-10-101-464A-73
5	33	63.5	426	9	US-10-214-766-43
6	33	63.5	478	9	US-09-924-340-108
7	33	63.5	478	9	US-09-992-600A-108
8	33	63.5	478	9	US-09-746-783-184
9	33	63.5	478	9	US-10-000-489-108
10	33	63.5	478	9	US-10-000-986-108
11	33	63.5	653	9	US-09-820-843A-26
12	32	61.5	254	10	US-09-947-387-66
13	32	61.5	289	9	US-09-778-927A-53
14	32	61.5	289	9	US-10-024-066-2
15	32	61.5	289	9	US-10-024-066-4
16	32	61.5	289	10	US-09-919-497-54
17	32	61.5	295	10	US-09-925-300-1061
18	32	61.5	529	10	US-09-923-304-4
19	32	61.5	691	9	US-10-101-921-4

20	61.5	691	10	US-09-925-731-2	Sequence 2, Appl1
21	61.5	1377	10	US-09-815-242-10384	Sequence 10384, A
22	61.5	2799	9	US-10-151-736-4	Sequence 4, Appl1
23	59.6	53	9	US-10-092-154-878	Sequence 878, App
24	59.6	53	10	US-09-764-847-878	Sequence 878, App
25	59.6	59	10	US-09-948-080-14	Sequence 14, Appl
26	59.6	161	9	US-09-738-626-5124	Sequence 5124, Ap
27	59.6	163	9	US-10-117-846-20	Sequence 20, Appl
28	59.6	192	9	US-09-986-480-171	Sequence 171, App
29	59.6	198	10	US-09-731-872-334	Sequence 334, App
30	59.6	223	9	US-09-738-626-6349	Sequence 6349, Ap
31	59.6	299	10	US-09-815-242-10697	Sequence 10697, A
32	59.6	381	9	US-09-975-139-5	Sequence 5, Appl1
33	59.6	702	9	US-10-280-403-2	Sequence 2, Appl1
34	59.6	702	10	US-09-907-479-2	Sequence 2, Appl1
35	59.6	763	9	US-09-738-626-4454	Sequence 4454, Ap
36	59.6	1053	10	US-09-815-242-5136	Sequence 5136, Ap
37	59.6	1407	10	US-09-815-242-10439	Sequence 10439, A
38	59.6	1426	10	US-09-912-020-340	Sequence 340, App
39	57.7	7	9	US-09-909-062-1	Sequence 1, Appl1
40	57.7	7	9	US-09-909-062-9	Sequence 9, Appl1
41	57.7	7	9	US-09-909-062-130	Sequence 130, App
42	57.7	121	9	US-09-852-797-68	Sequence 68, Appl
43	57.7	121	9	US-09-852-797-85	Sequence 85, Appl
44	57.7	121	10	US-09-853-161-68	Sequence 68, Appl
45	57.7	121	10	US-09-853-161-85	Sequence 85, Appl
46	57.7	121	10	US-09-852-659A-68	Sequence 68, Appl
47	57.7	121	10	US-09-852-659A-85	Sequence 85, Appl
48	57.7	135	9	US-09-992-598-359	Sequence 359, App
49	57.7	135	9	US-09-989-293A-359	Sequence 359, App
50	57.7	135	9	US-09-989-735-359	Sequence 359, App
51	57.7	135	9	US-09-990-444-359	Sequence 359, App
52	57.7	135	9	US-09-989-730-359	Sequence 359, App
53	57.7	135	9	US-09-990-436-359	Sequence 359, App
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55	57.7	135	9	US-09-993-687-359	Sequence 359, App
56	57.7	135	9	US-09-989-734-359	Sequence 359, App
57	57.7	135	9	US-09-997-653-359	Sequence 359, App
58	57.7	135	9	US-10-174-590-444	Sequence 444, App
59	57.7	135	9	US-10-176-758-444	Sequence 444, App
60	57.7	135	9	US-10-175-737-444	Sequence 444, App
61	57.7	135	9	US-09-993-667-359	Sequence 359, App
62	57.7	135	9	US-10-173-706-444	Sequence 444, App
63	57.7	135	9	US-10-175-738-444	Sequence 444, App
64	57.7	135	9	US-10-175-752-444	Sequence 444, App
65	57.7	135	9	US-10-176-482-444	Sequence 444, App
66	57.7	135	9	US-10-176-757-444	Sequence 444, App
67	57.7	135	9	US-10-176-913-444	Sequence 444, App
68	57.7	135	9	US-10-180-552-444	Sequence 444, App
69	57.7	135	9	US-10-180-557-444	Sequence 444, App
70	57.7	135	9	US-09-990-438-359	Sequence 359, App
71	57.7	135	9	US-09-990-562-359	Sequence 359, App
72	57.7	135	9	US-09-997-428-359	Sequence 359, App
73	57.7	135	9	US-09-997-666-359	Sequence 359, App
74	57.7	135	9	US-10-173-700-444	Sequence 444, App
75	57.7	135	9	US-10-174-572-444	Sequence 444, App

ALIGNMENTS

RESULT 1

US-10-027-806-4
; Sequence 4, Application US/10027806
; Patent No. US20020160476A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; APPLICANT: Schleper, Christa
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAUM SYMBIOSUM
; FILE REFERENCE: DCCORP.002A
; CURRENT APPLICATION NUMBER: US/10/027,806
; CURRENT FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3472
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-806-4

Query Match 73.1%; Score 38; DB 9; Length 3472;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXGMSYS 11
Db 2294 EDVIPRGISFS 2304
|:|:| |:|:|

RESULT 2
US-10-034-623-4
; Sequence 4, Application US/10034623
; Publication No. US20020198365A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; APPLICANT: Schleper, Christa
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCOIP.002A
; CURRENT APPLICATION NUMBER: US/10/034,623
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/408,020
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/102,294
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3472
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-034-623-4

Query Match 73.1%; Score 38; DB 9; Length 3472;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXGMSYS 11
Db 2294 EDVIPRGISFS 2304
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RESULT 3
US-10-027-801-4
; Sequence 4, Application US/10027801
; Publication No. US20030054364A1
; GENERAL INFORMATION:
; APPLICANT: Swanson, Ronald V.
; APPLICANT: Feldman, Robert A.
; APPLICANT: Schleper, Christa
; TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM
; FILE REFERENCE: DCOIP.002A
; CURRENT APPLICATION NUMBER: US/10/027,801
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/408,020
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 3472
; TYPE: PRT
; ORGANISM: Cenarchaeum symbiosum
US-10-027-801-4

Query Match 73.1%; Score 38; DB 9; Length 3472;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXGMSYS 11
Db 2294 EDVIPRGISFS 2304
|:|:| |:|:|

RESULT 4
US-10-101-464A-73
; Sequence 73, Application US/10101464A
; Publication No. US20030046728A1
; GENERAL INFORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Nieuwenhuizen, Nicolaas
; APPLICANT: Higgins, Colleen M.
; TITLE OF INVENTION: Compositions Isolated from Plant Cells
; TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
; FILE REFERENCE: 11000.1020c2
; CURRENT APPLICATION NUMBER: US/10/101,464A
; CURRENT FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: 09/704,302
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: 09/228,986
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/162,866
; PRIOR FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: PCT/US00/00724
; PRIOR FILING DATE: 2000-01-11
; NUMBER OF SEQ ID NOS: 989
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 73
; LENGTH: 947
; TYPE: PRT
; ORGANISM: Pinus radiata
US-10-101-464A-73

Query Match 65.4%; Score 34; DB 9; Length 947;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Db 686 VMPGSGISYS 694
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RESULT 5
US-10-214-766-43
; Sequence 43, Application US/10214766
; Publication No. US20030084473A1
; GENERAL INFORMATION:
; APPLICANT: Gocal, Greg
; TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS
; FILE REFERENCE: CA1138
; CURRENT APPLICATION NUMBER: US/10/214,766
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,734
; PRIOR FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-214-766-43

Query Match 63.5%; Score 33; DB 9; Length 426;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGMSY 10

Db 223 EFVIPAGQSY 232

RESULT 6
US-09-924-340-108
; Sequence 108, Application US/09924340
; Publication No. US20030027248A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US2.REG
; CURRENT APPLICATION NUMBER: US/09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR FILING DATE: 2001-07-13
; PRIOR FILING DATE: 2001-06-29
; PRIOR FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 108
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-924-340-108

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Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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II | | | | |
Db 239 EVAPAGASYN 248

RESULT 7
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; Sequence 108, Application US/09992600A
; Publication No. US20030027161A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US4.DIV
; CURRENT APPLICATION NUMBER: US/09/992,600A
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-08-06
; PRIOR FILING DATE: 2001-08-06
; PRIOR FILING DATE: 2001-08-06
; PRIOR FILING DATE: 2001-08-06
; PRIOR FILING DATE: 2001-07-13
; PRIOR FILING DATE: 2001-06-29
; PRIOR FILING DATE: 2001-06-15
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: JPatent
; SEQ ID NO 108
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-600A-108

Query Match 63.5%; Score 33; DB 9; Length 478;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 EVVPXGMSYS 11
II | | | | |
Db 239 EVAPAGASYN 248

RESULT 8
US-09-746-783-184
; Sequence 184, Application US/09746783
; Publication No. US20030044935A1
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallie, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Fechtel, Kim
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 231
; ENCODING THEM
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/746,783
; FILING DATE: 21-Dec-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Milasincic, Debra J.
; REGISTRATION NUMBER: 46,931
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 184:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 184:
US-09-746-783-184

Query Match 63.5%; Score 33; DB 9; Length 478;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EVVPXGMSYS 11
II | | | | |
Db 239 EVAPAGASYN 248

RESULT 9
US-10-000-489-108
; Sequence 108, Application US/10000489
; Publication No. US20030092011A1
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

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Query Match      63.5%; Score 33; DB 9; Length 478;
Best Local Similarity 60.0%; Pred. NO. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels

QY      2 EVVPXGMSYS 11
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Db      239 EVAPAGASIN 248
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RESULT 11

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Query Match	61.5%;	Score 32;	DB 10;	Length 10;
Best Local Similarity	50.0%;	Pred. No. 3.5;		
Matches	5;	Conservative	3;	Mismatches 2; Indels
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Db	1	DDIVPCSMYS	10	

RESULT 13
US-09-778-927A-53
; Sequence 53, Application US/09778927A
; Patent No. US20020068342A1
; GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Rami et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; FILE REFERENCE: 2786-0160P
; CURRENT APPLICATION NUMBER: US/09/778,927A
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: IL 134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL135341
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 53
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(254)
; OTHER INFORMATION: Xaa = any amino acid, unknown, or other
US-09-778-927A-53

Query Match 61.5%; Score 32; DB 10; Length 254;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10
||| | | |
Db 74 EEVFFPLAMNY 83

RESULT 14
US-10-024-066-2
; Sequence 2, Application US/10024066
; Patent No. US20020166134A1
; GENERAL INFORMATION:
; APPLICANT: Field, Loren J.
; TITLE OF INVENTION: CARDIOMYOCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
; FILE REFERENCE: 7037-450
; CURRENT APPLICATION NUMBER: US/10/024,066
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/139,942
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/US00/16827
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-024-066-2

Query Match 61.5%; Score 32; DB 9; Length 289;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10
||| | | |
Db 73 EEVFFPLAMNY 82

RESULT 15
US-10-024-066-4

; Sequence 4, Application US/10024066
; Patent No. US20020166134A1
; GENERAL INFORMATION:
; APPLICANT: Field, Loren J.
; TITLE OF INVENTION: CARDIOMYOCYTES WITH ENHANCED PROLIFERATIVE POTENTIAL,
; FILE REFERENCE: 7037-450
; CURRENT APPLICATION NUMBER: US/10/024,066
; PRIOR FILING DATE: 2001-12-18
; PRIOR APPLICATION NUMBER: 60/139,942
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: PCT/US00/16827
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-024-066-4

Query Match 61.5%; Score 32; DB 9; Length 289;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10
||| | | |
Db 74 EEVFFPLAMNY 83

RESULT 16
US-09-919-497-54
; Sequence 54, Application US/09919497
; Patent No. US20020106662A1
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-54

Query Match 61.5%; Score 32; DB 10; Length 289;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10
||| | | |
Db 74 EEVFFPLAMNY 83

RESULT 17
US-09-925-300-1061
; Sequence 1061, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08

; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1061
; LENGTH: 295
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (243)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (277)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1061

Query Match 61.5%; Score 32; DB 10; Length 295;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGMSYS 11
||| |||
Db 52 EVLPKMSYA 61

RESULT 18
US-09-923-304-4
; Sequence 4, Application US/09923304
; Patent No. US20020081612A1
; GENERAL INFORMATION:
; APPLICANT: KATZ, RUTH
; APPLICANT: JIANG, FENG
; TITLE OF INVENTION: DETECTION AND DIAGNOSIS OF SMOKING RELATED CANCERS
; FILE REFERENCE: UTSC:658US
; CURRENT APPLICATION NUMBER: US/09/923,304
; CURRENT FILING DATE: 2001-08-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 529
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-304-4

Query Match 61.5%; Score 32; DB 10; Length 529;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10
||| |||
Db 48 QEVLPPLKY 57

RESULT 19
US-10-101-921-4
; Sequence 4, Application US/10101921
; Publication No. US20030022199A1
; GENERAL INFORMATION:
; APPLICANT: Nezu, Jun-Ichi
; APPLICANT: Ose, Asuka
; APPLICANT: Tsuji, Akira
; TITLE OF INVENTION: TRANSPORTER GENES OATP-B, C, D, AND E
; FILE REFERENCE: 06501-104US1
; CURRENT APPLICATION NUMBER: US/10/101,921
; CURRENT FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: PCT/JP00/06416
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: JP 11/267835
; PRIOR FILING DATE: 1999-09-21
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4

; LENGTH: 691
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-101-921-4

Query Match 61.5%; Score 32; DB 9; Length 691;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMSY 10
||| |||
Db 188 IVPLGLSY 195

RESULT 20
US-09-925-731-2
; Sequence 2, Application US/09925731
; Patent No. US20020090622A1
; GENERAL INFORMATION:
; APPLICANT: ADEKUN, ANTHONI MONISOLA
; APPLICANT: AMBROSE, HELEN JEAN
; APPLICANT: CRESSWELL, CARL JOHN
; APPLICANT: DUDLEY, ADAM JESTON
; TITLE OF INVENTION: CHEMICAL COMPOUNDS
; FILE REFERENCE: DJB/009901/0282795
; CURRENT APPLICATION NUMBER: US/09/925,731
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/226,909
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 691
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-731-2

Query Match 61.5%; Score 32; DB 10; Length 691;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMSY 10
||| |||
Db 188 IVPLGLSY 195

RESULT 21
US-09-815-242-10384
; Sequence 10384, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10384
; LENGTH: 1377
; TYPE: PRT
; ORGANISM: Escherichia coli
US-09-815-242-10384

Query Match 61.5%; Score 32; DB 10; Length 1377;
Best Local Similarity 45.5%; Pred. No. 6.7e+02;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 EVVPXGMSYS 11
||| :|||
Db 369 EQLNPAGLSYT 379

RESULT 22

US-10-151-736-4
; Sequence 4, Application US/10151736
; Publication No. US20020192160A1
; GENERAL INFORMATION:
; APPLICANT: Callaghan, Michelle J.
; APPLICANT: Sutherland, Linfield
; APPLICANT: Watts, Colin K.
; TITLE OF INVENTION: No. US20020192160A1el Human Tumour Suppressor Gene
; FILE REFERENCE: RICE-010CON
; CURRENT APPLICATION NUMBER: US/10/151,736
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 09/403,402
; PRIOR FILING DATE: 1999-10-21
; PRIOR APPLICATION NUMBER: PCT/AU98/00280
; PRIOR FILING DATE: 1998-04-20
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 2799
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-736-4

Query Match 61.5%; Score 32; DB 9; Length 2799;
Best Local Similarity 60.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGMSYS 11
||| :|||
Db 2096 EVLPTRKMSYA 2105

RESULT 23

US-10-092-154-878
; Sequence 878, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 878
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: misc_feature
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-092-154-878

Query Match 59.6%; Score 31; DB 9; Length 53;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGMSYS 11
||| :|||
Db 39 VVPTAVSYS 47

RESULT 24

US-09-764-847-878
; Sequence 878, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 878
; LENGTH: 53
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (7)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-847-878

Query Match 59.6%; Score 31; DB 10; Length 53;
Best Local Similarity 66.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGMSYS 11
||| :|||
Db 39 VVPTAVSYS 47

RESULT 25

US-09-948-080-14
; Sequence 14, Application US/09948080
; Patent No. US20020102702A1
; GENERAL INFORMATION:
; APPLICANT: VAN DER OSTEN, CLAUS
; APPLICANT: HALKIER, TORDEN
; APPLICANT: ANDERSEN, CARSTEN
; APPLICANT: BAUDITZ, PETER
; APPLICANT: HANSEN, PETER KAMP
; TITLE OF INVENTION: PROTEASE VARIANTS AND COMPOSITIONS
; FILE REFERENCE: 4946,200-US
; CURRENT APPLICATION NUMBER: US/09/948,080
; CURRENT FILING DATE: 2001-09-06
; PRIOR APPLICATION NUMBER: US/08/963,851
; PRIOR FILING DATE: 1997-11-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-948-080-14

Query Match 59.6%; Score 31; DB 10; Length 59;
Best Local Similarity 45.5%; Pred. No. 37;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 BEVPXGMSYS 11
I: I I:
Db 38 EKHIPGGLEYS 48

Search completed: June 10, 2003, 14:35:46
Job time : 15.0714 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:31:15 ; Search time 11.2143 Seconds
(without alignments)
94.297 Million cell updates/sec

Title: US-09-909-164-47
Perfect score: 52
Sequence: 1 EEVVPXGMSYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	73.1	3472	T31308	hypothetical 367K
2	37	71.2	840	T39116	probable sulfate p
3	37	71.2	877	T40413	sulfate permease -
4	36	69.2	102	A42452	V1 protein - tobac
5	36	69.2	1498	B97355	DNA segregation AT
6	35	67.3	225	S57810	hypothetical prote
7	35	67.3	425	T24111	hypothetical prote
8	35	67.3	670	S22293	zinc finger protei
9	35	67.3	749	H82691	topoisomerase IV s
10	35	67.3	2717	A34203	DNA-binding protei
11	34	65.4	156	S54619	hypothetical prote
12	34	65.4	252	H69491	cell division inhi
13	34	65.4	544	C82900	probable ABC subst
14	33	63.5	94	T40758	hypothetical prote
15	33	63.5	116	E90544	50S ribosomal prot
16	33	63.5	165	D69493	hypothetical prote
17	33	63.5	253	C81374	hypothetical prote
18	33	63.5	259	T34536	hypothetical prote
19	33	63.5	284	S75817	hypothetical prote
20	33	63.5	298	T47670	beta-ketoacyl-ACP
21	33	63.5	368	F72281	hypothetical prote
22	33	63.5	426	D82163	3-phosphoshikimate
23	33	63.5	466	T43653	cdc37 protein - fi
24	33	63.5	653	D82352	iron(III) ABC tran
25	33	63.5	890	A30481	bacteriocin BCN5 -
26	33	63.5	1028	D83286	ATP-dependent DNA
27	33	63.5	1152	D87046	conserved hypotet
28	33	63.5	1394	A35626	transforming growt
29	33	63.5	1401	G82336	DNA-directed RNA p

ALIGNMENTS

RESULT 1

T31308
hypothetical 367K protein - Cenarchaeum symbiosum

C:Species: Cenarchaeum symbiosum

C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000

C:Accession: T31308

R:Schleper, C.; DeLong, E.F.; Preston, C.M.; Feldman, R.A.; Wu, K.Y.; Swanson, R.V.

J. Bacteriol. 180, 5003-5009, 1998

A:Title: Genomic analysis reveals chromosomal variation in natural populations of

A:Reference number: Z20994; MUID:984224450; PMID:9748430

A:Accession: T31308

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-3472 <SCH>

C:Cross-references: EMBL:AF083072; NID:g3599393; PID:g3599394; PIDN:AAC62699.1

C:Superfamily: Cenarchaeum symbiosum hypothetical 367K protein

Query Match 73.1%; Score 38; DB 2; Length 3472;
Best Local Similarity 54.5%; Pred. No. 59;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGMSYS 11

hypothetical prote
masking protein pr
hypothetical prote
transport protein
rho protein GPP-di
hypothetical prote
cyclin D2 - rat
cyclin D2 - mouse
cyclin D2 - human
cyclin D1 - Africa
cyclin D2 - Africa
cyclin D2 - chicke
cyclin D1 - zebra
cyclin D3 - human
cyclin D1 - human
cyclin D1 - mouse
cyclin D1 - rat
rhesF protein - Esc
conserved hypotet
tolB protein - Hae
conserved hypotet
conserved hypotet
agaA protein limpo
hypothetical prote
transport protein
infected cell prot
SCT1 protein - yea
hypothetical prote
maltooligosyltreha
RNA 1 protein - to
aggregation protei
rhaA protein precu
rhaA protein in rh
RhsH core protein
rhesC protein in rh
rhesC protein precu
RhsC core protein
rhaA core protein
rhesB protein precu
gene 11-1 protein
trans-regulatory s
hypothetical prote
probable cobH - My
probable purQ prot
phosphoribosylform

33 63.5 1548 2 T04456
33 63.5 1712 2 A38261
32 61.5 84 2 E97333
32 61.5 175 2 P00616
32 61.5 223 2 T01457
32 61.5 279 2 B72481
32 61.5 288 2 J04011
32 61.5 288 2 I58372
32 61.5 289 2 A41984
32 61.5 289 2 A42822
32 61.5 291 2 S57922
32 61.5 291 2 S57925
32 61.5 291 2 J04579
32 61.5 291 2 S62730
32 61.5 292 2 B42822
32 61.5 295 2 A38977
32 61.5 295 2 A56523
32 61.5 295 2 J02342
32 61.5 347 2 I55120
32 61.5 363 2 D69551
32 61.5 427 2 F64064
32 61.5 427 2 A99286
32 61.5 449 2 B06604
32 61.5 525 2 D98311
32 61.5 525 2 AF2971
32 61.5 726 2 T44000
32 61.5 726 2 T44187
32 61.5 759 2 S25330
32 61.5 889 2 S22659
32 61.5 922 2 AG1827
32 61.5 993 1 P1VXTA
32 61.5 1306 2 S22624
32 61.5 1377 2 C65159
32 61.5 1377 2 E86034
32 61.5 1394 2 H91236
32 61.5 1397 2 A85570
32 61.5 1397 2 C64805
32 61.5 1399 2 A99720
32 61.5 1409 2 F91187
32 61.5 1411 2 E65145
32 61.5 1948 2 S00485
31 59.6 124 1 VKLJ51
31 59.6 133 2 A71173
31 59.6 208 1 D70764
31 59.6 224 2 G70709
31 59.6 224 2 F87186

Db 2294 EDVIPRGSFS 2304

||||| |||

RESULT 2

T39116

probable sulfate permease - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T39116

R:Hunt, C.; Aves, S.; McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, November 1999

A:Reference number: Z21829

A:Accession: T39116

A:Status: preliminary; translated from GB/EMBL/DDBB

A:Molecule type: DNA

A:Residues: 1-840 <HUN>

A:Cross-references: EMBL:AL132779; PIDN:CAB60015.1; GSPDB:GN000066; SPDB:SPAC869.05c

A:Experimental source: strain 972h-; cosmid c869

C:Genetics:

A:Gene: SPDB:SPAC869.05c

A:Map position: 1

Query Match 71.2%; Score 37; DB 2; Length 840;

Best Local Similarity 77.8%; Pred. No. 21;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMSYS 11

|||||

Db 135 VVPOGMSYA 143

RESULT 3

T40413

sulfate permease - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T40413

R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Jimenez Martinez, J.

submitted to the EMBL Data Library, August 1998

A:Reference number: Z21926

A:Accession: T40413

A:Status: preliminary; translated from GB/EMBL/DDBB

A:Molecule type: DNA

A:Residues: 1-877 <LYN>

A:Cross-references: EMBL:AL031261; PIDN:CAA20298.1; GSPDB:GN000067; SPDB:SPBC3H7.02

A:Experimental source: strain 972h-; cosmid c3H7

C:Genetics:

A:Gene: SPDB:SPBC3H7.02

A:Map position: 2

Query Match 71.2%; Score 37; DB 2; Length 877;

Best Local Similarity 77.8%; Pred. No. 22;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMSYS 11

|||||

Db 148 VVPOGMSYA 156

RESULT 4

A42452

V1 protein - tobacco yellow dwarf virus (strain Australia)

C:Species: tobacco yellow dwarf virus

C>Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 08-Oct-1999

C:Accession: A42452

R:Morris, B.A.M.; Richardson, K.A.; Haley, A.; Zhan, X.; Thomas, J.E.

Virology 187, 633-642, 1992

A:Title: The nucleotide sequence of the infectious cloned DNA component of tobacco yellow

A:Reference number: A42452; MUID:92188538; PMID:1546458

A:Accession: A42452

A:Molecule type: DNA

A:Residues: 1-102 <MOR>

A:Cross-references: GB:M81103; NID:g335283; PIDN:AAA47947.1; PID:g335284

Query Match 69.2%; Score 36; DB 2; Length 102;

Best Local Similarity 60.0%; Pred. No. 3.5;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EVVPXGMSYS 11

|||||

Db 7 QVVPNGINYS 16

RESULT 5

B97355

DNA segregation ATPase, FtsK/SpoIIIE family, YUKA B. subtilis ortholog [imported]

C:Species: Clostridium acetobutylicum

C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C:Accession: B97355

R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.

J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacteri

A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: B97355

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1498 <KUR>

A:Cross-references: GB:AE001437; PIDN:AAK81629.1; PID:g15026814; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC3709

Query Match 69.2%; Score 36; DB 2; Length 1498;

Best Local Similarity 60.0%; Pred. No. 63;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10

|||||

Db 1276 EQKIPMGMSY 1285

RESULT 6

S57810

hypothetical protein precursor (clone TP11) - tomato

C:Species: Lycopersicon esculentum (tomato)

C>Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jul-2000

C:Accession: S57810

R:Milligan, S.B.; Gasser, C.S.

Plant Mol. Biol. 28, 691-711, 1995

A:Title: Nature and regulation of pistil-expressed genes in tomato.

A:Reference number: S57808; MUID:95375233; PMID:7647301

A:Accession: S57810

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-225 <ML>

A:Cross-references: EMBL:U20592; NID:g924625; PIDN:AAA80497.1; PID:g924626

C:Superfamily: plant kunitz-type proteinase inhibitor

Query Match 67.3%; Score 35; DB 2; Length 225;

Best Local Similarity 54.5%; Pred. No. 13;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMSYS 11

|||||

Db 32 DEWVPNGKTYA 42

RESULT 7

T24111

hypothetical protein R10D12.10 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T24111

R:Percy, C.

submitted to GenBank, June 2000

R;de Haan, M.; Grivell,

submitted to the Protein Sequence Database, July 1996

A:Reference number: S66877
 A:Accession: S66879
 A:Molecule type: DNA
 A:Residues: 1-156 <DEW>
 A:Cross-references: EMBL:Z74920; NID:q1420109; PIDN:CAA99201.1; PID:q1420111; MIPS:YOR013w
 A:Experimental source: strain S288C
 C:Genetics:
 A:Cross-references: SGD:S0005539
 A:Map position: 15R
 C:Superfamily: hypothetical protein YOR013w

Query Match 65.4%; Score 34; DB 2; Length 156;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGMSY 10
 ||:| |||
 Db 50 EVMLPGMDY 58

RESULT 12

H69491
 cell division inhibitor (mind-2) homolog - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999
 C:Accession: H69491
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 .; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
 A:Reference number: A69250; MUID:98049343; PMID:9389475
 A:Accession: H69491
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-252 <LKE>
 A:Cross-references: GB:AE000970; GB:AE000782; NID:g2689293; PIDN:AAB89318.1; PID:g264860
 C:Superfamily: cell division inhibitor mind

Query Match 65.4%; Score 34; DB 2; Length 252;
 Best Local Similarity 75.0%; Pred. No. 24;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EVVPXGMS 9
 ||:| |||
 Db 81 EVIPAGMS 88

RESULT 13

C82900
 probable ABC substrate-binding protein, iron UU359 [imported] - Ureaplasma urealyticum
 C:Species: Ureaplasma urealyticum
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
 C:Accession: C82900
 R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
 submitted to GenBank, February 2000
 A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a min
 A:Reference number: A82870
 A:Accession: C82900
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-544 <GLA>
 A:Cross-references: GB:AF002133; GB:AF222894; NID:g6899339; PIDN:AAF30768.1; GSPDB:GN001
 A:Experimental source: serovar 3; biovar 1
 C:Genetics:
 A:Gene: ABCsbp-5; UU359
 A:Genetic code: SGC3

Query Match 65.4%; Score 34; DB 2; Length 544;
 Best Local Similarity 70.0%; Pred. No. 55;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10
 ||||| :||
 Db 135 EEVVPYLSY 144

RESULT 14

I40758
 hypothetical protein 1 - Campylobacter jejuni (fragment)
 C:Species: Campylobacter jejuni
 C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 08-Oct-1999
 C:Accession: I40758; S47317
 R:Hani, E.K.; Chan, V.L.
 J. Bacteriol. 177, 2396-2402, 1995
 A:Title: Expression and characterization of Campylobacter jejuni benzoylglutamine am
 A:Reference number: I40758
 A:Accession: I40758
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-94 <RES>
 A:Cross-references: EMBL:Z36940; NID:g535805; PIDN:CAA85392.1; PID:g535806

Query Match 63.5%; Score 33; DB 2; Length 94;
 Best Local Similarity 55.6%; Pred. No. 13;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGMSY 10
 :|| ||||
 Db 26 DIPSPGMSY 34

RESULT 15

E90544
 50S ribosomal protein L20 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
 C:Species: Mycoplasma pulmonis
 C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
 R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Mosze
 Nucleic Acids Res. 29, 2145-2153, 2001
 A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma
 A:Reference number: A99512; MUID:21267165; PMID:11333084
 A:Accession: E90544
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-116 <KUR>
 A:Cross-references: GB:AL445566; PID:q14089674; PIDN:CAC13434.1; GSPDB:GN00153
 A:Experimental source: strain UAB CTIP
 C:Genetics:
 A:Gene: MYPU_2610
 A:Genetic code: SGC3
 C:Superfamily: Escherichia coli ribosomal protein L20

Query Match 53.5%; Score 33; DB 2; Length 116;
 Best Local Similarity 77.8%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGMSYS 11
 || |||||
 Db 68 VRPLGMSYS 76

RESULT 16

D69493
 hypothetical protein AF1949 - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 04-Mar-2000
 C:Accession: D69493
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.;
 .; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Syk

Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaea
 A:Reference number: A69250; MUID:98049343; PMID:9389475
 A:Accession: D69493

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA

A:Residues: 1-165 <KLE>
 A:Cross-references: GB:AE000968; GB:AE000782; NID:g2689291; PIDN:AAB89307.1; PID:g264859
 C:Superfamily: Archaeoglobus fulgidus hypothetical protein AF1949

Query Match 63.5%; Score 33; DB 2; Length 165;
 Best Local Similarity 60.0%; Pred. No. 25;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGMSY 10

Db 60 EESIPDGASY 69

RESULT 17

C81374 hypothetical protein Cj0990c [imported] - Campylobacter jejuni (strain NCTC 11168)

C:Species: Campylobacter jejuni
 C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
 C:Accession: C81374

R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chilling
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrel
 Nature 403, 665-668, 2000

A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
 A:Reference number: A81250; MUID:20150912; PMID:10688204

A:Accession: C81374

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-253 <PAR>

A:Cross-references: GB:AL139076; GB:AL111168; NID:g6968128; PIDN:CAB73246.1; PID:g696842

A:Experimental source: serotype O2, strain NCTC 11168

C:Genetics:

A:Gene: Cj0990c

Query Match 63.5%; Score 33; DB 2; Length 253;

Best Local Similarity 55.6%; Pred. No. 39;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 EVVPXGMSY 10

Db 185 DIFPSGMSY 193

RESULT 18

T34536

hypothetical protein DKFZp434C031.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999

C:Accession: T34536

R:Poustka, A.; Wellenreuther, R.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, October 1999

A:Reference number: Z21540

A:Accession: T34536

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-259 <POU>

A:Cross-references: EMBL:AL122063

A:Experimental source: adult testis; clone DKFZp434C031

C:Genetics:

A:Note: DKFZp434C031.1

Query Match 63.5%; Score 33; DB 2; Length 259;

Best Local Similarity 60.0%; Pred. No. 40;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EVVPXGMSY 11

Db 22 EVAPAGASYN 31

RESULT 19

S75817

hypothetical protein slr1275 - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C:Accession: S75817

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima

o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.;

DNA Res. 3, 109-136, 1996

A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecho

s.

A:Reference number: S74322; MUID:97061201; PMID:8905231

A:Accession: S75817

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-284 <KAN>

A:Cross-references: EMBL:D90913; GB:AB001339; NID:g1653348; PIDN:BAAL8276.1; PID:d

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 63.5%; Score 33; DB 2; Length 284;

Best Local Similarity 55.6%; Pred. No. 44;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VVPXGMSYS 11

Db 208 VIPAGVSYT 216

RESULT 20

T47670

beta-ketoacyl-ACP reductase-like protein - Arabidopsis thaliana

N:Alternate names: protein T26112.190

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 18-Aug-2000

C:Accession: T47670

R:Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Lemcke, K.; Mayer,

submitted to the Protein Sequence Database, February 2000

A:Reference number: Z24471

A:Accession: T47670

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-298 <MON>

A:Cross-references: EMBL:AL132954

A:Experimental source: cultivar Columbia; BAC clone T26112

C:Genetics:

A:Map position: 3

A:Introns: 25/3

A:Note: T26112.190

C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

Query Match 63.5%; Score 33; DB 2; Length 298;

Best Local Similarity 55.6%; Pred. No. 47;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VVPXGMSYS 11

Db 187 IVPGLAYS 195

RESULT 21

F72281

hypothetical protein TM1216 - Thermotoga maritima (strain MSB8)

C:Species: Thermotoga maritima

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: F72281

R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.;

Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richards

C.M.

A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from geno

Nature 399, 323-329, 1999

A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: F72281
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-368 <ARN>
A:Cross-references: GB:AE001778; GB:AE000512; NID:g4981757; PIDN:AAD36291.1; PID:g498178
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1216
C:Superfamily: NADH dehydrogenase (ubiquinone) 49K protein

Query Match 63.5%; Score 33; DB 2; Length 368;
Best Local Similarity 55.6%; Pred. No. 59;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VVPXGMSYS 11
Db 294 IVPKGMAYA 302
:|||:|:

RESULT 22

D82163
3-phosphoshikimate 1-carboxyvinyltransferase VC1732 [imported] - Vibrio cholerae (strain D82163)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: D82163
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, R.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82163
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-426 <HET>
A:Cross-references: GB:AE004251; GB:AE003852; NID:g9656248; PIDN:AAF94882.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1732
A:Map position: 1
C:Superfamily: 3-phosphoshikimate 1-carboxyvinyltransferase; 3-phosphoshikimate 1-carboxy

Query Match 63.5%; Score 33; DB 2; Length 426;
Best Local Similarity 60.0%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGMSY 10
Db 223 EFVIPAGQSY 232
|:|:|:|:

RESULT 23

T43653
cdc37 protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 18-Feb-2000
C:Accession: T43653; T40791; T43654
R:Westwood, P.K.; Preston, N.C.; Fantes, P.A.
submitted to the EMBL Data Library, March 1999
A:Description: Schizosaccharomyces pombe cdc37 cDNA.
A:Reference number: 222602
A:Accession: T43653
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-466 <WES>
A:Cross-references: EMBL:AJ132376; PIDN:CAB38757.1
R:Wood, V.; Raandream, M.A.; Barrall, B.G.; Volckaert, G.
submitted to the EMBL Data Library, May 1999
A:Reference number: 221875
A:Accession: T40791
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA

A:Residues: 1-466 <WOO>
A:Cross-references: EMBL:AL049769; PIDN:CAB42371.2; GSPDB:GN00067
A:Experimental source: strain 972h-; cosmid c9B6
R:Westwood, P.K.; Preston, N.C.; Fantes, P.A.
submitted to the EMBL Data Library, March 1999
A:Description: Schizosaccharomyces pombe cdc37 gene.
A:Reference number: 222603
A:Accession: T43654
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-466 <WE2>
A:Cross-references: EMBL:AJ132377; PIDN:CAB38758.1
C:Genetics:
A:Gene: cdc37; SPAC9B6.10
A:Map position: 2
A:Introns: 8/2; 17/2; 21/1

Query Match 63.5%; Score 33; DB 2; Length 466;
Best Local Similarity 50.0%; Pred. No. 76;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EEVVPXGMSY 10
Db 98 DSAIPGMSY 107
:|:|:|:

RESULT 24

D82352
Iron(III) ABC transporter, permease protein VC0203 [imported] - Vibrio cholerae (strain D82352)
C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C:Accession: D82352
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, R.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: D82352
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-653 <HEI>
A:Cross-references: GB:AE004110; GB:AE003852; NID:g9654600; PIDN:AAF93379.1; GSPDB:GN001
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0203
A:Map position: 1

Query Match 63.5%; Score 33; DB 2; Length 653;
Best Local Similarity 66.7%; Pred. No. 11e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EEVVPXGMS 9
Db 300 EEVVPSGIT 308
|:|:|:|:

RESULT 25

A30481
bacteriocin BCN5 - Clostridium perfringens plasmid pIP404
C:Species: Clostridium perfringens
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 24-Nov-1999
C:Accession: A30481; S03779
R:Garnier, T.; Cole, S.T.
J. Bacteriol. 168, 1189-1196, 1986
A:Title: Characterization of a bacteriocinogenic plasmid from Clostridium perfringens
A:Reference number: J70354; MUID:87057020; PMID:2877971
A:Accession: A30481
A:Molecule type: DNA
A:Residues: 1-890 <GAR>
A:Cross-references: GB:M32882; GB:J03309; NID:g150738; PIDN:AAA98249.1; PID:g150738
C:Genetics:
A:Gene: bcn

A:Genome: plasmid
C:Superfamily: Clostridium perfringens plasmid pIP404 bacteriocin BCN5
C:Keywords: bacteriocin

Query Match 63.5%; Score 33; DB 2; Length 890;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGMSY 10
|||||:
Db 170 EVVPGGFTY 178

Search completed: June 10, 2003, 13:49:19
Job time : 12.2143 secs

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OM protein - protein search, using sw model

Run on: June 10, 2003, 13:25:04 ; Search time 4.5 seconds
(without alignments)
101.387 Million cell updates/sec

Title: US-09-909-164-47

Perfect score: 52

Sequence: 1 EEVVPXGMSYS 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	73.1	1058	1 CARB_FUSNN	Q8986 fusobacteri
2	37	71.2	877	1 SULH_SCHPO	O74377 schizosacch
3	36	69.2	102	1 YILK_TYDVA	P31619 tobacco yel
4	36	69.2	1498	1 YIA9_CLOAB	Q04351 clostridium
5	35	67.3	2717	1 ZEP1_HUMAN	P15822 homo sapien
6	34	65.4	788	1 CY14_NEUCR	P23622 neurospora
7	34	65.4	1499	1 A10C_HUMAN	O60312 homo sapien
8	33	63.5	116	1 RL20_MYCPU	Q98qvo mycoplasma
9	33	63.5	253	1 Y990_CAWJE	P45489 campylobact
10	33	63.5	426	1 AROA_VIECH	Q9krb0 vibrio chol
11	33	63.5	466	1 CC37_SCHPO	O94740 schizosacch
12	33	63.5	478	1 GSR2_HUMAN	Q9nzm5 homo sapien
13	33	63.5	890	1 BCN5_CLOPE	P08696 clostridium
14	33	63.5	1394	1 LTBS_HUMAN	P22064 homo sapien
15	33	63.5	1401	1 RPOC_VIECH	Q9kv29 vibrio chol
16	33	63.5	1595	1 LTBI_HUMAN	Q14766 homo sapien
17	33	63.5	1712	1 LTBI_RAT	Q00918 rattus norv
18	32	61.5	288	1 CGD2_RAT	Q04827 rattus norv
19	32	61.5	289	1 CGD2_HUMAN	Q30279 homo sapien
20	32	61.5	289	1 CGD2_MOUSE	P30280 mus musculus
21	32	61.5	291	1 CGD1_BRARE	Q90459 brachydanio
22	32	61.5	291	1 CGD1_XENLA	P50755 xenopus lae
23	32	61.5	291	1 CGD2_CHICK	P49706 gallus gall
24	32	61.5	291	1 CGD2_XENLA	P53782 xenopus lae
25	32	61.5	292	1 CGD1_CHICK	P55169 gallus gall
26	32	61.5	292	1 CGD3_HUMAN	P30281 homo sapien
27	32	61.5	295	1 CGD1_HUMAN	P24385 homo sapien
28	32	61.5	295	1 CGD1_MOUSE	P25322 mus musculus
29	32	61.5	295	1 CGD1_RAT	P39948 rattus norv
30	32	61.5	427	1 TOLB_HAEIN	P44677 haemophilus
31	32	61.5	529	1 ENP3_HUMAN	O75355 homo sapien
32	32	61.5	691	1 OAT6_HUMAN	Q9Y616 homo sapien
33	32	61.5	726	1 PRTP_HSV6U	P52384 human herpe

34	61.5	759	1	SCT1_YEAST	P32784 saccharomyc
35	61.5	920	1	EDD_RAT	Q64671 rattus norv
36	61.5	993	1	VIA_TAV	P28931 tomato aspe
37	61.5	1377	1	RHSA_ECOLI	P16916 escherichia
38	61.5	1397	1	RHSC_ECOLI	P16918 escherichia
39	61.5	1411	1	RHSB_ECOLI	P16917 escherichia
40	61.5	2799	1	EDD_HUMAN	O95071 homo sapien
41	59.6	124	1	REV_SIVC2	P17280 chimpanzee
42	59.6	208	1	COBH_MYCTU	Q10676 mycobacteri
43	59.6	223	1	PURQ_PYRHO	O59619 pyrococcus
44	59.6	224	1	PURQ_HALN1	Q9hnu2 halobacteri
45	59.6	224	1	PURQ_MYCLE	O05756 mycobacteri
46	59.6	224	1	PURQ_MYCTU	P1841 mycobacteri
47	59.6	225	1	PURQ_CORAM	Q9zhx0 corynebacte
48	59.6	240	1	GDIR_ARATH	Q9sf6c arabidopsi
49	59.6	276	1	Y939_METJA	Q58349 methanococc
50	59.6	319	1	YHAI_CRYPA	P10941 cryptoneutr
51	59.6	432	1	PURA_YEAST	P80210 saccharomyc
52	59.6	488	1	NOM2_PSEAE	Q9htr0 pseudomonas
53	59.6	670	1	OATP_RAT	P46720 rattus norv
54	59.6	706	1	ADDG_HUMAN	Q9uey8 homo sapien
55	59.6	706	1	ADDG_MOUSE	Q9qyb5 mus musculu
56	59.6	827	1	PLSB_MOUSE	Q61586 mus musculu
57	59.6	828	1	PLSB_RAT	P97564 rattus norv
58	59.6	1047	1	EF3_SCHPO	O94489 schizosacch
59	59.6	1407	1	RPOC_ECOLI	P00577 escherichia
60	59.6	1426	1	RHSD_ECOLI	P16919 escherichia
61	59.6	2145	1	U520_CAEEL	Q9u290 caenorhabdi
62	58.7	472	1	ET2A_XENLA	P19102 xenopus lae
63	57.7	81	1	YE47_ARCFU	O28825 archaeoglob
64	57.7	121	1	TKNK_HUMAN	Q9uhf0 homo sapien
65	57.7	132	1	ATPE_AQUAE	O86903 aquifex aeo
66	57.7	146	1	ATPE_LACAC	Q99y0 lactobacill
67	57.7	218	1	PURQ_METH	O36270 methanobact
68	57.7	223	1	PURQ_RHIME	Q92p11 rhizobium m
69	57.7	223	1	RPIA_BUCAI	P57489 buchnera ap
70	57.7	230	1	PURQ_METJA	O59042 methanococc
71	57.7	232	1	SCOA_HELPI	Q9zle3 helicobacte
72	57.7	232	1	SCOA_HELPI	P56006 helicobacte
73	57.7	286	1	CXAC_RAT	P28233 rattus norv
74	57.7	356	1	GBA2_USTMA	P87033 ustilago ma
75	57.7	361	1	RFBB_SALTY	P26391 salmonella

ALIGNMENTS

RESULT 1
CARB_FUSNN
ID CARB_FUSNN STANDARD; PRT; 1058 AA.
AC Q8RG86;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Carbamoyl-phosphate synthase large chain (EC 6.3.5.5) (Carbamoyl-phosphate synthetase ammonia chain).
GN CARB OR FN0422.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RA Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharya A., Bartman A., Gardner W., Grechkin G., Zhu L., Larsen N., D'Souza M., Kogan Y., Chaga O., Goltzman E., Bernal A., Fonstein M., Kyripides N., Walunas T., Pusch G., Haselkorn R., Overbeek R., "Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 25586." J. Bacteriol. 184:2005-2018(2002).

CC -!- CATALYTIC ACTIVITY: 2 ATP + L-glutamine + CO(2) + H(2)O -> 2 ADP +

phosphate + L-glutamate + carbamoyl phosphate.
 -1- COFACTOR: Binds three manganese ions (By similarity).
 -1- PATHWAY: Arginine biosynthesis.
 -1- PATHWAY: Pyrimidine biosynthesis; first step.
 -1- SUBUNIT: Composed of two chains; the small (or glutamine) chain promotes the hydrolysis of glutamine to ammonia, which is used by the large (or ammonia) chain to synthesize carbamoyl phosphate (By similarity).
 -1- SIMILARITY: BELONGS TO THE CARB FAMILY.

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 EMBL: AE010554; RAL94625.1; ALT_INIT.
 InterPro: IPR005483; CPase_L.
 InterPro: IPR005479; CPase_L_D2.
 InterPro: IPR005480; CPase_L_D3.
 InterPro: IPR005481; CPase_L_N.
 InterPro: IPR004362; MGS-like.
 Pfam: PF00289; CPase_L_Chain; 2.
 Pfam: PF02786; CPase_L_D2; 2.
 Pfam: PF02787; CPase_L_D3; 1.
 Pfam: PF02142; MGS; 1.
 PRINTS: PR00098; CPASE.
 PROSITE: PS00866; CPASE_1; 2.
 PROSITE: PS00867; CPASE_2; 2.
 Arginine biosynthesis: Pyrimidine biosynthesis; Ligase; Repeat;
 KW ATP-binding; Manganese; Complete proteome.
 FT DOMAIN 1 401 CARBOXYPHOSPHATE SYNTHETIC DOMAIN.
 FT DOMAIN 402 546 OLIGOMERIZATION DOMAIN.
 FT DOMAIN 547 929 CARBAMOYL PHOSPHATE SYNTHETIC DOMAIN.
 FT DOMAIN 930 1058 ALLOSTERIC DOMAIN.
 FT REPEAT 1 546
 FT REPEAT 547 1058
 FT NP_BIND 153 210 ATP (POTENTIAL).
 FT NP_BIND 302 352 ATP (POTENTIAL).
 FT METAL 284 298 MANGANESE 1 (BY SIMILARITY).
 FT METAL 298 298 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 300 300 MANGANESE 2 (BY SIMILARITY).
 FT METAL 820 820 MANGANESE 3 (BY SIMILARITY).
 FT METAL 832 832 MANGANESE 3 (BY SIMILARITY).
 SQ SEQUENCE 1058 AA; 117451 MW; ED7037AF77C1E39F CRC64;
 Query Match 73.1%; Score 38; DB 1; Length 1058;
 Best Local Similarity 60.0%; Pred. No. 6.2;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 EVVPXGMSYS 11
 I: I I I I I
 Db 190 EIVPGLNYS 199
 RESULT 2
 SULH_SCHPO ID SULH_SCHPO STANDARD; PRT; 877 AA.
 AC Q74377;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Probable sulfate permease C3H7.02.
 GN SPBC3H7.02.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-972;
 RX MEDLINE-21848401; PubMed-11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Howarth T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James P., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney K., Moule S., Mungall K., Murphy L., Niblett D., Odeh C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford J., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grymonprez B.,
 RA Weltyens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of Schizosaccharomyces pombe."
 RL Nature 415:871-880(2002).
 -1- FUNCTION: HIGH AFFINITY UPTAKE OF SULFATE INTO THE CELL (BY SIMILARITY).
 -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 -1- SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS.
 -1- SIMILARITY: CONTAINS 1 STAS DOMAIN.

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 EMBL: AL031261; CAA20298.1;
 InterPro: IPR002645; STAS
 InterPro: IPR001902; Sulfate_transp.
 Pfam: PF00916; Sulfate_transp; 1.
 Pfam: PF01740; STAS; 1.
 DR TIGREMS: TIGR00815; sulp; 1.
 DR PROSITE: PS01130; SLC26A; 1.
 DR PROSITE: PS50801; STAS; 1.
 KW Transport; Transmembrane.
 FT TRANSMEM 133 153 POTENTIAL.
 FT TRANSMEM 161 181 POTENTIAL.
 FT TRANSMEM 186 206 POTENTIAL.
 FT TRANSMEM 221 241 POTENTIAL.
 FT TRANSMEM 243 263 POTENTIAL.
 FT TRANSMEM 292 312 POTENTIAL.
 FT TRANSMEM 329 349 POTENTIAL.
 FT TRANSMEM 384 404 POTENTIAL.
 FT TRANSMEM 424 444 POTENTIAL.
 FT TRANSMEM 461 481 POTENTIAL.
 FT TRANSMEM 484 504 POTENTIAL.
 FT TRANSMEM 518 538 POTENTIAL.
 FT TRANSMEM 543 563 POTENTIAL.
 FT DOMAIN 594 747 STAS.
 SQ SEQUENCE 877 AA; 96373 MW; 56995A8493371E43 CRC64;
 Query Match 71.2%; Score 37; DB 1; Length 877;
 Best Local Similarity 77.8%; Pred. No. 8.3;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 VVPXGMSYS 11
 I I I I I I I I I I I

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Db          148 VVPQGMSSYA 156

RESULT 3
Y1LK_TYDVA
ID Y1LK_TYDVA      STANDARD;      PRT;      102 AA.
AC P31619;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-OCT-1993 (Rel. 27, Last annotation update)
DE Hypothetical 11.2 kDa protein.
GN Y1.
OS Tobacco yellow dwarf virus (strain Australia) (TYDV).
OC Viruses; ssDNA viruses; Geminiviridae; Mastrevirus.
OX NCBI_TaxID=31599;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92188538; PubMed=1546458;
RA Morris B.A.M., Richardson K.A., Haley A., Zhan X., Thomas J.E.;
RT "The nucleotide sequence of the infectious cloned DNA component of
RT tobacco yellow dwarf virus reveals features of geminiviruses
RT infecting monocotyledonous plants.";
RL Virology 187:633-642(1992).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M81103; AAA47947.1;
DR PIR; A42452; A42452.
DR InterPro; IPR002621; Gemini_mov.
DR Pfam; PF01708; Gemini_mov; 1.
KW Hypothetical protein.
SQ SEQUENCE 102 AA; 11178 MW; A40ECF1E0AF55B67 CRC64;

Query Match          69.2%; Score 36; DB 1; Length 102;
Best Local Similarity 60.0%; Pred. No. 1.4;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY          2 EVVPXGMSYS 11
           :||| |::||
Db          7 QVVPXGINS 16

RESULT 4
Y1A9_CLOAB
ID Y1A9_CLOAB      STANDARD;      PRT;      1498 AA.
AC Q04351;
DT 01-FEB-1994 (Rel. 28, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein CAC3709.
GN CAC3709.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=ATCC 824 / DSM 792 / VKM B-1787;
RA Noelling J., Breton G., Omeichenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
RA Tatusev R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
RN [2]

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RP SEQUENCE OF 1-108 FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RA MEDLINE=93273706; PubMed=8501044;
RX Sauer U., Duerre P.;
RT "Sequence and molecular characterization of a DNA region encoding a
RT small heat shock protein of Clostridium acetobutylicum.";
RL J. Bacteriol. 175:3394-3400(1993).
CC -!- SIMILARITY: BELONGS TO THE FTSK/SPOIIIE FAMILY.
CC -!- CAUTION: Ref. 2 sequence differs from that shown due to frameshifts
CC in positions 76 and 106.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE007866; AAK81629.1;
DR EMBL; X65276; CAA46379.1; ALT_FRAME.
DR InterPro; IPR002543; FtsK_SpoIIIE.
DR Pfam; PF01580; FtsK_SpoIIIE; 2.
KW Hypothetical protein; ATP-binding; Complete proteome.
FT NP_BIND 675 682 ATP (POTENTIAL)
SQ SEQUENCE 1498 AA; 168968 MW; FF42037A335A9649 CRC64;

Query Match          69.2%; Score 36; DB 1; Length 1498;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY          1 ERVVPXGMSY 10
           |:::|
Db          1276 EQKIPGMSY 1285

RESULT 5
ZEPL_HUMAN
ID ZEPL_HUMAN      STANDARD;      PRT;      2717 AA.
AC P15822;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Zinc finger protein 40 (Human immunodeficiency virus type I enhancer-
DE binding protein 1) (HIV-Ep1) (Major histocompatibility complex binding
DE protein 1) (MBP-1) (Positive regulatory domain II binding factor 1)
DE (PRDII-BF1).
GN HIVP1 OR ZNF40.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90169514; PubMed=2106471;
RA Fan C.M., Maniatis T.;
RT "A DNA-binding protein containing two widely separated zinc finger
RT motifs that recognize the same DNA sequence.";
RL Genes Dev. 4:29-42(1990).
RN [2]
RP STRUCTURE BY NMR OF 2113-2142.
RX MEDLINE=91064333; PubMed=2248949;
RA Omichinski J.G., Clore G.M., Appella E., Sakaguchi K.,
RA Gronenborn A.M.;
RT "High-resolution three-dimensional structure of a single zinc finger
RT from a human enhancer binding protein in solution.";
RL Biochemistry 29:9324-9334(1990).
RN [3]
RP STRUCTURE BY NMR OF 2087-2142.
RX MEDLINE=92232884; PubMed=1567844;
RA Omichinski J.G., Clore G.M., Robien M., Sakaguchi K., Appella E.,
RA Gronenborn A.M.;
RT "High-resolution solution structure of the double Cys2His2 zinc

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finger from the human enhancer binding protein MBP-1.";
 Biochemistry 31:3907-3917(1992).
 -1- FUNCTION: THIS PROTEIN SPECIFICALLY BINDS TO THE DNA SEQUENCE
 5'-GGGACTTCC-3' WHICH IS FOUND IN THE ENHANCER ELEMENTS OF
 NUMEROUS VIRAL PROMOTERS SUCH AS THOSE OF SV40, CMV, OR HIV1.
 IN ADDITION, RELATED SEQUENCES ARE FOUND IN THE ENHANCER ELEMENTS
 OF A NUMBER OF CELLULAR PROMOTERS, INCLUDING THOSE OF THE CLASS I
 MHC, INTERLEUKIN-2 RECEPTOR, AND INTERFERON-BETA GENES. IT MAY ACT
 IN T-CELL ACTIVATION.
 -1- SUBCELLULAR LOCATION: Nuclear.
 -1- INDUCTION: BY MITOGEN AND PHORBOL ESTER.
 -1- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY
 SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
 ZINC-FINGER IN-BETWEEN.
 -1- SIMILARITY: STRONG, TO HIVP2.

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 EMBL: X51435; CAA35798.1; -
 EMBL: A34203; A34203.
 PDB: 3ZNF; 15-JAN-92.
 PDB: 4ZNF; 15-JAN-92.
 PDB: 1BBO; 31-OCT-93.
 TRANSFAC: T00497; -
 Genew: HGNC:4920; HIVEP1.
 MIM: 194540; -
 InterPro: IPR000822; Znf_C2H2.
 Pfam: PF00096; zf-C2H2; 5.
 PRINTS: PR00048; ZINCFINGER.
 SMART: SM00355; Znf_C2H2; 4.
 PROSITE: PS00028; ZINC_FINGER_C2H2_1; 4.
 PROSITE: PS00157; ZINC_FINGER_C2H2_2; 4.
 Transcription regulation: Zinc-finger; Metal-binding; DNA-binding;
 Nuclear protein; Repeat; 3D-structure.
 FT DOMAIN 406 456 ZINC FINGERS.
 FT ZN_FING 406 428 ZN_FING
 FT ZN_FING 434 456 C2H2-TYPE
 FT DOMAIN 803 806 POLY-SER.
 FT ZN_FING 958 981 ZHC-TYPE (POTENTIAL).
 FT DOMAIN 2087 2139 ZINC FINGERS.
 FT ZN_FING 2087 2109 C2H2-TYPE.
 FT ZN_FING 2115 2139 C2H2-TYPE.
 FT STRAND 2088 2088 C2H2-TYPE.
 FT TURN 2090 2092
 FT STRAND 2095 2095
 FT HELIX 2099 2108
 FT TURN 2109 2109
 FT STRAND 2115 2116
 FT STRAND 2123 2124
 FT HELIX 2127 2135
 SQ SEQUENCE 2717 AA; 297217 MW; D45D3CA951FEA561 CRC64;
 Query Match 67.3%; Score 35; DB 1; Length 2717;
 Best Local Similarity 66.7%; Pred. No. 70;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 VVPXGMSYS 11
 Db 2405 VVPAGLTYS 2413
 RESULT 6
 CY14_NEUCR
 ID CY14_NEUCR STANDARD; PRT; 788 AA.
 AC P23622;
 DT 01-NOV-1991 (Rel. 20, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Sulfate permease II.
 GN CYS-14.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OC NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91129256; PubMed=1825178;
 RA Ketter J.S., Jarai G., Fu Y.-H., Marzluf G.A.;
 RT "Nucleotide sequence, messenger RNA stability, and DNA recognition
 elements of cys-14," the structural gene for sulfate permease II in
 Neurospora crassa.;
 RL Biochemistry 30:1780-1787(1991).
 RN [2]
 RP PROBABLE REVISIONS.
 RX MEDLINE=94188926; PubMed=8140616;
 RA Sandal N.N., Marcker K.A.;
 RT "Similarities between a soybean nodulin, Neurospora crassa sulphate
 permease II and a putative human tumour suppressor.";
 RL Trends Biochem. Sci. 19:19-19(1994).
 CC -1- FUNCTION: UPTAKE OF SULFATE INTO THE CELL.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- INDUCTION: Highly expressed, but only in cells subject to sulfur
 limitation, and it is turned on by the positive-acting Cys-3
 sulfur regulatory protein.
 CC -1- MISCELLANEOUS: SULFATE PERMEASE II IS MAINLY FOUND IN MYCELIA.
 CC -1- SIMILARITY: BELONGS TO THE SLC26A FAMILY OF TRANSPORTERS.

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 EMBL: M59167; AAA33615.1; ALT_SEQ.
 PIR: A37956; A37956.
 InterPro: IPR001902; Sulfate_transp.
 Pfam: PF00916; Sulfate_transp; 1.
 TIGRFAMS: TIGR00815; sulp; 1.
 PROSITE: PS01130; SLC26A; 1.
 KW Transport; Transmembrane; Glycoprotein.
 FT TRANSMEM 71 91 POTENTIAL.
 FT TRANSMEM 103 123 POTENTIAL.
 FT TRANSMEM 128 148 POTENTIAL.
 FT TRANSMEM 171 191 POTENTIAL.
 FT TRANSMEM 193 213 POTENTIAL.
 FT TRANSMEM 271 291 POTENTIAL.
 FT TRANSMEM 326 346 POTENTIAL.
 FT TRANSMEM 363 383 POTENTIAL.
 FT TRANSMEM 451 471 POTENTIAL.
 FT TRANSMEM 474 494 POTENTIAL.
 FT CARBOHYD 23 23 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 578 578 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 788 AA; 87864 MW; 4FC604B60798CE77 CRC64;
 Query Match 65.4%; Score 34; DB 1; Length 788;
 Best Local Similarity 66.7%; Pred. No. 32;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 VVPXGMSYS 11
 Db 90 VVPQGMAYA 98
 RESULT 7
 A10C_HUMAN
 ID A10C_HUMAN STANDARD; PRT; 1499 AA.
 AC O60312; Q96914;
 DT 30-MAY-2000 (Rel. 39, Created)

15-JUN-2002 (Rel. 41, Last sequence update)
 15-JUN-2002 (Rel. 41, Last annotation update)
 Potential phospholipid-transporting ATPase VC (EC 3.6.3.1) (ATPVC)
 (Aminophospholipid translocase VC).
 GN ATP10C OR ATPVC OR KIAA0566.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21225279; PubMed=11326269;
 RA Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S.,
 RT Oshimura M.;
 "A novel maternally expressed gene, ATP10C, encodes a putative
 aminophospholipid translocase associated with Angelman syndrome.";
 Nat. Genet. 28:19-20(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2131119; PubMed=11353404;
 RA Herzog L.B.K., Kim S.-J., Cook E.H. Jr., Ledbetter D.H.;
 "The human aminophospholipid-transporting ATPase gene ATP10C maps
 adjacent to UBE3A and exhibits similar imprinted expression.";
 Am. J. Hum. Genet. 68:1501-1505(2001).
 RN [3]
 RP SEQUENCE OF 337-1499 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98290545; PubMed=9628581;
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
 RA Nomura N., Ohara O.;
 "Prediction of the coding sequences of unidentified human genes. IX.
 The complete sequences of 100 new cDNA clones from brain which can
 code for large proteins in vitro.";
 DNA Res. 5:31-39(1998).
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O = ADP + phosphate.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- TISSUE SPECIFICITY: Wide expression, with highest levels in
 kidney, followed by lung, brain, prostate, testis, ovary, and
 small intestine.
 CC -1- DISEASE: Defects in ATP10C may be a cause of Angelman syndrome
 (AS), also known as 'happy puppet syndrome'.
 CC -1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2
 ATPASES). SUBFAMILY IV.

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 or send an email to license@isb-sib.ch)

 DR EMBL; AB051358; BAB47392.1; -.
 DR EMBL; AY029504; AAK33100.1; -.
 DR EMBL; AY029487; AAK33100.1; JOINED.
 DR EMBL; AY029488; AAK33100.1; JOINED.
 DR EMBL; AY029489; AAK33100.1; JOINED.
 DR EMBL; AY029490; AAK33100.1; JOINED.
 DR EMBL; AY029491; AAK33100.1; JOINED.
 DR EMBL; AY029492; AAK33100.1; JOINED.
 DR EMBL; AY029493; AAK33100.1; JOINED.
 DR EMBL; AY029494; AAK33100.1; JOINED.
 DR EMBL; AY029495; AAK33100.1; JOINED.
 DR EMBL; AY029496; AAK33100.1; JOINED.
 DR EMBL; AY029497; AAK33100.1; JOINED.
 DR EMBL; AY029498; AAK33100.1; JOINED.
 DR EMBL; AY029499; AAK33100.1; JOINED.
 DR EMBL; AY029500; AAK33100.1; JOINED.
 DR EMBL; AY029501; AAK33100.1; JOINED.
 DR EMBL; AY029502; AAK33100.1; JOINED.
 DR EMBL; AY029503; AAK33100.1; JOINED.
 DR EMBL; AB011138; BAA25492.1; -.
 DR Genew; HGNC:13547; ATP10C.

DR MIM; 605855; -.
 DR MIM; 105830; -.
 DR InterPro; IPR001757; ATPase_E1-E2.
 DR InterPro; IPR001454; Hlgase/hydrase.
 DR Pfam; PF00702; Hydrolase; 1.
 DR PRINTS; PR00119; CATAPASE.
 DR PROSITE; PS00154; ATPASE_E1_E2; 1.
 KW Hydrolase; Transmembrane; Phosphorylation; Magnesium; ATP-binding;
 KW Multigene family.
 FT DOMAIN 1 86 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 87 106 POTENTIAL.
 FT DOMAIN 107 110 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 111 128 POTENTIAL.
 FT DOMAIN 129 309 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 310 332 POTENTIAL.
 FT DOMAIN 337 362 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 363 384 POTENTIAL.
 FT DOMAIN 385 1087 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1108 1108 POTENTIAL.
 FT DOMAIN 1109 1119 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1120 1140 POTENTIAL.
 FT DOMAIN 1141 1170 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1171 1192 POTENTIAL.
 FT DOMAIN 1193 1199 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1200 1222 POTENTIAL.
 FT DOMAIN 1223 1228 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 1229 1249 POTENTIAL.
 FT DOMAIN 1250 1267 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1268 1292 POTENTIAL.
 FT DOMAIN 1293 1499 CYTOPLASMIC (POTENTIAL).
 FT MOD_RES 427 427 PHOSPHORYLATION (BY SIMILARITY).
 FT METAL 1031 1031 MAGNESIUM (BY SIMILARITY).
 FT METAL 1035 1035 MAGNESIUM (BY SIMILARITY).
 FT DOMAIN 467 470 POLY-GLU.
 FT CONFLICT 388 388 Q -> R (IN REF. 3).
 SQ SEQUENCE 1499 AA; 167687 MW; D49964D0635A68D CRC64;
 Query Match 65.4%; Score 34; DB 1; Length 1499;
 Best Local Similarity 72.7%; Pred. No. 62;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 EEVVPXGMSYS 11
 Db 469 EEVVPXGMSYS 479
 RESULT 8
 RL20_MYCPU
 ID RL20_MYCPU STANDARD; PRT; 116 AA.
 AC Q98QV0;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 50S ribosomal protein L20.
 GN RPLT OR MYPU.2610.
 OS Mycoplasma pulmonis.
 CC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2107;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=UAB CTIP;
 RX MEDLINE=21267165; PubMed=11353084;
 RA Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
 RA Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
 BLANCHARD A.;
 "The complete genome sequence of the murine respiratory pathogen
 Mycoplasma pulmonis.";
 Nucleic Acids Res. 29:2145-2153(2001).
 CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS
 NECESSARY TO THE IN VITRO ASSEMBLY PROCESS OF THE 50S RIBOSOMAL
 SUBUNIT; IT IS NOT INVOLVED IN THE PROTEIN SYNTHESIZING FUNCTIONS
 OF THAT SUBUNIT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE L20P FAMILY OF RIBOSOMAL PROTEINS.

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DR EMBL; AL445563; CAC13434.1; -
 DR MyuList; MYPU_2610; -
 DR InterPro; IPR001081; Ribosomal_L20.
 DR Pfam; PF00453; Ribosomal_L20; 1.
 DR PRINTS; PR00062; Ribosomal_L20.
 DR ProDom; PD002389; Ribosomal_L20; 1.
 DR TIGRFAMs; TIGR01032; rplT_bact; 1.
 DR PROSITE; PS00937; RIBOSOMAL_L20; 1.
 DR Ribosomal protein; rRNA-binding; Complete proteome.
 KW RIBOSOMAL L20; 1.
 SQ SEQUENCE 116 AA; 13565 MW; C59C748901B181F14 CRC64;

Query Match 63.5%; Score 33; DB 1; Length 116;
 Best Local Similarity 77.8%; Pred. No. 7;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 VVPXGMSYS 11
 DB 68 VRPLGMSYS 76

RESULT 9
 Y990_CAMJE STANDARD; PRT; 253 AA.
 AC P45489; Q9PNV0; PRT; 253 AA.
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein Cj0990C.
 GN Cj0990C.
 OS Campylobacter jejuni.
 OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
 CC Campylobacter.
 OX NCBI_TaxID=137;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=NCCTC 11168;
 RX MEDLINE=20150912; PubMed=10688204;
 RA Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
 RA Basham D., Chillingworth T., Davies R.M., Feltwell T., Holtroyd S.,
 RA Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
 RA Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
 RA Whitehead S., Barrell B.G.;
 RA "The genome sequence of the food-borne pathogen Campylobacter jejuni
 RT reveals hypervariable sequences.";
 RL Nature 403:665-668(2000).
 RN [2]
 RC SEQUENCE OF 160-253 FROM N.A.
 RP STRAIN=ATCC 43431 / TGH 9011.
 RX MEDLINE=95247673; PubMed=7730270;
 RA Hani E.K., Chan V.L.;
 RA "Expression and characterization of Campylobacter jejuni
 RT benzoylglycine amidohydrolase (Hippuricase) gene in Escherichia
 RT coli.";
 RL J. Bacteriol. 177:2396-2402(1995).
 CC -----
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DR EMBL; AL139076; CAB73246.1; -

DR EMBL; Z36940; CAA85392.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 253 AA; 29783 MW; F96D3FF3265F8A6A CRC64;

Query Match 63.5%; Score 33; DB 1; Length 253;
 Best Local Similarity 55.6%; Pred. No. 16;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EYVPXGMSY 10
 DB 185 DIFPQMSY 193

RESULT 10
 AROA_VIBCH STANDARD; PRT; 426 AA.
 ID AROA_VIBCH STANDARD; PRT; 426 AA.
 AC Q9KRE0;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) (5-
 DE enolpyruvylshikimate-3-phosphate synthase) (EPSP synthase) (EPSPs).
 GN AROA OR VCI732.
 OS Vibrio cholerae.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 OX NCBI_TaxID=666;
 RN [1]
 RC SEQUENCE FROM N.A.
 RP STRAIN=El Tor N16961 / Serotype O1;
 RX MEDLINE=20406833; PubMed=10952301;
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Niernan W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RA "DNA sequence of both chromosomes of the cholera pathogen Vibrio
 RT cholerae.";
 RL Nature 406:477-483(2000).
 CC -!- CATALYTIC ACTIVITY: Phosphoenolpyruvate + 3-phosphoshikimate =
 CC phosphate + 5-O-(1-carboxyvinyl)-3-phosphoshikimate.
 CC -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
 CC sixth step.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -!- SIMILARITY: BELONGS TO THE EPSP SYNTHASE FAMILY.
 CC -----
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DR EMBL; AE004251; AAF94882.1; -
 DR TIGR; VC1732; -
 DR InterPro; IPR001986; EPSP_synthase.
 DR Pfam; PF00275; EPSP_synthase; 1.
 DR ProDom; PD001867; EPSP_synthase; 1.
 DR PROSITE; PS00104; EPSP_SYNTHASE_1; 1.
 DR PROSITE; PS00885; EPSP_SYNTHASE_2; 1.
 KW Aromatic amino acid biosynthesis; Transferase; Complete proteome.
 SQ SEQUENCE 426 AA; 46101 MW; 38852D6483BFEC13 CRC64;

Query Match 63.5%; Score 33; DB 1; Length 426;
 Best Local Similarity 60.0%; Pred. No. 27;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EYVPXGMSY 10
 DB 223 EFVIPAGQSY 232

[illegible]

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vivo and in vitro."
Mol. Microbiol. 2:607-614(1988).
-1- FUNCTION: MAY FUNCTION AS AN IONOPHORE.
-1- INDUCTION: BY UV IRRADIATION.
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EMBL; M14481; AAA98248.1; -
EMBL; M32882; AAA98249.1; -
PIR; A30481; A30481.
InterPro; IPR003646; SH3_bac.
SMART; SM00287; SH3D; 3.
Antibiotic; Bacteriocin; Plasmid.
DOMAIN 815 869 HYDROPHOBIC.
SEQUENCE 890 AA; 96699 MW; F4E5E8971C31C6C6 CRC64;
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Query Match 63.5%; Score 33; DB 1; Length 890;
Best Local Similarity 66.7%; Pred. No. 58;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 2 EVVPXGMSY 10
DB 170 EVVPGGFTY 178
|||||
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RESULT 14
LTBS HUMAN STANDARD; PRT; 1394 AA.
AC P22064;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Latent transforming growth factor beta binding protein 1s precursor
DE (Transforming growth factor beta-1 binding protein 1) (TGF-beta1-BP-
DE 1).
DE LTBP1.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP TISSUE=Fibroblast, and Platelet;
RC MIML=100000000; PubMed=2350783;
RX Kanzaki T., Olofsson A., Maren A., Wernstedt C., Hellman U.,
RA Miyazono K., Claesson-Welsh L., Heldin C.-H.;
RA "TGF-beta 1 binding protein: a component of the large latent complex
RT of TGF-beta 1 with multiple repeat sequences.";
RL Cell 61:1051-1061(1990).
CC -1- SUBUNIT: THE LARGE LATENT COMPLEX OF TGF-BETA1 FROM PLATELETS IS
CC COMPOSED OF THE TGF-BETA1 MOLECULE NONCOVALENTLY ASSOCIATED WITH
CC A DISULFIDE-BONDED COMPLEX OF A DIMER OF THE N-TERMINAL PROPEPTIDE
CC OF THE TGF-BETA1 PRECURSOR AND A THIRD COMPONENT DENOTED TGF-
CC BETA1-BP. TGF-BETA1-BP DOES NOT BIND DIRECTLY TO ACTIVE TGF-BETA1.
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; a short form (shown here) and a
CC long form (AC Q14766); are produced by alternative splicing.
CC -1- PTM: CONTAINS HYDROXYLATED ASPARAGINE RESIDUES..
CC -1- PTM: The N-terminus is blocked.
CC -1- SIMILARITY: CONTAINS 16 EGF-LIKE DOMAINS.
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FT	DISULFID	902	915	BY SIMILARITY.
FT	DISULFID	921	933	BY SIMILARITY.
FT	DISULFID	927	942	BY SIMILARITY.
FT	DISULFID	944	957	BY SIMILARITY.
FT	DISULFID	963	975	BY SIMILARITY.
FT	DISULFID	970	984	BY SIMILARITY.
FT	DISULFID	986	1000	BY SIMILARITY.
FT	DISULFID	1101	1114	BY SIMILARITY.
FT	DISULFID	1109	1123	BY SIMILARITY.
FT	DISULFID	1125	1138	BY SIMILARITY.
FT	DISULFID	1144	1155	BY SIMILARITY.
FT	DISULFID	1150	1164	BY SIMILARITY.
FT	DISULFID	1166	1179	BY SIMILARITY.
FT	DISULFID	1298	1309	BY SIMILARITY.
FT	DISULFID	1304	1318	BY SIMILARITY.
FT	DISULFID	1320	1333	BY SIMILARITY.
FT	DISULFID	1339	1354	BY SIMILARITY.
FT	DISULFID	1349	1363	BY SIMILARITY.
FT	DISULFID	1365	1378	BY SIMILARITY.
FT	MOD_RES	647	647	HYDROXYLATION.
FT	MOD_RES	810	810	HYDROXYLATION.
FT	CARBOHYD	21	21	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	52	52	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	98	98	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	294	294	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	870	870	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	923	923	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1039	1039	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	1394 AA;	152791 MW; DFFCA81A40B2C7D1 CRC64;	/FTID=CAR_000184.
Query Match		63.5%;	Score 33; DB 1; Length 1394;	
Best Local Similarity		45.5%;	Pred. No. 93;	
Matches	5; Conservative	3; Mismatches	3; Indels	0; Gaps
Qy	1 EEVVPXGMSYS 11			
	! ! ! ! !			
Db	399 KEICPGMGY 409			
RESULT 15				
RPOC_VIBCH				
ID	RPOC_VIBCH	STANDARD;	PRT;	1401 AA.
AC	Q9KV29;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase			
DE	beta' chain) (RNA polymerase beta' subunit).			
GN	RPOC OR VC0329.			
OS	Vibrio cholerae.			
OC	Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.			
OX	NCBI_TaxID=666;			
RN	[1]			
RN	SEQUENCE FROM N.A.			
RP	STRAIN=El Tor N16961 / Serotype O1;			
RC	MEDLINE=20406833; Pubmed=10952301;			
RX	Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,			
RA	Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,			
RA	Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,			
RA	Emolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,			
RA	McDonald L., Uitterback T., Fleischmann R.D., Nierman W.C., White O.,			
RA	Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,			
RA	Fraser C.M.;			
RT	"DNA sequence of both chromosomes of the cholera pathogen Vibrio			
RT	cholerae."			
RL	Nature 406:477-483(2000).			
CC	- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION			
CC	OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS			
CC	SUBSTRATES (By similarity).			
CC	- CATALYTIC ACTIVITY: N nucleoside triphosphate - N diphosphate +			
CC	[RNA](N).			
CC	- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE			

FT DISULFID 998 1009 BY SIMILARITY.
 FT DISULFID 1004 1018 BY SIMILARITY.
 FT DISULFID 1020 1033 BY SIMILARITY.
 FT DISULFID 1039 1051 BY SIMILARITY.
 FT DISULFID 1046 1060 BY SIMILARITY.
 FT DISULFID 1062 1074 BY SIMILARITY.
 FT DISULFID 1080 1092 BY SIMILARITY.
 FT DISULFID 1086 1101 BY SIMILARITY.
 FT DISULFID 1103 1116 BY SIMILARITY.
 FT DISULFID 1122 1134 BY SIMILARITY.
 FT DISULFID 1128 1143 BY SIMILARITY.
 FT DISULFID 1145 1158 BY SIMILARITY.
 FT DISULFID 1164 1176 BY SIMILARITY.
 FT DISULFID 1171 1185 BY SIMILARITY.
 FT DISULFID 1187 1201 BY SIMILARITY.
 FT DISULFID 1302 1315 BY SIMILARITY.
 FT DISULFID 1310 1324 BY SIMILARITY.
 FT DISULFID 1326 1339 BY SIMILARITY.
 FT DISULFID 1345 1356 BY SIMILARITY.
 FT DISULFID 1351 1365 BY SIMILARITY.
 FT DISULFID 1367 1380 BY SIMILARITY.
 FT DISULFID 1499 1510 BY SIMILARITY.
 FT DISULFID 1505 1519 BY SIMILARITY.
 FT DISULFID 1521 1534 BY SIMILARITY.
 FT DISULFID 1540 1555 BY SIMILARITY.
 FT DISULFID 1550 1564 BY SIMILARITY.
 FT DISULFID 1566 1579 BY SIMILARITY.
 FT MOD_RES 848 848 HYDROXYLATION (BY SIMILARITY).
 FT MOD_RES 1011 1011 HYDROXYLATION (BY SIMILARITY).
 FT CARBOHYD 495 495 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1071 1071 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1121 1124 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1240 1240 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1595 AA; 173229 MW; 6A091EBA8556D8E5 CRC64;

Query Match 63.58; Score 33; DB 1; Length 1595;
 Best Local Similarity 45.5%; Pred. No. 1.1e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSYS 11
 Db 600 KEICPGMGYT 610
 :|: |||:

RESULT 17
 LTBL_RAT STANDARD; PRT; 1712 AA.
 AC Q00918;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DE Latent transforming growth factor beta binding protein 1 precursor
 DE (Transforming growth factor beta-1 binding protein 1) (TGF-beta1-BP-1)
 DE 1) (Transforming growth factor beta-1 masking protein, large subunit).
 GN LTBL.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=91062373; PubMed=2247454;
 RA Tsuji T., Okada F., Yamaguchi K., Nakamura T.;
 RT "Molecular cloning of the large subunit of transforming growth factor type beta masking protein and expression of the mRNA in various rat tissues.";
 RT Proc. Natl. Acad. Sci. U.S.A. 87:8835-8839(1990).
 RL -1- SUBUNIT: THE LARGE LATENT COMPLEX OF TGF-BETA1 FROM PLATELETS IS COMPOSED OF THE TGF-BETA1 MOLECULE NONCOVALENTLY ASSOCIATED WITH A MASKING PROTEIN CONSISTING OF A DISULFIDE-BONDED COMPLEX OF A DIMER OF THE N-TERMINAL PROPEPTIDE OF THE TGF-BETA1 PRECURSOR AND A THIRD COMPONENT DENOTED TGF-BETA1-BP (OR MP LARGE SUBUNIT).
 CC TGF-BETA1-BP DOES NOT BIND DIRECTLY TO ACTIVE TGF-BETA1.

CC -1- SIMILARITY: CONTAINS 18 EGF-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL; M55431; AAA42235.1; --
 DR PIR; A38261; A38261.
 DR HSP; P16109; JFSP.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF-Ca.
 DR InterPro; IPR002212; Fibril-assoc.
 DR Pfam; PF00008; EGF; 16.
 DR Pfam; PF00683; TB; 4.
 DR SMART; SM00179; EGF_Ca; 13.
 DR SMART; SM00001; EGF_Like; 5.
 DR PROSITE; PS00010; ASX_HYDROXYL; 13.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 10.
 DR PROSITE; PS01187; EGF_Ca; 15.
 KW Growth factor binding; Repeat; EGF-like domain; Hydroxylation; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT PROPEP 21 736 POTENTIAL.
 FT CHAIN 737 1577 LATENT TRANSFORMING GROWTH FACTOR BETA BINDING PROTEIN 1.
 FT SITE 734 736 CLEAVAGE (POTENTIAL).
 FT SITE 1575 1577 CLEAVAGE (POTENTIAL).
 FT PROPEP 1578 1712 POTENTIAL.
 FT DOMAIN 181 213 EGF-LIKE 1.
 FT DOMAIN 391 423 EGF-LIKE 2.
 FT REPEAT 551 604 EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 618 658 EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
 FT REPEAT 671 721 INTERNAL REPEAT 2.
 FT DOMAIN 865 906 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 907 948 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 949 989 EGF-LIKE 7, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 990 1029 EGF-LIKE 8, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1030 1070 EGF-LIKE 9, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1071 1111 EGF-LIKE 10, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1112 1152 EGF-LIKE 11, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1153 1193 EGF-LIKE 12, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1194 1235 EGF-LIKE 13, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1236 1277 EGF-LIKE 14, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1278 1320 INTERNAL REPEAT 3.
 FT REPEAT 1340 1392 EGF-LIKE 15, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1415 1457 EGF-LIKE 16, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1458 1498 EGF-LIKE 17.
 FT REPEAT 1517 1568 EGF-LIKE 18, CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 1612 1652 EGF-LIKE 19.
 FT DOMAIN 1653 1697 EGF-LIKE 20, CALCIUM-BINDING (POTENTIAL).
 FT DISULFID 185 195 BY SIMILARITY.
 FT DISULFID 199 201 BY SIMILARITY.
 FT DISULFID 203 212 BY SIMILARITY.
 FT DISULFID 395 405 BY SIMILARITY.
 FT DISULFID 399 411 BY SIMILARITY.
 FT DISULFID 413 422 BY SIMILARITY.
 FT DISULFID 622 633 BY SIMILARITY.
 FT DISULFID 628 642 BY SIMILARITY.
 FT DISULFID 644 657 BY SIMILARITY.
 FT DISULFID 869 881 BY SIMILARITY.
 FT DISULFID 876 890 BY SIMILARITY.
 FT DISULFID 892 905 BY SIMILARITY.
 FT DISULFID 911 923 BY SIMILARITY.
 FT DISULFID 918 932 BY SIMILARITY.
 FT DISULFID 934 947 BY SIMILARITY.
 FT DISULFID 953 964 BY SIMILARITY.
 FT DISULFID 959 973 BY SIMILARITY.
 FT DISULFID 976 988 BY SIMILARITY.

FT DISULFID 994 1005 BY SIMILARITY.
 FT DISULFID 1000 1014 BY SIMILARITY.
 FT DISULFID 1017 1028 BY SIMILARITY.
 FT DISULFID 1034 1045 BY SIMILARITY.
 FT DISULFID 1040 1054 BY SIMILARITY.
 FT DISULFID 1056 1069 BY SIMILARITY.
 FT DISULFID 1075 1086 BY SIMILARITY.
 FT DISULFID 1081 1095 BY SIMILARITY.
 FT DISULFID 1097 1110 BY SIMILARITY.
 FT DISULFID 1116 1127 BY SIMILARITY.
 FT DISULFID 1122 1136 BY SIMILARITY.
 FT DISULFID 1138 1151 BY SIMILARITY.
 FT DISULFID 1157 1169 BY SIMILARITY.
 FT DISULFID 1164 1178 BY SIMILARITY.
 FT DISULFID 1180 1192 BY SIMILARITY.
 FT DISULFID 1198 1210 BY SIMILARITY.
 FT DISULFID 1204 1219 BY SIMILARITY.
 FT DISULFID 1221 1234 BY SIMILARITY.
 FT DISULFID 1240 1252 BY SIMILARITY.
 FT DISULFID 1246 1261 BY SIMILARITY.
 FT DISULFID 1263 1276 BY SIMILARITY.
 FT DISULFID 1282 1294 BY SIMILARITY.
 FT DISULFID 1289 1303 BY SIMILARITY.
 FT DISULFID 1305 1319 BY SIMILARITY.
 FT DISULFID 1419 1432 BY SIMILARITY.
 FT DISULFID 1427 1441 BY SIMILARITY.
 FT DISULFID 1443 1456 BY SIMILARITY.
 FT DISULFID 1462 1473 BY SIMILARITY.
 FT DISULFID 1468 1482 BY SIMILARITY.
 FT DISULFID 1484 1497 BY SIMILARITY.
 FT DISULFID 1616 1627 BY SIMILARITY.
 FT DISULFID 1622 1636 BY SIMILARITY.
 FT DISULFID 1638 1651 BY SIMILARITY.
 FT DISULFID 1657 1672 BY SIMILARITY.
 FT DISULFID 1667 1681 BY SIMILARITY.
 FT DISULFID 1683 1696 BY SIMILARITY.
 FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 370 370 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 416 416 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1042 1042 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1242 1242 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 1357 1357 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1712 AA; 186598 MW; 650BCEAA691FD134 CRC64;

Query Match 63.5%; Score 33; DB 1; Length 1712;
 Best Local Similarity 45.5%; Pred. No. 1.le+02;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSYS 11

Db 718 KEICPGMGYT 728

RESULT 18

CGD2_RAT

ID CGD2_RAT STANDARD; PRT; 288 AA.

AC Q04827;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE GL/S-specific cyclin D2 (Vin-1 proto-oncogene).

GN CCND2 OR VIN-1.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93275661; PubMed=8502486;

RA Hanna Z., Jankowski M., Tremblay P., Jiang X.M., Milatovich A.,

RA Francke U., Jolicœur P.;

RT "The Vin-1 gene, identified by provirus insertional mutagenesis, is

RT the cyclin D2.";
 RL Oncogene 8:1661-1666(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95011623; PubMed=7926809;
 RA Hosokawa Y., Onga T., Nakashima K.;
 RT "Induction of D2 and D3 cyclin-encoding genes during promotion of the
 RT G1/S transition by prolactin in rat Nb2 cells.";
 RL Gene 147:249-252(1994).
 CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
 CC (START) TRANSITION
 CC -1- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM
 CC A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
 CC IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
 CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
 CC -----
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EMBL; L09752; AAA1010.1; .
 EMBL; D16308; BAA03815.1; .
 InterPro; IPR004366; Cyclin.
 InterPro; IPR004367; Cyclin_Cterm.
 Pfam; PF00134; cyclin; 1.
 Pfam; PF02984; cyclin_C; 1.
 SMART; SM00385; CYCLIN; 1.
 PROSITE; PS00292; CYCLINS; 1.

KW Cyclin; Cell cycle; Cell division; Multigene family; Proto-oncogene.
 FT CONFLICT 68 68 E -> G (IN REF. 2).
 FT CONFLICT 104 104 C -> V (IN REF. 2).
 FT CONFLICT 232 232 T -> A (IN REF. 2).
 SQ SEQUENCE 288 AA; 32826 MW; 4B522BF4E9835FC1 CRC64;

Query Match 61.5%; Score 32; DB 1; Length 288;
 Best Local Similarity 60.0%; Pred. No. 29;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10

Db 73 EEVFPAMNY 82

RESULT 19

CGD2_HUMAN

ID CGD2_HUMAN STANDARD; PRT; 289 AA.

AC P30279; Q13955;

DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE GL/S-specific cyclin D2.

GN CCND2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92347851; PubMed=1386336;

RA Xiong Y., Menninger J., Beach D., Ward D.C.;

RT "Molecular cloning and chromosomal mapping of CCND genes encoding

RT human D-type cyclins.";

RL Genomics 13:575-584(1992).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=93205384; PubMed=8455931;

RA Palmero I., Holder A., Sinclair A.J., Dickson C., Peters G.;

RT "Cyclins D1 and D2 are differentially expressed in human B-lymphoid

RT cell lines.";

RL Oncogene 8:1049-1054(1993).
 RP [3]
 RP SEQUENCE FROM N.A.
 RA Miyajima N.;
 RL Submitted (MAR-1993) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone marrow;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 1-240 FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=92347850; PubMed=1386335;
 RA Inaba T., Matsushime H., Valentine M., Roussel M.F., Sherr C.J.,
 RA Look A.T.;
 RT "genomic organization, chromosomal localization, and independent
 expression of human cyclin D genes.";
 RL Genomics 13:565-574(1992).
 CC -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
 (START) TRANSITION.
 CC -!- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM
 A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
 IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
 CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; M90813; AAA51926.1; -;
 DR EMBL; X68452; CAA48493.1; -;
 DR EMBL; D13639; BAA02802.1; -;
 DR EMBL; BC010958; AAH10958.1; -;
 DR EMBL; M88083; AAA51928.1; -;
 DR EMBL; M88080; AAA51928.1; JOINED.
 DR EMBL; M88081; AAA51928.1; JOINED.
 DR EMBL; M88082; AAA51928.1; JOINED.
 DR PIR; A42822; A42822.
 DR PIR; S26580; S26580.
 DR Genew; HGNC:1583; CCND2.
 DR MIM; 123833; -;
 DR InterPro; IPR004366; Cyclin.
 DR InterPro; IPR004367; Cyclin_Cterm.
 DR Pfam; PF00134; cyclin; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLINS; 1.
 DR Cyclin; Cell cycle; Cell division; Multigene family.
 FT CONFLICT 166 167 KL -> NV (IN REF. 5).
 FT CONFLICT 224 224 T -> H (IN REF. 5).
 SQ SEQUENCE 289 AA; 33067 MW; E4E5FEF476D76D90 CRC64;

 Query Match 61.5%; Score 32; DB 1; Length 289;
 Best Local Similarity 60.0%; Pred. No. 29;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

 QY 1 EEVVPXGMSY 10
 ||| | | | |
 Db 74 EEVFPFLANNY 83

 RESULT 20
 CGD2_MOUSE
 ID CGD2_MOUSE STANDARD; PRT; 289 AA.
 AC P30280;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE G1/S-specific cyclin D2.
 GN CCND2 OR CYL-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92196134; PubMed=1372445;
 RA Kiyokawa H., Busquets X., Powell C.T., Ngo L., Rifkind R.A.,
 RA Marks P.A.;
 RT "Cloning of a D-type cyclin from murine erythroleukemia cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2444-2447(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91235305; PubMed=1827757;
 RA Matsushime H., Roussel M.F., Ashmun R.A., Sherr C.J.;
 RT "Colony-stimulating factor 1 regulates novel cyclins during the G1
 phase of the cell cycle.";
 RL Cell 65:701-713(1991).
 CC -!- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
 (START) TRANSITION.
 CC -!- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM
 A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
 IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
 CC -!- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
 CC -----
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 CC -----
 DR EMBL; M83749; AAA37519.1; -;
 DR EMBL; M86182; AAA37503.1; -;
 DR PIR; B40035; B40035.
 DR PIR; A41984; A41984.
 DR MGD; MGI:88314; Ccnd2.
 DR InterPro; IPR004366; Cyclin.
 DR InterPro; IPR004367; Cyclin_Cterm.
 DR Pfam; PF00134; cyclin; 1.
 DR Pfam; PF02984; cyclin_C; 1.
 DR SMART; SM00385; CYCLIN; 1.
 DR PROSITE; PS00292; CYCLINS; 1.
 DR Cyclin; Cell cycle; Cell division; Multigene family.
 KW SEQUENCE 289 AA; 32897 MW; 58F322771DD1DA3D CRC64;

 Query Match 61.5%; Score 32; DB 1; Length 289;
 Best Local Similarity 60.0%; Pred. No. 29;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

 QY 1 EEVVPXGMSY 10
 ||| | | | |
 Db 73 EEVFPFLANNY 82

 RESULT 21
 CGD1_BRARE
 ID CGD1_BRARE STANDARD; PRT; 291 AA.
 AC Q90459;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE G1/S-specific cyclin D1.
 GN CGD1.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=96138542; PubMed=8547308;
RA Yarden A., Salomon D., Geiger B.;
RT "zebrafish cyclin D1 is differentially expressed during early
RL embryogenesis.";
RL Biochim. Biophys. Acta 1264:257-260(1995).
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
CC (START) TRANSITION.
CC -1- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM
CC A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
CC IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; X87581; CAA60885.1; -
CC ZFIN; ZDB-GENE-980526-176; cycl1.
CC InterPro; IPR004366; Cyclin.
CC Pfam; PF00134; cyclin; 1.
CC Pfam; PF02984; cyclin_C; 1.
CC SMART; SM00385; CYCLIN; 1.
CC PROSITE; PS00292; CYCLINS; 1.
CC Cyclin; Cell cycle; Cell division.
CC KW SEQUENCE 291 AA; 33067 MW; FA5274CB1B46D5EF CRC64;
CC
CC Query Match 61.5%; Score 32; DB 1; Length 291;
CC Best Local Similarity 60.0%; Pred. No. 29;
CC Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
CC
CC QY 1 EEVVPXGMSY 10
CC III I I I
CC Db 75 EEVFPPLANNY 84
CC
CC RESULT 22
CC CGDI_XENLA
CC ID PGD1_XENLA STANDARD; PRT; 291 AA.
CC AC P50755;
CC DT 01-OCT-1996 (Rel. 34, Created)
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE G1/S-specific cyclin D1.
CC GN CCND1.
CC OS Xenopus laevis (African clawed frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
CC OC Xenopodinae; Xenopus.
CC OX NCBI_TaxID=8355;
CC [1]
CC SEQUENCE FROM N.A.
CC Cockerill M.J., Hunt T.;
CC Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
CC (START) TRANSITION.
CC -1- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM
CC A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
CC IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
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CC or send an email to license@isb-sib.ch).
CC
CC QY 1 EEVVPXGMSY 10
CC III I I I
CC Db 75 EEVFPPLANNY 84
CC
CC RESULT 22
CC CGDI_XENLA
CC ID PGD1_XENLA STANDARD; PRT; 291 AA.
CC AC P50755;
CC DT 01-OCT-1996 (Rel. 34, Created)
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE G1/S-specific cyclin D1.
CC GN CCND1.
CC OS Xenopus laevis (African clawed frog).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
CC OC Xenopodinae; Xenopus.
CC OX NCBI_TaxID=8355;
CC [1]
CC SEQUENCE FROM N.A.
CC Cockerill M.J., Hunt T.;
CC Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
CC (START) TRANSITION.
CC -1- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM
CC A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
CC IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
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CC or send an email to license@isb-sib.ch).
CC
CC QY 1 EEVVPXGMSY 10
CC III I I I
CC Db 75 EEVFPPLANNY 84
CC
CC RESULT 22
CC CGD2_CHICK
CC ID CGD2_CHICK STANDARD; PRT; 291 AA.
CC AC P49706;
CC DT 01-OCT-1996 (Rel. 34, Created)
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE G1/S-specific cyclin D2.
CC GN CCND2.
CC OS Gallus gallus (Chicken).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC OC Gallus.
CC OX NCBI_TaxID=9031;
CC [1]
CC SEQUENCE FROM N.A.
CC RP MEDLINE=96144302; PubMed=8566807;
CC Li H., Grenet J., Kidd V.J.;
CC "Structure and gene expression of avian cyclin D2.";
CC Gene 167:341-342(1995).
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
CC (START) TRANSITION.
CC -1- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM
CC A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
CC IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U28980; AAA96955.1; -
CC InterPro; IPR004366; Cyclin.
CC InterPro; IPR004367; Cyclin_Cterm.
CC Pfam; PF00134; cyclin; 1.
CC Pfam; PF02984; cyclin_C; 1.
CC SMART; SM00385; CYCLIN; 1.
CC PROSITE; PS00292; CYCLINS; 1.
CC Cyclin; Cell cycle; Cell division; Multigene family.
CC KW SEQUENCE 291 AA; 33163 MW; 43A7E646AEAF3109 CRC64;
CC
CC Query Match 61.5%; Score 32; DB 1; Length 291;
CC Best Local Similarity 60.0%; Pred. No. 29;
CC Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
CC
CC QY 1 EEVVPXGMSY 10
CC III I I I
CC Db 74 EEVFPPLANNY 83

CC EMBL; X89475; CAA61664.1; -
DR InterPro; IPR004366; Cyclin.
DR InterPro; IPR004367; Cyclin_Cterm.
DR Pfam; PF00134; cyclin; 1.
DR Pfam; PF02984; cyclin_C; 1.
DR SMART; SM00385; CYCLIN; 1.
DR PROSITE; PS00292; CYCLINS; 1.
DR Cyclin; Cell cycle; Cell division; Multigene family.
KW SEQUENCE 291 AA; 32953 MW; A4747C5BD1679087 CRC64;
SQ
CC Query Match 61.5%; Score 32; DB 1; Length 291;
CC Best Local Similarity 60.0%; Pred. No. 29;
CC Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
CC
CC QY 1 EEVVPXGMSY 10
CC III I I I
CC Db 73 EEVFPPLANNY 82
CC
CC RESULT 23
CC CGD2_CHICK
CC ID CGD2_CHICK STANDARD; PRT; 291 AA.
CC AC P49706;
CC DT 01-OCT-1996 (Rel. 34, Created)
CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
CC DT 16-OCT-2001 (Rel. 40, Last annotation update)
CC DE G1/S-specific cyclin D2.
CC GN CCND2.
CC OS Gallus gallus (Chicken).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
CC OC Gallus.
CC OX NCBI_TaxID=9031;
CC [1]
CC SEQUENCE FROM N.A.
CC RP MEDLINE=96144302; PubMed=8566807;
CC Li H., Grenet J., Kidd V.J.;
CC "Structure and gene expression of avian cyclin D2.";
CC Gene 167:341-342(1995).
CC -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
CC (START) TRANSITION.
CC -1- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM
CC A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
CC IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U28980; AAA96955.1; -
CC InterPro; IPR004366; Cyclin.
CC InterPro; IPR004367; Cyclin_Cterm.
CC Pfam; PF00134; cyclin; 1.
CC Pfam; PF02984; cyclin_C; 1.
CC SMART; SM00385; CYCLIN; 1.
CC PROSITE; PS00292; CYCLINS; 1.
CC Cyclin; Cell cycle; Cell division; Multigene family.
KW SEQUENCE 291 AA; 33163 MW; 43A7E646AEAF3109 CRC64;
SQ
CC Query Match 61.5%; Score 32; DB 1; Length 291;
CC Best Local Similarity 60.0%; Pred. No. 29;
CC Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
CC
CC QY 1 EEVVPXGMSY 10
CC III I I I
CC Db 74 EEVFPPLANNY 83

```
RESULT 24
CGD2_XENLA          STANDARD;          PRT;    291 AA.
AC  P33782;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  16-OCT-2001 (Rel. 40, Last annotation update)
DE  G1/S-specific cyclin D2.
GN  CCND2.
OS  Xenopus laevis (African clawed frog).
OC  Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC  Xenopodinae; Xenopus.
OX  NCBI_TaxID=8355;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Cockerill M.J., Hunt T.;
RL  Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
[2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=97380591; PubMed=9237366;
RA  Taieb F., Jessus C.; cloning and expression in oocytes and during
RT  early development.;
RL  Biol. Cell 88:99-111(1996).
CC  -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
CC  (START) TRANSITION.
CC  -1- SUBUNIT: INTERACTS WITH THE CDK4 AND CDK6 PROTEIN KINASES TO FORM
CC  A SERINE/THREONINE KINASE HOLOENZYME COMPLEX. THE CYCLIN SUBUNIT
CC  IMPARTS SUBSTRATE SPECIFICITY TO THE COMPLEX.
CC  -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
-----
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-----
DR  EMBL; X89476; CAA61665.1; -
DR  EMBL; X83503; CAA58493.1; -
DR  InterPro; IPR004366; Cyclin.
DR  InterPro; IPR004367; Cyclin_Cterm.
DR  Pfam; PF00134; cyclin; 1.
DR  Pfam; PF02984; cyclin_C; 1.
DR  SMART; SM00385; CYCLIN; 1.
DR  PROSITE; PS00292; CYCLINS; 1.
KW  Cyclin; Cell cycle; Cell division; Multigene family.
SQ  SEQUENCE 291 AA; 32959 MW; 9A290F04F1531E89 CRC64;

Query Match          61.5%; Score 32; DB 1; Length 291;
Best Local Similarity 60.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY  1 EEVVPXGMSY 10
DB  ||||| |
    74 EEVFPAMNYY 83

RESULT 25
CGD1_CHICK          STANDARD;          PRT;    292 AA.
AC  P35169;
DT  01-OCT-1996 (Rel. 34, Created)
DT  01-OCT-1996 (Rel. 34, Last sequence update)
DT  15-JUL-1999 (Rel. 38, Last annotation update)
DE  G1/S-specific cyclin D1.
GN  CCND1.
OS  Gallus gallus (Chicken).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Query Match          61.5%; Score 32; DB 1; Length 291;
Best Local Similarity 60.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY  1 EEVVPXGMSY 10
DB  ||||| |
    74 EEVFPAMNYY 83

Gallus.
OX  NCBI_TaxID=9031;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Li H., Lahti J.M., Kidd V.J.;
RL  Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC  -1- FUNCTION: ESSENTIAL FOR THE CONTROL OF THE CELL CYCLE AT THE G1/S
CC  (START) TRANSITION. INTERACTS WITH THE CDK4 AND CDK6 PROTEIN
CC  KINASES (BY SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO THE CYCLIN FAMILY. CYCLIN D SUBFAMILY.
-----
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CC  or send an email to license@isb-sib.ch).
-----
DR  EMBL; U40844; AAA83271.1; -
DR  InterPro; IPR004366; Cyclin.
DR  InterPro; IPR004367; Cyclin_Cterm.
DR  Pfam; PF00134; cyclin; 1.
DR  Pfam; PF02984; cyclin_C; 1.
DR  SMART; SM00385; CYCLIN; 1.
DR  PROSITE; PS00292; CYCLINS; 1.
KW  Cyclin; Cell cycle; Cell division; Multigene family.
SQ  SEQUENCE 292 AA; 33263 MW; 7B543029DB45A67D CRC64;

Query Match          61.5%; Score 32; DB 1; Length 292;
Best Local Similarity 60.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY  1 EEVVPXGMSY 10
DB  ||||| |
    75 EEVFPAMNYY 84

Search completed: June 10, 2003, 13:40:25
Job time : 4.5 secs
```


GenCore version 5.1.6
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OM protein - protein search., using sw model

Run on: June 10, 2003, 13:30:25 ; Search time 25.7857 Seconds
(without alignments)
87.898 Million cell updates/sec

Title: US-09-909-164-47
Perfect score: 52
Sequence: 1 BEVVPXGMSYS 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :

SPTREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phase:*
10: sp.plant:*
11: sp.prodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.rvirus:*
16: sp.bacteriaph:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	73.1	387	16 Q98FX1	Q98fx1 rhizobium 1
2	38	73.1	1063	16 Q8RG86	Q8rg86 fusobacteri
3	38	73.1	3472	1 Q74056	Q74056 cenarchaeum
4	37	71.2	840	3 Q9URY8	Q9ury8 schizosacch
5	36	69.2	471	11 Q8R126	Q8r126 mus musculu
6	36	69.2	484	11 Q8VD18	Q8vd18 mus musculu
7	35	67.3	225	10 Q40129	Q40129 lycopersico
8	35	67.3	425	5 Q9XVK4	Q9xvk4 caenorhabdi
9	35	67.3	556	4 Q43733	Q43733 homo sapien
10	35	67.3	583	5 Q9BH85	Q9bha5 plasmodium
11	35	67.3	583	5 Q9BH83	Q9bh83 plasmodium
12	35	67.3	670	11 Q01487	Q01487 rattus norv
13	35	67.3	749	16 Q9PDM6	Q9pdm6 xylella fas
14	35	67.3	1902	4 Q14122	Q14122 homo sapien
15	34	65.4	156	3 Q12479	Q12479 saccharomyc
16	34	65.4	219	17 Q971S2	Q971s2 sulfolobus

17	34	65.4	252	17	Q28342	O28342 archaeoglob
18	34	65.4	290	4	Q96MU1	Q96mu1 homo sapien
19	34	65.4	387	16	Q92MD6	Q92md6 rhizobium m
20	34	65.4	541	16	Q98BP5	Q98bp5 rhizobium l
21	34	65.4	544	16	Q9PQD2	Q9pqd2 ureaplasma
22	34	65.4	842	3	Q9URR4	Q9urr4 penicillium
23	34	65.4	1049	16	Q8XT05	Q8xt05 ralstonia s
24	34	65.4	1499	4	Q96914	Q96914 homo sapien
25	33	63.5	143	17	Q8TX62	Q8tx62 methanopyru
26	33	63.5	162	11	Q9CX04	Q9cxq4 mus musculu
27	33	63.5	165	17	Q28330	O28330 archaeoglob
28	33	63.5	193	2	Q8VUA8	Q8vuua8 lactococcc
29	33	63.5	209	16	Q8RE56	Q8re56 fusobacteri
30	33	63.5	284	16	P74187	P74187 synechocyst
31	33	63.5	298	10	Q9M3C0	Q9m3c0 arabidopsis
32	33	63.5	326	12	Q9Q9Q9	Q9q9q9 soil-borne
33	33	63.5	326	12	Q9Q9Q5	Q9q9q5 soil-borne
34	33	63.5	326	12	Q9QCE7	Q9qce7 soil-borne
35	33	63.5	326	12	Q9DJG4	Q9djg4 soil-borne
36	33	63.5	326	12	Q91DN1	Q91dn1 soil-borne
37	33	63.5	326	12	Q9Q9Q7	Q9q9q7 soil-borne
38	33	63.5	327	12	Q9G360	Q9g360 soil-borne
39	33	63.5	332	10	Q9FNL4	Q9fnl4 arabidopsis
40	33	63.5	368	16	Q9X003	Q9x0u3 thermotoga
41	33	63.5	393	5	Q9V914	Q9v914 drosophila
42	33	63.5	479	4	Q96CS0	Q96cs0 homo sapien
43	33	63.5	548	11	Q9D2X9	Q9d2x9 mus musculu
44	33	63.5	584	16	Q8R8K6	Q8r8k6 thermoanaer
45	33	63.5	648	4	Q96MB2	Q96mb2 homo sapien
46	33	63.5	653	16	Q9KVE3	Q9kve3 vibrio chol
47	33	63.5	676	5	Q9VA55	Q9va55 drosophila
48	33	63.5	676	5	Q8T8Z7	Q8t8z7 drosophila
49	33	63.5	678	12	Q9ELX6	Q9elx6 cercopithe
50	33	63.5	746	3	Q9URR3	Q9urr3 penicillium
51	33	63.5	791	4	Q9H2K5	Q9h2k5 homo sapien
52	33	63.5	793	4	Q9H2K6	Q9h2k6 homo sapien
53	33	63.5	844	11	Q922D4	Q922d4 mus musculu
54	33	63.5	1028	16	Q8YJ11	Q8yj11 brucella me
55	33	63.5	1152	16	Q9CC95	Q9cc95 mycobacteri
56	33	63.5	1305	5	Q9V7C7	Q9v7c7 drosophila
57	33	63.5	1394	4	Q8TD95	Q8td95 homo sapien
58	33	63.5	1442	17	Q96YH5	Q96yh5 sulfolobus
59	33	63.5	1548	10	Q65531	O65531 arabidopsis
60	33	63.5	1713	11	Q88349	Q88349 mus musculu
61	32	61.5	84	16	Q97DE7	Q97de7 clostridium
62	32	61.5	103	11	Q9D0H9	Q9d0h9 mus musculu
63	32	61.5	108	1	Q9UX33	Q9ux33 sulfolobus
64	32	61.5	153	13	P79919	P79919 xenopus lae
65	32	61.5	156	11	Q9D8L9	Q9d8l9 mus musculu
66	32	61.5	174	10	Q9M3T4	Q9m3t4 betula verr
67	32	61.5	190	13	Q57481	Q57481 stizostedio
68	32	61.5	191	11	Q9NBA4	Q9nba4 rattus norv
69	32	61.5	200	17	Q97CD0	Q97cd0 thermoplasm
70	32	61.5	207	2	Q47284	Q47284 escherichia
71	32	61.5	234	2	O32330	O32330 clostridium
72	32	61.5	236	10	Q9SXF1	Q9sxf1 arabidopsis
73	32	61.5	240	11	Q9DB09	Q9db09 mus musculu
74	32	61.5	243	12	Q9LEW1	Q9lew1 cydia pomon
75	32	61.5	279	17	Q9F8Z4	Q9f8z4 aeropyrum p

ALIGNMENTS

RESULT 1
Q98FX1 PRELIMINARY; PRT; 387 AA.
ID Q98FX1
AC Q98FX1;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Hippurate hydrolase.
GN MLR3583.

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OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
CC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003002; BAB50445.1; -
DR InterPro: IPR002933; Peptidase_M20.
DR Pfam; PF01546; Peptidase_M20; 1.
DR Hydrolase; Complete proteome.
KW Hydrolase; Complete proteome.
SQ SEQUENCE 387 AA; 41180 MW; 131BFF8E64306829 CRC64;

Query Match 73.1%; Score 38; DB 16; Length 387;
Best Local Similarity 60.0%; Pred. No. 9.8;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EVVPXGMSY 10
Db 367 DEAIHPGMSY 376

RESULT 2
ID Q8RG86 PRELIMINARY; PRT; 1063 AA.
AC Q8RG86;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Carbamoyl-phosphate synthase large chain (EC 6.3.5.5).
GN FN0422.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25586;
RX MEDLINE=21886394; PubMed=11889109;
RA Kapatal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fonstein M., Kyripides N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
RT nucleatum strain ATCC 25586."
RL J. Bacteriol. 184:2005-2018(2002).
DR EMBL; AE010534; AAL94625.1; -
DR Ligase; Complete proteome.
KW Ligase; Complete proteome.
SQ SEQUENCE 1063 AA; 118008 MW; 39700E10B7CCE411 CRC64;

Query Match 73.1%; Score 38; DB 16; Length 1063;
Best Local Similarity 60.0%; Pred. No. 23;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EVVPXGMSY 11
Db 195 EIVPGLNYS 204

RESULT 3
ID Q74056 PRELIMINARY; PRT; 3472 AA.
AC Q74056;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)

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DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 367.1 kDa protein.
OS Cenarchaeum symbiosum.
OC Archaea; Crenarchaeota; Cenarchaeum.
OX NCBI_TaxID=46770;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B;
RX MEDLINE=98422450; PubMed=9748430;
RA Schleper C., Delong E.F., Preston C.M., Feldman R.A., Wu K.Y.,
RA Swanson R.V.;
RT "Genomic analysis reveals chromosomal variation in natural populations
RT of the uncultured psychrophilic archaeon 'Cenarchaeum symbiosum.'";
RL J. Bacteriol. 180:5003-5009(1998).
CC 1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AF083072; AAC62699.1; -
DR InterPro: IPR000515; BPD_transp.
DR InterPro: IPR001680; WD40.
DR Pfam; PF00400; WD40; 4.
DR SMART; SM00320; WD40; 2.
DR PROSITE; PS00402; BPD_TRANS_INN_MEMBER; UNKNOWN_1.
KW Hypothetical protein; Repeat; WD repeat.
SQ SEQUENCE 3472 AA; 367058 MW; 37F80707030F9355 CRC64;

Query Match 73.1%; Score 38; DB 1; Length 3472;
Best Local Similarity 54.5%; Pred. No. 1e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EVVPXGMSY 11
Db 2294 EDVPRGISFS 2304

RESULT 4
ID Q9URY8 PRELIMINARY; PRT; 840 AA.
AC Q9URY8;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Probable sulfate permease.
GN SPAC869.05C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972H-;
RA Hunt C., Aves S., McDougall R.C., Rajandream M.A., Barrell B.G.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; ALI32779; CAB60015.1; -
DR InterPro: IPR002645; STAS.
DR InterPro: IPR001902; Sulfate_transp.
DR Pfam; PF01740; STAS; 1.
DR Pfam; PF00916; Sulfate_transp; 1.
DR TIGRFAMs; TIGR00815; sulP; 1.
SQ SEQUENCE 840 AA; 93517 MW; ED4833E162B69077 CRC64;

Query Match 71.2%; Score 37; DB 3; Length 840;
Best Local Similarity 77.8%; Pred. No. 37;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 VVPXGMSY 11
Db 135 VVPOGMSYA 143

RESULT 5
ID Q8R126 PRELIMINARY; PRT; 471 AA.

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RP  SEQUENCE FROM N.A.
RC  STRAIN-VF36; TISSUE=PISTIL;
RX  MEDLINE=93375233; PubMed=7647301;
RA  Milligan S.B., Gasser C.S.;
RT  "Nature and regulation of pistil-expressed genes in tomato.";
RL  Plant Mol. Biol. 28:691-711(1995).
DR  EMBL; U20592; AAA80497.1; -.
DR  InterPro; IPR002160; Kunitz_legume.
DR  Pfam; PF00197; Kunitz_legume; 1.
DR  ProDom; PD000891; Kunitz_legume; 1.
DR  SMART; SM00452; STI; 1.
DR  PROSITE; PS00283; SOYBEAN_KUNITZ; UNKNOWN_1.
KW  Hypothetical protein; Signal.
FT  SIGNAL 1 20 POTENTIAL.
FT  CHAIN 21 225 UNKNOWN.
SQ  SEQUENCE 225 AA; 25188 MW; 1074C261D20CFDAD CRC64;

Query Match 67.3%; Score 35; DB 10; Length 225;
Best Local Similarity 54.5%; Pred. No. 24;
Matches 6; Conservative 3; Mismatches 2; Indels 0

Qy 1 EEVVPXGMSYS 11
Db 32 DEVVPGKTYA 42
:|||||:|:|

RESULT 8
Q9XVK4 PRELIMINARY; PRT; 425 AA.
ID Q9XVK4
AC Q9XVK4;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE R10D12.10 protein.
GN R10D12.10.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabdi
OC Rhabditidae; Peloderinae; Caenorhabditis.
OC NCBI_TaxID=6239;
[1]
RP SEQUENCE FROM N.A.
RA Percy C.M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
[2]
RX SEQUENCE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).
DR EMBL; Z81109; CAB03241.1; -.
DR InterPro; IPR000719; Euk.pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW ATP-binding; Transferase.
SQ SEQUENCE 425 AA; 49410 MW; 5D96E29B08C8E9D6 CRC64;

Query Match 67.3%; Score 35; DB 5; Length 425;
Best Local Similarity 50.0%; Pred. No. 48;
Matches 5; Conservative 3; Mismatches 2; Indels 0

Qy 1 EEVVPXGMSY 10
Db 335 EQIVPGGLQY 344
|:|:|:|:|

RESULT 9
O43733 PRELIMINARY; PRT; 556 AA.
ID O43733
AC O43733;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)

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DT 01-JUN-1998 (Tremblrel. 06, Last annotation update)
 DE DNA binding protein (Fragment).
 GN DJ451B15.2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Tubby B.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z98050; CAB10847.1; -;
 FT NON_TER 1
 SQ SEQUENCE 556 AA; 59059 MW; ECB00E4033FB2528 CRC64;

Query Match 67.3%; Score 35; DB 4; Length 556;
 Best Local Similarity 66.7%; Pred. No. 64;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 VVPXGMSYS 11
 ||| |::||
 DB 244 VVPAGLTYS 252

RESULT 10
 Q9BHA5 PRELIMINARY; PRT; 583 AA.
 AC Q9BHA5;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Choline transporter.
 GN SC1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ben Mamoun C., Gluzman I.Y., Goldberg D.E.;
 RT "Plasmodium falciparum choline transporter (PfSC1) gene.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY007372; AAK14816.1; -;
 DR EMBL; AY007375; AAG17947.1; -;
 DR InterPro; IPR002123; Acyltransferase.
 DR Pfam; PF01553; Acyltransferase; 1
 SQ SEQUENCE 583 AA; 66917 MW; 2B2BFAE3E395E049 CRC64;

Query Match 67.3%; Score 35; DB 5; Length 583;
 Best Local Similarity 55.6%; Pred. No. 67;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 VVPXGMSYS 11
 ::| |::||
 DB 227 IIPVGLSYS 235

RESULT 11
 Q9BH83 PRELIMINARY; PRT; 583 AA.
 AC Q9BH83;
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
 DE Choline transporter.
 GN SC1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ben Mamoun C., Gluzman I.Y., Goldberg D.E.;
 RT "Plasmodium falciparum choline transporter (PfSC1) gene.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY007374; AAK14818.1; -;
 DR EMBL; AY007373; AAK14817.1; -;
 DR InterPro; IPR002123; Acyltransferase.
 DR Pfam; PF01553; Acyltransferase; 1.
 SQ SEQUENCE 583 AA; 66918 MW; 4DF83D7530527474 CRC64;

Query Match 67.3%; Score 35; DB 5; Length 583;
 Best Local Similarity 55.6%; Pred. No. 67;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 3 VVPXGMSYS 11
 ::| |::||
 DB 227 IIPVGLSYS 235

RESULT 12
 Q01487 PRELIMINARY; PRT; 670 AA.
 ID Q01487;
 AC Q01487;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE DNA-binding protein AT-BP2 (ALPHA1-antitrypsin promoter binding protein 2) (Fragment).
 DE Rattus norvegicus (Rat).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE=THYROID;
 RX MEDLINE-91187610; PubMed-1901405;
 RA Mitchelmore C., Traboni C., Cortese R.;
 RT "Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-antitrypsin promoter and to the major histocompatibility complex class I enhancer.";
 RT Nucleic Acids Res. 19:141-147(1991).
 CC -!- FUNCTION: BINDS TO THE ALPHA1-ANTITRYPSIN PROMOTER, TO THE KAPPA IMMUNOGLOBULIN GENE ENHANCER, AND TO THE MAJOR HISTOCOMPATIBILITY COMPLEX CLASS I ENHANCER; IT PLAYS A ROLE AS TRANSCRIPTIONAL REGULATOR. CONCERNING THE ALPHA1-ANTITRYPSIN EXPRESSION IT MAY ACT AS A NEGATIVE REGULATOR BY INTERFERING AT THE ALPHA1-ANTITRYPSIN PROMOTOR WITH ANOTHER NUCLEAR PROTEIN, CALLED LF-B.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- MISCELLANEOUS: ACIDIC AMINO ACID REGION MAY BE INVOLVED IN TRANSCRIPTIONAL ACTIVATION.
 CC -!- SIMILARITY: HIGHLY SIMILAR TO AT-BP1 AND TO THE PRDII-BF1 FACTOR.
 DR EMBL; X54250; CAA38151.1; -;
 DR HSP; P15822; 1BBO.
 DR InterPro; IPR000822; Znf_C2H2.
 DR Pfam; PF00096; Zf-C2H2; 2.
 DR SMART; SM00355; Znf_C2H2; 2.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
 DR PROSITE; PS50157; ZINC_FINGER_C2H2_2; 2.
 KW Zinc-finger; Nuclear protein; DNA-binding; Transcription regulation;
 KW Metal-binding; Multigene family.
 FT NON_TER 1
 FT DOMAIN 54 104 ZINC-FINGERS.
 FT DOMAIN 140 160 ACIDIC.
 FT ZN_FING 54 74 C(2)H(2) CLASS.
 FT ZN_FING 82 104 C(2)H(2) CLASS.
 SQ SEQUENCE 670 AA; 71233 MW; CDD2324152590C17 CRC64;

Query Match 67.3%; Score 35; DB 11; Length 670;
 Best Local Similarity 66.7%; Pred. No. 78;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 VVPXGMSYS 11
 ||| |::||
 DB 376 VVPAGLTYS 384

RESULT 13

Q9PDM6
ID Q9PDM6 PRELIMINARY; PRT; 749 AA.
AC Q9PDM6
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Topoisomerase IV subunit.
GN XF1353.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvares R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Canargo A.A., Canargo L.E.A., Carraro D.M., Carver H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facchini A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohenfeld J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.B., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.V., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshakho M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa";
RL Nature 406:151-159(2000).
DR EMBL: AF003967; AAF84162.1;
DR HSSP: P09097; 1AB4.
DR InterPro: IPR002205; DNA_topoisomIV.
DR Pfam: PF00521; DNA_topoisomIV; 1.
DR ProDom: PD000742; DNA_topoisomIV; 1.
DR SMART: SM00434; TOP4c; 1.
DR TIGRFAMs: TIGR01062; parC_Gneg; 1.
KW Complete proteome.
SQ SEQUENCE 749 AA; 83344 MW; 4DCD10F480EE0257 CRC64;
Query Match 67.3%; Score 35; DB 16; Length 749;
Best Local Similarity 77.8%; Pred. No. 88;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPGMSY 10
Db 526 EVDPSGMSY 534
II I I I I I I

RESULT 14
Q14122
ID Q14122 PRELIMINARY; PRT; 1902 AA.
AC Q14122;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-2002 (TREMBLrel. 20, Last annotation update)
DE DNA-binding protein (Mbp-1) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90205917; PubMed=2108316;
RA Baldwin A.S., Leclair K.P., Singh H., Sharp P.A.;
RT "A large protein containing zinc finger domains binds to related
RT sequence elements in the enhancers of the class I major
RT histocompatibility complex and kappa immunoglobulin genes.";
RL Mol. Cell. Biol. 10:1406-1414(1990).
DR EMBL: M32019; AAA17534.1;
DR HSSP: P15822; 1BBO.
DR InterPro: IPR000822; znf_C2H2.
DR Pfam: PF00096; zf-C2H2; 3.
DR SMART: SM00355; znf_C2H2; 2.
DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 2.
DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 2.
KW DNA-binding; Metal-binding; Zinc-finger.
FT NON_TER 1
SQ SEQUENCE 1902 AA; 207457 MW; 35BBF0D961E6ED20 CRC64;
Query Match 67.3%; Score 35; DB 4; Length 1902;
Best Local Similarity 66.7%; Pred. No. 2.4e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 VVPXGMSYS 11
Db 1590 VVPAGLTYS 1598
III I I I I I

RESULT 15
Q12479
ID Q12479 PRELIMINARY; PRT; 156 AA.
AC Q12479;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE ORF YOR013W.
GN YOR013W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA De haan M., Grivell L.A., Maarse A.C.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MIPS;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RA De haan M., Maarse A.C., Grivell L.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RA Dumont M.E., Schlichter J.B., Cardillo T.S., Hayes M.K., Bethlenny G.,
RX MEDLINE=94019318; PubMed=8413243;
RA Sherman F.;
RT "CYC2 encodes a factor involved in mitochondrial import of yeast
RT cytochrome c.";
RL Mol. Cell. Biol. 13:6442-6451(1993).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=FY1679;
RX MEDLINE=94169519; PubMed=7764548;
RA Lee Y.S., Shimizu J., Yoda K., Yamasaki M.;
RT "Molecular cloning of a gene, DHS1, which complements a drug-
RT hypersensitive mutation of the yeast Saccharomyces cerevisiae.";
RT Biosci. Biotechnol. Biochem. 58:391-395(1994).

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DR EMBL; Z74920; CAA99201.1; -
DR EMBL; X87331; CAA60762.1; -
DR SGD; S0005539; YOR013W;
SQ SEQUENCE 156 AA; 17881 MW; 380442B74C272B41 CRC64;

Query Match
Best Local Similarity 65.4%; Score 34; DB 3; Length 156;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EVVPXGMSY 10
||:| | |
DB 50 EYVPLGMDY 58

RESULT 16
Q371S2
ID Q971S2 PRELIMINARY; PRT; 219 AA.
AC Q971S2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE putative ribose 5-phosphate isomerase.
GN ST1302.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC Sulfolobus.
OX NCBI_TaxID=111955;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-JCM 10545 / 7;
RX PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
RA Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka K., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermoacidophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
DR EMBL; AP000985; BAB6348.1; -
DR InterPro; IPR004788; RPIA; 1.
DR ProDom; PD005813; RPIA; 1.
KW Isomerase; Hypothetical protein; Complete proteome.
SQ SEQUENCE 219 AA; 24541 MW; A4E9A3F2C4006D90 CRC64;

Query Match
Best Local Similarity 65.4%; Score 34; DB 17; Length 219;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EVVPXGMSY 10
||| | |
DB 131 EVVPGVAY 139

RESULT 17
O28342
ID O28342 PRELIMINARY; PRT; 252 AA.
AC O28342;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cell division inhibitor (MIND-2).
GN AFI937.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_TaxID=2234;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=96049343; PubMed=9389475;
RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,

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RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyriakides N.C.,
RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artlich P., Kaine B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
DR EMBL; AE000970; AAB89318.1; -
DR TIGR; AFI937; -
DR InterPro; IPR000707; ATPase_Para.
DR Pfam; PF00991; Para; 1.
KW Hypothetical protein; Cell division; Complete proteome.
SQ SEQUENCE 252 AA; 27130 MW; A401DC1F93E8C538 CRC64;

Query Match
Best Local Similarity 65.4%; Score 34; DB 17; Length 252;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EVVPXGMS 9
||:| | |
DB 81 EVIPAGMS 88

RESULT 18
Q96MU1
ID Q96MU1 PRELIMINARY; PRT; 290 AA.
AC Q96MU1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE CDNA FL31891 fis, clone NT2RP7003304, weakly similar to YceA protein
DE homolog ybfQ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanehori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK056453; BAB71188.1; -
DR InterPro; IPR001763; Rhodanese-like.
DR Pfam; PF00581; Rhodanese; 1.
SQ SEQUENCE 290 AA; 32972 MW; 41FB7FB0217C1421 CRC64;

Query Match
Best Local Similarity 65.4%; Score 34; DB 4; Length 290;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EEVVPXGMS 9
||:| | |
DB 35 EEIVPMGIS 43

RESULT 19
Q92MD6
ID Q92MD6 PRELIMINARY; PRT; 387 AA.
AC Q92MD6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

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01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 Putative HIPPURATE hydrolase protein (EC 3.5.1.32).
 GN H1P01 OR R02690 OR SMC00682.
 OS Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OX NCBI_TaxID=382;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=1021;
 RX MEDLINE=21396507; PubMed=11481430;
 RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
 RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
 RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
 RA Pohl T., Portetelle D., Puehler A., Purnelle B., Rampsperger F.,
 RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
 RT "Analysis of the chromosome sequence of the legume symbiont
 RT Sinorhizobium meliloti strain 1021.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 DR EMBL; AL591791; CAC47269.1; -.
 DR InterPro; IPR002933; Peptidase_M20.
 DR Pfam; PF01546; Peptidase_M20; 1.
 KW Hydrolase; Complete proteome.
 SQ SEQUENCE 387 AA; 41074 MW; 342763088907A6E3 CRC64;
 Query Match 65.4%; Score 34; DB 16; Length 387;
 Best Local Similarity 50.0%; Pred. No. 70;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGMSY 10
 : : : : :
 Db 367 DEAIHPGISY 376
 RESULT 20
 Q98BP5 PRELIMINARY; PRT; 541 AA.
 AC Q98BP5;
 DT 01-OCT-2001 (TREMBlrel. 18, Created)
 DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Probable DNA ligase.
 GN MLL5481.
 OS Rhizobium loti (Mesorhizobium loti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Phyllobacteriaceae; Mesorhizobium.
 OX NCBI_TaxID=381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF303099;
 RX MEDLINE=21082930; PubMed=11214968;
 RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
 RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
 RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
 RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
 RA Takeuchi C., Yamada M., Tabata S.;
 RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
 RT Mesorhizobium loti.";
 RL DNA Res. 7:331-336(2000).
 DR EMBL; AP003006; BAB51927.1; -.
 DR InterPro; IPR000977; DNA_ligase.
 DR Pfam; PF01068; DNA_ligase; 1.
 DR PROSITE; PS00697; DNA_LIGASE_A1; UNKNOWN_1.
 DR PROSITE; PS0160; DNA_LIGASE_A3; 1.
 KW Ligase; Complete proteome.
 SQ SEQUENCE 541 AA; 60645 MW; 2EEFF705453F28F8 CRC64;
 Query Match 65.4%; Score 34; DB 16; Length 541;
 Best Local Similarity 60.0%; Pred. No. 1e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGMSY 10

Db 445 EELVPVGKAY 454
 RESULT 21
 Q9PQD2 PRELIMINARY; PRT; 544 AA.
 AC Q9PQD2;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Putative ABC substrate-binding protein-iron.
 GN ABCSEP-5 OR UN359.
 OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Ureaplasma.
 OX NCBI_TaxID=134821;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SEROVAR 3;
 RX MEDLINE=20500219; PubMed=11048724;
 RA Glass J.I., Lefkowitz E.J., Glass J.S., Helner C.R., Chen E.Y.,
 RA Casseil G.H.;
 RT "The complete sequence of the mucosal pathogen Ureaplasma
 RT urealyticum.";
 RL Nature 407:757-762(2000).
 DR EMBL; AE002133; AAF30768.1; -.
 KW Complete proteome.
 SQ SEQUENCE 544 AA; 61291 MW; CF8756202A389C00 CRC64;
 Query Match 65.4%; Score 34; DB 16; Length 544;
 Best Local Similarity 70.0%; Pred. No. 1e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EEVVPXGMSY 10
 : : : : :
 Db 135 EEVVPHYLSY 144
 RESULT 22
 Q9URR4 PRELIMINARY; PRT; 842 AA.
 AC Q9URR4;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Sulfate permease SUTB.
 GN SUTB.
 OS Penicillium chrysogenum.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
 OX NCBI_TaxID=5076;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Q176;
 RX MEDLINE=20042342; PubMed=10572125;
 RA Van de Kamp M., Pizzini E., Vos A., Van der Lende T.R.,
 RA Schuur T.A., Newbert R.W., Turner G., Konings W.N., Driessen A.J.M.;
 RT "Sulfate Transport in Penicillium chrysogenum: Cloning and
 RT Characterization of the SUTB and SUTB Genes.";
 RL J. Bacteriol. 181:7228-7234(1999).
 DR EMBL; AF163974; AAF14539.1; -.
 DR InterPro; IPR002645; STAS.
 DR InterPro; IPR001902; Sulfate_transp.
 DR Pfam; PF01740; STAS; 1.
 DR Pfam; PF00916; Sulfate_transp; 1.
 DR TIGRFAMs; TIGR00815; sulp; 1.
 DR PROSITE; PS01130; SULFATE_TRANS; UNKNOWN_1.
 SQ SEQUENCE 842 AA; 91865 MW; 839A55486E73D15 CRC64;
 Query Match 65.4%; Score 34; DB 3; Length 842;
 Best Local Similarity 66.7%; Pred. No. 1.6e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      3 VVPXGMSYS 11
Db      111 VVPOGMAYA 119

RESULT 23
Q8XT05
ID      Q8XT05      PRELIMINARY;      PRT; 1049 AA.
AC      Q8XT05;
DT      01-MAR-2002 (TREMBlrel. 20, Created)
DT      01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE      Probable multidrug efflux system transmembrane protein.
GN      MEXD OR RSP0312 OR RS05457.
OS      Ralstonia solanacearum (Pseudomonas solanacearum).
OC      Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
OC      Ralstonia.
OX      NCBI_TaxID=305;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21681879; PubMed=11823852;
RA      Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA      Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA      Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA      Gaspin C., Lavie M., Molisan A., Robert C., Saurin W., Schliex T.,
RA      Siquier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA      Welssenbach J., Boucher C.A.;
RA      "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL      Nature 415:497-502(2002).
DR      EMBL; AL646078; CAD17463.1; -.
DR      InterPro; IPR001036; Acrlflvin_res.
DR      InterPro; IPR004764; HAEI.
DR      InterPro; IPR000731; HMGCR/patch_5TM.
DR      Pfam; PF00873; ACR_tran; 1
DR      PRINTS; PR00702; ACRIFLAVINRP.
DR      TIGRFAMs; TIGR00915; 2A0602; 1.
DR      PROSITE; PS0156; SSD; 1.
KW      Plasmid; Complete proteome.
SQ      SEQUENCE 1049 AA; 111769 MW; CB59674B670089CE CRC64;

Query Match      65.4%; Score 34; DB 16; Length 1049;
Best Local Similarity 75.0%; Pred. NO. 2.le+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 VVPXGMSYS 11
Db      317 MPAGMSYS 324

RESULT 24
Q96914
ID      Q96914      PRELIMINARY;      PRT; 1499 AA.
AC      Q96914;
DT      01-DEC-2001 (TREMBlrel. 19, Created)
DT      01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE      Putative aminophospholipid translocase (Aminophospholipid-transporting
DE      ATPase).
GN      ATP10C.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21225279; PubMed=11326269;
RA      Meguro M., Kashiwagi A., Mitsuya K., Nakao M., Kondo I., Saitoh S.,
RA      Oshimura M.;
RT      "A novel maternally expressed gene, ATP10C, encodes a putative
RT      aminophospholipid translocase associated with Angelman syndrome.";
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RL      Nat. Genet. 28:19-20(2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21313119; PubMed=11353404;
RA      Herzing L.B.K., Kim S.J., Cook E.H. Jr., Ledbetter D.H.;
RT      "The human aminophospholipid-transporting ATPase gene ATP10C maps
RT      adjacent to UBE3A and exhibits similar imprinted expression.";
RL      Am. J. Hum. Genet. 68:1501-1505(2001).
DR      EMBL; AB051358; BAB47392.1; -.
DR      EMBL; AY029504; AAK33100.1; -.
DR      EMBL; AY029487; AAK33100.1; JOINED.
DR      EMBL; AY029488; AAK33100.1; JOINED.
DR      EMBL; AY029489; AAK33100.1; JOINED.
DR      EMBL; AY029490; AAK33100.1; JOINED.
DR      EMBL; AY029491; AAK33100.1; JOINED.
DR      EMBL; AY029492; AAK33100.1; JOINED.
DR      EMBL; AY029493; AAK33100.1; JOINED.
DR      EMBL; AY029494; AAK33100.1; JOINED.
DR      EMBL; AY029495; AAK33100.1; JOINED.
DR      EMBL; AY029496; AAK33100.1; JOINED.
DR      EMBL; AY029497; AAK33100.1; JOINED.
DR      EMBL; AY029498; AAK33100.1; JOINED.
DR      EMBL; AY029499; AAK33100.1; JOINED.
DR      EMBL; AY029500; AAK33100.1; JOINED.
DR      EMBL; AY029501; AAK33100.1; JOINED.
DR      EMBL; AY029502; AAK33100.1; JOINED.
DR      InterPro; IPR001757; ATPase_E1-E2.
DR      InterPro; IPR001064; Crystallin.
DR      InterPro; IPR001454; Hlgnaase/hydrilase.
DR      Pfam; PF00702; Hydrilase; 1.
DR      PROSITE; PS00154; ATPASE_E1_E2; UNKNOWN_1.
DR      PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
SQ      SEQUENCE 1499 AA; 167687 MW; D4996A4D0635A68D CRC64;

Query Match      65.4%; Score 34; DB 4; Length 1499;
Best Local Similarity 72.7%; Pred. NO. 3e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 EEVVPXGMSYS 11
Db      469 EEVPRGGSVS 479

RESULT 25
Q8TX62
ID      Q8TX62      PRELIMINARY;      PRT; 143 AA.
AC      Q8TX62;
DT      01-JUN-2002 (TREMBlrel. 21, Created)
DT      01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      Uncharacterized conserved protein.
GN      MK0814.
OS      Methanopyrus kandleri.
OC      Archaea; Euryarchaeota; Methanopyri; Methanopyraces; Methanopyraceae;
OC      Methanopyrus.
OX      NCBI_TaxID=2320;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      STRAIN=AV19 / DSM 6324 / JCM 9639;
RX      MEDLINE=21927647; PubMed=11930014;
RA      Slesarev A.I., Mezhevaya K.V., Makarova K.S., Polushin N.N.,
RA      Shcherbinina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA      Natale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA      Malykh A.G., Koonin E.V., Kozyavkin S.A.;
RT      "The complete genome of hyperthermophile Methanopyrus kandleri AV19
RT      and monophyly of archaeal methanogens.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR      EMBL; AE010372; AAK02027.1; -.
KW      Complete proteome.
SQ      SEQUENCE 143 AA; 15734 MW; 4C8B28A1FBEDD0B CRC64;

Query Match      63.5%; Score 33; DB 17; Length 143;
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Best Local Similarity 60.0%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EEVVPXGMSY 10
 ||:| | |
Db 75 EELVPQAGY 84

Search completed: June 10, 2003, 13:46:39
Job time : 25.7857 secs

